

SEQUENCE LISTING

<110> MEMORIAL SLOAN-KETTERING CANCER CENTER

<120> ENHANCED CHIMERIC ANTIGEN RECEPTORS AND USES THEREOF

<130> 072734.0816

<140> PCT/US2018/068134

<141> 2018-12-31

<150> 62/612,031

<151> 2017-12-29

<160> 119

<170> PatentIn version 3.5

<210> 1

<211> 345

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Gln His His Leu Trp Ile Leu Leu Leu Cys Leu Gln Thr Trp
1 5 10 15

Pro Glu Ala Ala Gly Lys Asp Ser Glu Ile Phe Thr Val Asn Gly Ile
20 25 30

Leu Gly Glu Ser Val Thr Phe Pro Val Asn Ile Gln Glu Pro Arg Gln
35 40 45

Val Lys Ile Ile Ala Trp Thr Ser Lys Thr Ser Val Ala Tyr Val Thr
50 55 60

Pro Gly Asp Ser Glu Thr Ala Pro Val Val Thr Val Thr His Arg Asn
65 70 75 80

Tyr Tyr Glu Arg Ile His Ala Leu Gly Pro Asn Tyr Asn Leu Val Ile
85 90 95

Ser Asp Leu Arg Met Glu Asp Ala Gly Asp Tyr Lys Ala Asp Ile Asn

100	105	110
Thr Gln Ala Asp Pro Tyr Thr Thr Thr Lys Arg Tyr Asn Leu Gln Ile		
115	120	125
Tyr Arg Arg Leu Gly Lys Pro Lys Ile Thr Gln Ser Leu Met Ala Ser		
130	135	140
Val Asn Ser Thr Cys Asn Val Thr Leu Thr Cys Ser Val Glu Lys Glu		
145	150	155
Glu Lys Asn Val Thr Tyr Asn Trp Ser Pro Leu Gly Glu Glu Gly Asn		
165	170	175
Val Leu Gln Ile Phe Gln Thr Pro Glu Asp Gln Glu Leu Thr Tyr Thr		
180	185	190
Cys Thr Ala Gln Asn Pro Val Ser Asn Asn Ser Asp Ser Ile Ser Ala		
195	200	205
Arg Gln Leu Cys Ala Asp Ile Ala Met Gly Phe Arg Thr His His Thr		
210	215	220
Gly Leu Leu Ser Val Leu Ala Met Phe Phe Leu Leu Val Leu Ile Leu		
225	230	235
Ser Ser Val Phe Leu Phe Arg Leu Phe Lys Arg Arg Gln Gly Arg Ile		
245	250	255
Phe Pro Glu Gly Ser Cys Leu Asn Thr Phe Thr Lys Asn Pro Tyr Ala		
260	265	270
Ala Ser Lys Lys Thr Ile Tyr Thr Tyr Ile Met Ala Ser Arg Asn Thr		
275	280	285
Gln Pro Ala Glu Ser Arg Ile Tyr Asp Glu Ile Leu Gln Ser Lys Val		
290	295	300

Leu Pro Ser Lys Glu Glu Pro Val Asn Thr Val Tyr Ser Glu Val Gln
 305 310 315 320

Phe Ala Asp Lys Met Gly Lys Ala Ser Thr Gln Asp Ser Lys Pro Pro
 325 330 335

Gly Thr Ser Ser Tyr Glu Ile Val Ile
 340 345

<210> 2
 <211> 75
 <212> DNA
 <213> Homo sapiens

<400> 2
 ttgctgagcg tgctggctat gttctttctg cttgttctca ttctgtcttc agtgtttttg 60
 ttccgtttgt tcaag 75

<210> 3
 <211> 583
 <212> PRT
 <213> Homo sapiens

<400> 3
 Met Glu Ser Lys Gly Ala Ser Ser Cys Arg Leu Leu Phe Cys Leu Leu
 1 5 10 15

Ile Ser Ala Thr Val Phe Arg Pro Gly Leu Gly Trp Tyr Thr Val Asn
 20 25 30

Ser Ala Tyr Gly Asp Thr Ile Ile Ile Pro Cys Arg Leu Asp Val Pro
 35 40 45

Gln Asn Leu Met Phe Gly Lys Trp Lys Tyr Glu Lys Pro Asp Gly Ser
 50 55 60

Pro Val Phe Ile Ala Phe Arg Ser Ser Thr Lys Lys Ser Val Gln Tyr
 65 70 75 80

Asp Asp Val Pro Glu Tyr Lys Asp Arg Leu Asn Leu Ser Glu Asn Tyr
85 90 95

Thr Leu Ser Ile Ser Asn Ala Arg Ile Ser Asp Glu Lys Arg Phe Val
100 105 110

Cys Met Leu Val Thr Glu Asp Asn Val Phe Glu Ala Pro Thr Ile Val
115 120 125

Lys Val Phe Lys Gln Pro Ser Lys Pro Glu Ile Val Ser Lys Ala Leu
130 135 140

Phe Leu Glu Thr Glu Gln Leu Lys Lys Leu Gly Asp Cys Ile Ser Glu
145 150 155 160

Asp Ser Tyr Pro Asp Gly Asn Ile Thr Trp Tyr Arg Asn Gly Lys Val
165 170 175

Leu His Pro Leu Glu Gly Ala Val Val Ile Ile Phe Lys Lys Glu Met
180 185 190

Asp Pro Val Thr Gln Leu Tyr Thr Met Thr Ser Thr Leu Glu Tyr Lys
195 200 205

Thr Thr Lys Ala Asp Ile Gln Met Pro Phe Thr Cys Ser Val Thr Tyr
210 215 220

Tyr Gly Pro Ser Gly Gln Lys Thr Ile His Ser Glu Gln Ala Val Phe
225 230 235 240

Asp Ile Tyr Tyr Pro Thr Glu Gln Val Thr Ile Gln Val Leu Pro Pro
245 250 255

Lys Asn Ala Ile Lys Glu Gly Asp Asn Ile Thr Leu Lys Cys Leu Gly
260 265 270

Asn Gly Asn Pro Pro Pro Glu Glu Phe Leu Phe Tyr Leu Pro Gly Gln
275 280 285

Pro Glu Gly Ile Arg Ser Ser Asn Thr Tyr Thr Leu Thr Asp Val Arg
290 295 300

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

Met Ile Ala Ser Thr Ala Ile Thr Val His Tyr Leu Asp Leu Ser Leu
325 330 335

Asn Pro Ser Gly Glu Val Thr Arg Gln Ile Gly Asp Ala Leu Pro Val
340 345 350

Ser Cys Thr Ile Ser Ala Ser Arg Asn Ala Thr Val Val Trp Met Lys
355 360 365

Asp Asn Ile Arg Leu Arg Ser Ser Pro Ser Phe Ser Ser Leu His Tyr
370 375 380

Gln Asp Ala Gly Asn Tyr Val Cys Glu Thr Ala Leu Gln Glu Val Glu
385 390 395 400

Gly Leu Lys Lys Arg Glu Ser Leu Thr Leu Ile Val Glu Gly Lys Pro
405 410 415

Gln Ile Lys Met Thr Lys Lys Thr Asp Pro Ser Gly Leu Ser Lys Thr
420 425 430

Ile Ile Cys His Val Glu Gly Phe Pro Lys Pro Ala Ile Gln Trp Thr
435 440 445

Ile Thr Gly Ser Gly Ser Val Ile Asn Gln Thr Glu Glu Ser Pro Tyr
450 455 460

Ile Asn Gly Arg Tyr Tyr Ser Lys Ile Ile Ile Ser Pro Glu Glu Asn
 465 470 475 480

Val Thr Leu Thr Cys Thr Ala Glu Asn Gln Leu Glu Arg Thr Val Asn
 485 490 495

Ser Leu Asn Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp
 500 505 510

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

Ile Val Gly Ile Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly
 530 535 540

Val Val Tyr Trp Leu Tyr Met Lys Lys Ser Lys Thr Ala Ser Lys His
 545 550 555 560

Val Asn Lys Asp Leu Gly Asn Met Glu Glu Asn Lys Lys Leu Glu Glu
 565 570 575

Asn Asn His Lys Thr Glu Ala
 580

<210> 4

<211> 78

<212> DNA

<213> Homo sapiens

<400> 4

ctaattgtgg gaatcgttgt tggcttcctc cttgctgccc ttgttgctgg tgtcgtctac 60

tggctgtaca tgaagaag 78

<210> 5

<211> 235

<212> PRT

<213> Homo sapiens

<400> 5

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 Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
20 25 30

Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
35 40 45

Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
50 55 60

Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65 70 75 80

Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
85 90 95

Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
100 105 110

Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
115 120 125

Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
130 135 140

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

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

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

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His

195

200

205

Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
 210 215 220

Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
 225 230 235

<210> 6

<211> 75

<212> DNA

<213> Homo sapiens

<400> 6

atctacatct gggcgccctt ggccgggact tgtgggggtcc ttctcctgtc actggttatc 60

accctttact gcaac 75

<210> 7

<211> 221

<212> PRT

<213> Homo sapiens

<400> 7

Met Arg Pro Arg Leu Trp Leu Leu Leu Ala Ala Gln Leu Thr Val Leu
 1 5 10 15

His Gly Asn Ser Val Leu Gln Gln Thr Pro Ala Tyr Ile Lys Val Gln
 20 25 30

Thr Asn Lys Met Val Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser
 35 40 45

Asn Met Arg Ile Tyr Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp
 50 55 60

Ser His His Glu Phe Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile
 65 70 75 80

His Gly Glu Glu Val Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala

85

90

95

Ser Arg Phe Ile Leu Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly
 100 105 110

Ile Tyr Phe Cys Met Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys
 115 120 125

Gly Thr Gln Leu Ser Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro
 130 135 140

Thr Lys Lys Ser Thr Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro
 145 150 155 160

Glu Thr Gln Lys Gly Pro Leu Cys Ser Pro Ile Thr Leu Gly Leu Leu
 165 170 175

Val Ala Gly Val Leu Val Leu Leu Val Ser Leu Gly Val Ala Ile His
 180 185 190

Leu Cys Cys Arg Arg Arg Arg Ala Arg Leu Arg Phe Met Lys Gln Leu
 195 200 205

Arg Leu His Pro Leu Glu Lys Cys Ser Arg Met Asp Tyr
 210 215 220

<210> 8

<211> 75

<212> DNA

<213> Homo sapiens

<400> 8

atcacccttg gcctgctggt ggctggcgctc ctggttctgc tggtttccct gggagtggcc 60

atccacctgt gctgc 75

<210> 9

<211> 199

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 10
<211> 75
<212> DNA
<213> Homo sapiens

<400> 10
ttctgggttac ccataggatg tgcagccttt gttgtagtct gcattttggg atgcatactt 60
atttgttggc ttaca 75

<210> 11
<211> 223
<212> PRT
<213> Homo sapiens

<400> 11
Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15

Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30

Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60

Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80

Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 12
<211> 75
<212> DNA
<213> Homo sapiens

<400> 12
ttcctcctct ggatccttgc agcagttagt tcggggttgt ttttttatag ctttctcctc 60
acagctgttt ctttg 75

<210> 13
<211> 532
<212> PRT
<213> Homo sapiens

<400> 13
Met Ala Pro Ser Ser Pro Arg Pro Ala Leu Pro Ala Leu Leu Val Leu
1 5 10 15

Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr Ser Val Ser
20 25 30

Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys
35 40 45

Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu
50 55 60

Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
65 70 75 80

Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
85 90 95

Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
100 105 110

Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
115 120 125

Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
130 135 140

Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
145 150 155 160

Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
165 170 175

Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
180 185 190

Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
195 200 205

Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
210 215 220

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

Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
245 250 255

Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
260 265 270

Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
275 280 285

Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
290 295 300

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

Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
325 330 335

Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
340 345 350

Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
355 360 365

Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
370 375 380

Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
385 390 395 400

Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
 405 410 415

Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
 420 425 430

Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
 435 440 445

Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
 450 455 460

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

Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met Gly Thr Ala
 485 490 495

Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
 500 505 510

Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln
 515 520 525

Ala Thr Pro Pro
 530

<210> 14
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 14
 attgtcatca tcaactgtggt agcagccgca gtcataatgg gcactgcagg cctcagcacg 60
 tacctctata accgccagcg g 81

<210> 15
 <211> 39

<212> PRT

<213> Homo sapiens

<400> 15

Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn
1 5 10 15

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
20 25 30

Phe Pro Gly Pro Ser Lys Pro
35

<210> 16

<211> 117

<212> DNA

<213> Homo sapiens

<400> 16

caagagctga cttacacgtg tacagcccag aaccctgtca gcaacaattc tgactccatc 60

tctgcccggc agctctgtgc agacatcgca atgggcttcc gtactcacca caccggg 117

<210> 17

<211> 116

<212> DNA

<213> Homo sapiens

<400> 17

accaactgga gagaacagta aactccttga atgtctctgc tataagtatt ccagaacacg 60

atgaggcaga cgagataagt gatgaaaaca gagaaaaggt gaatgaccag gcaaaa 116

<210> 18

<211> 138

<212> DNA

<213> Homo sapiens

<400> 18

cccaccacga cgccagcgcc gcgaccacca acaccggcgc ccaccatcgc gtcgcagccc 60

ctgtccctgc gcccagaggc gtgccggcca gcggcggggg gcgcagtgca cacgaggggg 120

ctggacttcg cctgtgat 138

<210> 19
 <211> 117
 <212> DNA
 <213> Homo sapiens

<400> 19
 ctgagtgtgg ttgatttcct tcccaccact gcccagccca ccaagaagtc caccctcaag 60
 aagagagtgt gccggttacc caggccagag acccagaagg gccactttg tagcccc 117

<210> 20
 <211> 117
 <212> DNA
 <213> Homo sapiens

<400> 20
 tctcatgcca actattactt ctgcaaccta tcaatTTTTg atcctcctcc ttttaaagta 60
 actcttacag gaggatattt gcatatttat gaatcacaac tttgttgcca gctgaag 117

<210> 21
 <211> 117
 <212> DNA
 <213> Homo sapiens

<400> 21
 gacacgggac tctacatctg caaggtggag ctcatgtacc caccgccata ctacctgggc 60
 ataggcaacg gaaccagat ttatgtaatt gatccagaac cgtgcccaga ttctgac 117

<210> 22
 <211> 117
 <212> DNA
 <213> Homo sapiens

<400> 22
 ggggaatcag tgactgtcac tcgagatctt gagggcacct acctctgtcg ggccaggagc 60
 actcaagggg aggtcaccg caaggtgacc gtgaatgtgc tctcccccg gtatgag 117

<210> 23
 <211> 22
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 23

Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr
1				5				10					15		

Asp	Val	Leu	Asp	Lys	Arg
			20		

<210> 24

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24

cagaaccagc	tctataacga	gctcaatcta	ggacgaagag	aggagtacga	tgttttggac	60
aagaga						66

<210> 25

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 25

Gln	Asn	Gln	Leu	Phe	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Phe
1				5				10					15		

Asp	Val	Leu	Asp	Lys	Arg
			20		

<210> 26

<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 26
cagaaccagc tctttaacga gctcaatcta ggacgaagag aggagttcga tgttttggac 60

aagaga 66

<210> 27
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 27
Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
1 5 10 15

Tyr Ser Glu Ile Gly Met Lys
20

<210> 28
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 28
caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgagatt 60

gggatgaaa 69

<210> 29
<211> 23

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 29
Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
1 5 10 15

Phe Ser Glu Ile Gly Met Lys
20

<210> 30
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 30
caggaaggcc tgttcaatga actgcagaaa gataagatgg cggaggcctt cagtgagatt 60
gggatgaaa 69

<210> 31
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 31
His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
1 5 10 15

Asp Ala Leu His Met Gln
20

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

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 35
Lys Arg Arg Gly Arg
1 5

<210> 36
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 36
aagagacgtg gccgg

15

<210> 37
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 37
Lys Pro Arg Arg Lys
1 5

<210> 38
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 38
aagccgagaa ggaag 15

<210> 39
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 39
Lys Gly Glu Arg Arg Arg Gly Lys
1 5

<210> 40
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 40
aaaggcgagc gccggagggg caag 24

<210> 41
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 41
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp

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

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 42

<211> 1458

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 42

atggctctcc cagtgcctgc cctactgctt cccctagcgc ttctcctgca tgcagagggtg	60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact ggggtgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
gggtggagggtg gatcagggtg aggtggatct ggtggagggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660

ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720
tattttctgtc aacaatataa caggatatccg tacacgtccg gagggggggac caagctggag	780
atcaaacggg cggccgcaat tgaagttatg tatcctcctc cttacctaga caatgagaag	840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctattttccc	900
ggaccttcta agcccttttg ggtgctgggtg gtggttgggtg gagtcctggc ttgctatagc	960
ttgctagtaa cagtggcctt tattatatttc tgggtgagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgcagcc tatcgtcca gagtgaagtt cagcaggagc	1140
gcagacgccc ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga	1200
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatggggggga	1260
aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg	1320
gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat	1380
ggcctttacc agggctctcag tacagccacc aaggacacct acgacgccct tcacatgcag	1440
gccctgcccc ctcgctaa	1458

<210> 43

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 43

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

His	Ala	Glu	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro
			20					25					30		

Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
 50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
 65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
 85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
 100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
 115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
 145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
 165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
 180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
 195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
 210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
 225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
275 280 285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
370 375 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385 390 395 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Phe
420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe Ser Glu Ile Gly
 435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Phe Gln
 450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala Leu His Met Gln
 465 470 475 480

Ala Leu Pro Pro Arg
 485

<210> 44

<211> 1458

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 44

atggctctcc cagtgcactgc cctactgctt cccctagcgc ttctcctgca tgcagaggtg	60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtgaa gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggatggaggtg gatcaggtgg aggtggatct ggtggaggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa ttagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660

ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac 720
 tattttctgtc aacaatataa caggatatccg tacacgtccg gagggggggac caagctggag 780
 atcaaacggg cggccgcaat tgaagttatg tatcctcctc cttacctaga caatgagaag 840
 agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctattttccc 900
 ggaccttcta agcccttttg ggtgctgggtg gtggttgggtg gagtcctggc ttgctatagc 960
 ttgctagtaa cagtggcctt tattatttttc tgggtgagga gtaagaggag caggctcctg 1020
 cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag 1080
 ccctatgccc caccacgcga cttcgcagcc tatcgtcca gagtgaagtt cagcaggagc 1140
 gcagacgccc ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga 1200
 cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatggggggga 1260
 aagccgagaa ggaagaaccc tcaggaaggc ctgttcaatg aactgcagaa agataagatg 1320
 gcggaggcct tcagtgaatg tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat 1380
 ggcctttttcc aggggctcag tacagccacc aaggacacct tcgacgccct tcacatgcag 1440
 gccctgcccc ctcgctaa 1458

<210> 45

<211> 416

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 45

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

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
 20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
 35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
275 280 285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
370 375 380

Ala Tyr Gln Gln Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
385 390 395 400

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
405 410 415

<210> 46

<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 46

atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagaggtg	60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgataactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggtaggaggtg gatcagggtg aggtggatct ggtggaggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa ttagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720
tatttctgtc aacaatataa caggatatccg tacacgtccg gaggggggac caagctggag	780
atcaaacggg cggccgcaat tgaagttatg tatcctctc cttacctaga caatgagaag	840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc	900
ggaccttcta agcccttttg ggtgctgggt gtggttggtg gagtcctggc ttgctatagc	960
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgcagcc tatcgtcca gagtgaagtt cagcaggagc	1140
gcagacgccc ccgcgtacca gcagggccac gatggccttt accaggggct cagtacagcc	1200
accaaggaca cctacgacgc cttcacatg caggccctgc cccctcgcta a	1251

<210> 47
<211> 416
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 47
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
275 280 285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
370 375 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385 390 395 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
405 410 415

<210> 48

<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 48

atggctctcc cagtgcactgc cctactgctt cccctagcgc ttctcctgca tgcagaggtg	60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggatggaggtg gatcagggtgg aggtggatct ggtggaggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa ttagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720

tattttctgtc aacaatataa caggtatccg tacacgtccg gaggggggac caagctggag	780
atcaaacggg cggccgcaat tgaagttatg taccctctc cttacctaga caatgagaag	840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctattttccc	900
ggaccttcta agcccttttg ggtgctgggtg gtggttgggtg gagtcctggc ttgctatagc	960
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cgccccgggc ccaccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgcagcc tatcgtcca gagtgaagtt cagcaggagc	1140
gcagacgccc ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga	1200
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctta a	1251

<210> 49

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 49

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

His	Ala	Glu	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro
			20					25					30		

Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Ser
		35					40					45			

Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu
	50					55					60				

Trp	Ile	Gly	Gln	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	Gly
65					70				75						80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
275 280 285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
370 375 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Phe Asn Glu Leu Asn Leu Gly
385 390 395 400

Arg Arg Glu Glu Phe Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Phe
420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln

465

470

475

480

Ala Leu Pro Pro Arg
485

<210> 50

<211> 1458

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 50

atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagagggtg	60
aagctgcagc agtctggggc tgagctgggtg aggcctgggt cctcagtga gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgataactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggatggagggtg gatcagggtg aggtggatct ggtggagggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720
tatttctgtc aacaatataa caggatatccg tacacgtccg gaggggggac caagctggag	780
atcaaacggg cggccgcaat tgaagttatg tatcctcctc cttacctaga caatgagaag	840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc	900
ggaccttcta agcccttttg ggtgctgggtg gtggttgggtg gagtcctggc ttgctatagc	960

ttgctagtaa cagtggcctt tattatitttc tgggtgagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgcagcc tatcgtcca gagtgaagtt cagcaggagc	1140
gcagacgccc ccgcgtacca gcagggccag aaccagctct ttaacgagct caatctagga	1200
cgaagagagg agttcgatgt tttggacaag agacgtggcc gggaccctga gatgggggga	1260
aagccgagaa ggaagaaccc tcaggaaggc ctgttcaatg aactgcagaa agataagatg	1320
gcggaggcct tcagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat	1380
ggcctttacc aggttctcag tacagccacc aaggacacct acgacgccct tcacatgcag	1440
gccctgcccc ctcgctaa	1458

<210> 51

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 51

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

His	Ala	Glu	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro
			20					25					30		

Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Ser
		35					40					45			

Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu
	50					55					60				

Trp	Ile	Gly	Gln	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	Gly
65				70					75						80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val

275

280

285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
 290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
 305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
 325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
 340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
 355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 370 375 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Phe Asn Glu Leu Asn Leu Gly
 385 390 395 400

Arg Arg Glu Glu Phe Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 52
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 52
atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagagggtg 60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc 120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga 180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga 240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag 300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt 360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca 420
ggtaggagggt gatcagggtg aggtggatct ggtggagggt gatctgacat tgagctcacc 480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc 540
agtcagaatg tgggtactaa ttagcctgg tatcaacaga aaccaggaca atctcctaaa 600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt 660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac 720
tatttctgtc aacaatataa caggatatccg tacacgtccg gagggggggac caagctggag 780
atcaaacggg cggccgcaat tgaagttatg tatcctctc cttacctaga caatgagaag 840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc 900
ggaccttcta agcccttttg ggtgctgggt gtggttgggt gagtcctggc ttgctatagc 960
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg 1020

cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag 1080
 ccctatgccc caccacgcga cttcgcagcc tatcgctcca gagtgaagtt cagcaggagc 1140
 gcagacgccc ccgcgtacca gcagggccag aaccagctct ttaacgagct caatctagga 1200
 cgaagagagg agttcgatgt tttggacaag agacgtggcc gggaccctga gatgggggga 1260
 aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg 1320
 gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat 1380
 ggccctttacc agggctctcag tacagccacc aaggacacct acgacgccct tcacatgcag 1440
 gccctgcccc ctcgctaa 1458

<210> 53

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 53

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

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
 20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
 35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
 50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
 65 70 75 80

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

85

90

95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
 100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
 115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
 145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
 165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
 180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
 195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
 210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
 225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
 245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
 260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
 275 280 285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
 290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
 305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
 325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
 340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
 355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 370 375 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Phe Asn Glu Leu Asn Leu Gly
 385 390 395 400

Arg Arg Glu Glu Phe Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Phe Gln
 450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala Leu His Met Gln
 465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 54
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 54
atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagaggtg 60
aagctgcagc agtctggggc tgagctgggt aggcctgggt ctcagtgaa gatttcctgc 120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga 180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga 240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag 300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt 360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca 420
ggatggaggtg gatcaggtgg aggtggatct ggtggaggtg gatctgacat tgagctcacc 480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcggtcac ctgcaaggcc 540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa 600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt 660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac 720
tatttctgtc aacaatataa caggatatccg tacacgtccg gaggggggac caagctggag 780
atcaaacggg cggccgcaat tgaagttatg tatcctcctc cttacctaga caatgagaag 840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc 900
ggaccttcta agcccttttg ggtgctgggt gtggttgggt gagtcctggc ttgctatagc 960
ttgctagtaa cagtggcctt tattattttt tgggtgagga gtaagaggag caggctcctg 1020

cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgcagcc tatcgtcca gagtgaagtt cagcaggagc	1140
gcagacgccc ccgcgtacca gcagggccag aaccagctct ttaacgagct caatctagga	1200
cgaagagagg agttcgatgt tttggacaag agacgtggcc gggaccctga gatgggggga	1260
aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg	1320
gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat	1380
ggccttttcc aggggctcag tacagccacc aaggacacct tcgacgccct tcacatgcag	1440
gccctgcccc ctcgctaa	1458

<210> 55

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 55

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

His	Ala	Glu	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro
			20					25						30	

Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Ser
			35				40					45			

Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu
	50					55					60				

Trp	Ile	Gly	Gln	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	Gly
65				70					75						80

Lys	Phe	Lys	Gly	Gln	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr
				85					90					95	

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
275 280 285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
 290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
 305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
 325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
 340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
 355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 370 375 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
 385 390 395 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Phe Gln
 450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala Leu His Met Gln
 465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 56
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 56
atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagagggtg 60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc 120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga 180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga 240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag 300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt 360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca 420
ggatggagggt gatcagggtg aggtggatct ggtggagggt gatctgacat tgagctcacc 480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcggtcac ctgcaaggcc 540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa 600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt 660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac 720
tatttctgtc aacaatataa caggatatccg tacacgtccg gaggggggac caagctggag 780
atcaaacggg cggccgcaat tgaagttatg tatcctcctc cttacctaga caatgagaag 840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc 900
ggaccttcta agcccttttg ggtgctgggt gtggttgggt gaggcctggc ttgctatagc 960
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg 1020
cacagtgact acatgaacat gactccccgc cgccccgggc ccaccgcaa gcattaccag 1080

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ccctatgccc caccacgcga cttgcgagcc tatcgctcca gagtgaagtt cagcaggagc      1140
gcagacgccc ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga      1200
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga      1260
aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg      1320
gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat      1380
ggccttttcc aggggctcag tacagccacc aaggacacct tcgacgccct tcacatgcag      1440
gccctgcccc ctcgctaa                                                    1458

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<210> 57

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 57

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

```

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His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
20          25          30

```

```

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
35          40          45

```

```

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50          55          60

```

```

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65          70          75          80

```

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Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85          90          95

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Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
260 265 270

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
275 280 285

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
290 295 300

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
305 310 315 320

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
370 375 380

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385 390 395 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg
450 455

<210> 58

<211> 1368

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 58

atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagagggtg	60
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aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgataactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggtggagggtg gatcagggtgg aggtggatct ggtggagggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720
tatttctgtc aacaatataa caggatatccg tacacgtccg gaggggggac caagctggag	780
atcaaacggg cggccgcaat tgaagttatg tatcctctc cttacctaga caatgagaag	840
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc	900
ggaccttcta agcccttttg ggtgctgggtg gtgggtgggtg gagtcctggc ttgctatagc	960
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgcagcc tatcgctcca gagtgaagtt cagcaggagc	1140
gcagacgccc ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga	1200
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga	1260
aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg	1320

gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggtaa

1368

<210> 59

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 59

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

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
 145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
 165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
 180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
 195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
 210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
 225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
 245 250 255

Thr Lys Leu Glu Ile Lys Arg Asn Gln Leu Glu Arg Thr Val Asn Ser
 260 265 270

Leu Asn Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp Glu
 275 280 285

Ile Ser Asp Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu Ile
 290 295 300

Val Gly Ile Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly Val
 305 310 315 320

Val Tyr Trp Leu Tyr Met Lys Lys Arg Ser Lys Arg Ser Arg Leu Leu
 325 330 335

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg

340

345

350

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
355 360 365

Lys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
370 375 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
385 390 395 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
405 410 415

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
420 425 430

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
435 440 445

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
450 455 460

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
465 470 475 480

Arg

<210> 60

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 60

atggctctcc cagtgcactgc cctactgctt cccctagcgc ttctcctgca tgcagagggtg	60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggtaggagggt gatcagggtgg aggtggatct ggtggagggt gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720
tatttctgtc aacaatataa caggatatccg tacacgtccg gaggggggac caagctggag	780
atcaaacgga accaactgga gagaacagta aactccttga atgtctctgc tataagtatt	840
ccagaacacg atgaggcaga cgagataagt gatgaaaaca gagaaaagg gaatgaccag	900
gcaaaaactaa ttgtgggaat cgttggttgg ctcctccttg ctgcccttgt tgctggtgtc	960
gtctactggc tgtacatgaa gaagaggagt aagaggagca ggctcctgca cagtgcactac	1020
atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgccccca	1080
ccacgcgact tcgcagccta tcgcaaaaaga gtgaagttca gcaggagcgc agacgcccc	1140
gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag	1200
tacgatgttt tggacaagag acgtggccgg gaccctgaga tggggggaaa gccgagaagg	1260
aagaaccctc aggaaggcct gtacaatgaa ctgcagaaag ataagatggc ggaggcctac	1320
agtgcagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg cttttaccag	1380
ggctctcagta cagccaccaa ggacacctac gacgcccttc acatgcaggc cctgccccct	1440
cgctaa	1446

<210> 61

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 61

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

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr

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

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
355 360 365

Lys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
370 375 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
385 390 395 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
405 410 415

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln
420 425 430

Lys Asp Lys Met Ala Glu Ala Phe Ser Glu Ile Gly Met Lys Gly Glu
435 440 445

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Phe Gln Gly Leu Ser Thr
450 455 460

Ala Thr Lys Asp Thr Phe Asp Ala Leu His Met Gln Ala Leu Pro Pro
465 470 475 480

Arg

<210> 62

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 62

atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagaggtg

60

aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggctcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggatggagggtg gatcagggtg aggtggatct ggtggagggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720
tatttctgtc aacaatataa caggtatccg tacacgtccg gaggggggac caagctggag	780
atcaaacgga accaactgga gagaacagta aactccttga atgtctctgc tataagtatt	840
ccagaacacg atgaggcaga cgagataagt gatgaaaaca gagaaaagggt gaatgaccag	900
gcaaaaactaa ttgtgggaat cgttggttgg ctcctccttg ctgcccttgt tgctggtgtc	960
gtctactggc tgtacatgaa gaagaggagt aagaggagca ggctcctgca cagtgactac	1020
atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgccccca	1080
ccacgcgact tcgcagccta tcgcaaaaga gtgaagttca gcaggagcgc agacgcccc	1140
gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag	1200
tacgatgttt tggacaagag acgtggccgg gaccctgaga tggggggaaa gccgagaagg	1260
aagaaccctc aggaaggcct gttcaatgaa ctgcagaaag ataagatggc ggaggccttc	1320
agtgagattg ggatgaaagg cgagcgccgg aggggcaagg ggcacgatgg ctttttccag	1380
ggctctcagta cagccaccaa ggacaccttc gacgcccttc acatgcaggc cctgccccct	1440
cgctaa	1446

<210> 63

<211> 412

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 63

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

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val
165 170 175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
245 250 255

Thr Lys Leu Glu Ile Lys Arg Asn Gln Leu Glu Arg Thr Val Asn Ser
260 265 270

Leu Asn Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp Glu
275 280 285

Ile Ser Asp Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu Ile
290 295 300

Val Gly Ile Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly Val
305 310 315 320

Val Tyr Trp Leu Tyr Met Lys Lys Arg Ser Lys Arg Ser Arg Leu Leu
325 330 335

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
340 345 350

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
 355 360 365

Lys Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
 370 375 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 385 390 395 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405 410

<210> 64

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 64

atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagaggtg	60
aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc	120
aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga	180
cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga	240
aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag	300
ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt	360
tcggtagtag atttctactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca	420
ggatggaggtg gatcagggtg aggtggatct ggtggaggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa ttagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660

ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac 720
 tattttctgtc aacaatataa caggatatccg tacacgtccg gagggggggac caagctggag 780
 atcaaacgga accaactgga gagaacagta aactccttga atgtctctgc tataagtatt 840
 ccagaacacg atgaggcaga cgagataagt gatgaaaaca gagaaaaggt gaatgaccag 900
 gcaaaaactaa ttgtgggaat cgttggttggc ctcctccttg ctgcccttgt tgctggtgtc 960
 gtctactggc tgtacatgaa gaagaggagt aagaggagca ggctcctgca cagtgactac 1020
 atgaacatga ctccccgccg ccccgggccc acccgcaagc attaccagcc ctatgccccca 1080
 ccacgcgact tcgcagccta tcgcaaaaga gtgaagttca gcaggagcgc agacgcccccc 1140
 gcgtaccagc agggccagaa ccagctctat aacgagctca atctaggacg aagagaggag 1200
 tacgatgttt tggacaagag acgtggccgg gacccttaa 1239

<210> 65
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 65
 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
 20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
 35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 66

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 66

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 67

<211> 20

<212> PRT

<213> Homo sapiens

<400> 67

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 68

<211> 20

<212> PRT

<213> Mus musculus

<400> 68

Met Tyr Ser Met Gln Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu
1 5 10 15

Leu Val Asn Ser
20

<210> 69

<211> 20

<212> PRT

<213> Homo sapiens

<400> 69

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly
20

<210> 70

<211> 20

<212> PRT

<213> Mus musculus

<400> 70

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly
20

<210> 71
<211> 21
<212> PRT
<213> Homo sapiens

<400> 71
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
20

<210> 72
<211> 18
<212> PRT
<213> Homo sapiens

<400> 72
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala

<210> 73
<211> 16
<212> PRT
<213> Homo sapiens

<400> 73
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Ser Ser Ala Tyr Ser
1 5 10 15

<210> 74
<211> 30
<212> PRT
<213> Homo sapiens

<400> 74
Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1 5 10 15

Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser
20 25 30

<210> 75

<211> 272

<212> PRT

<213> Homo sapiens

<400> 75

Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val
1 5 10 15

Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
20 25 30

Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
35 40 45

Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
50 55 60

Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro
65 70 75 80

Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
85 90 95

Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly
100 105 110

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
115 120 125

Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg
130 135 140

Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser
145 150 155 160

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
165 170 175

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
180 185 190

Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser
195 200 205

Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu
210 215 220

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

Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr
245 250 255

Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys
260 265 270

<210> 76

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 76

Gly Tyr Ala Phe Ser Ser
1 5

<210> 77

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 77
Tyr Pro Gly Asp Gly Asp
1 5

<210> 78
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 78
Lys Thr Ile Ser Ser Val Val Asp Phe
1 5

<210> 79
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 79
Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
1 5 10

<210> 80
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 80
Ser Ala Thr Tyr Arg Asn
1 5

<210> 81
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 81
Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr
1 5

<210> 82
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 82
Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

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

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 83
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 83
Asp Ile Glu Leu Thr Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile
35 40 45

Tyr Ser Ala Thr Tyr Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80

Lys Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr
85 90 95

Thr Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 84
<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 84

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

His Ala Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
20 25 30

Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser
35 40 45

Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly
65 70 75 80

Lys Phe Lys Gly Gln Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr
85 90 95

Ala Tyr Met Gln Leu Ser Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Phe Cys Ala Arg Lys Thr Ile Ser Ser Val Val Asp Phe Tyr Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
145 150 155 160

Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Val

165

170

175

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln
 180 185 190

Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr Ser Ala Thr Tyr
 195 200 205

Arg Asn Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
 210 215 220

Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser Lys Asp Leu Ala Asp
 225 230 235 240

Tyr Phe Cys Gln Gln Tyr Asn Arg Tyr Pro Tyr Thr Ser Gly Gly Gly
 245 250 255

Thr Lys Leu Glu Ile Lys Arg
 260

<210> 85

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 85

atggctctcc cagtgactgc cctactgctt cccctagcgc ttctcctgca tgcagaggtg 60

aagctgcagc agtctggggc tgagctgggt aggcctgggt cctcagtga gatttcctgc 120

aaggcttctg gctatgcatt cagtagctac tggatgaact gggatgaagca gaggcctgga 180

cagggtcttg agtggattgg acagatttat cctggagatg gtgatactaa ctacaatgga 240

aagttcaagg gtcaagccac actgactgca gacaaatcct ccagcacagc ctacatgcag 300

ctcagcggcc taacatctga ggactctgcg gtctatttct gtgcaagaaa gaccattagt 360

tcggtagtag atttctactt tgactactgg ggccaagggga ccacgggtcac cgtctcctca	420
ggatggagggtg gatcagggtgg aggtggatct ggtggagggtg gatctgacat tgagctcacc	480
cagtctccaa aattcatgtc cacatcagta ggagacaggg tcagcgtcac ctgcaaggcc	540
agtcagaatg tgggtactaa tgtagcctgg tatcaacaga aaccaggaca atctcctaaa	600
ccactgattt actcggcaac ctaccggaac agtggagtcc ctgatcgctt cacaggcagt	660
ggatctggga cagatttcac tctcaccatc actaacgtgc agtctaaaga cttggcagac	720
tatttctgtc aacaatataa caggatatccg tacacgtccg gagggggggac caagctggag	780
atcaaacgg	789

<210> 86
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 86
 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 Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
 20 25 30

Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
 35 40 45

Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
 50 55 60

Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
 65 70 75 80

Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
 85 90 95

Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
 100 105 110

Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
115 120 125

Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
130 135 140

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

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

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

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
195 200 205

Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
210 215 220

Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
225 230 235

<210> 87
<211> 247
<212> PRT
<213> Mus musculus

<400> 87
Met Ala Ser Pro Leu Thr Arg Phe Leu Ser Leu Asn Leu Leu Leu Met
1 5 10 15

Gly Glu Ser Ile Ile Leu Gly Ser Gly Glu Ala Lys Pro Gln Ala Pro
20 25 30

Glu Leu Arg Ile Phe Pro Lys Lys Met Asp Ala Glu Leu Gly Gln Lys

35

40

45

Val Asp Leu Val Cys Glu Val Leu Gly Ser Val Ser Gln Gly Cys Ser
 50 55 60

Trp Leu Phe Gln Asn Ser Ser Ser Lys Leu Pro Gln Pro Thr Phe Val
 65 70 75 80

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

Asn Ser Ser Lys Leu Phe Ser Ala Val Arg Asp Thr Asn Asn Lys Tyr
 100 105 110

Val Leu Thr Leu Asn Lys Phe Ser Lys Glu Asn Glu Gly Tyr Tyr Phe
 115 120 125

Cys Ser Val Ile Ser Asn Ser Val Met Tyr Phe Ser Ser Val Val Pro
 130 135 140

Val Leu Gln Lys Val Asn Ser Thr Thr Thr Lys Pro Val Leu Arg Thr
 145 150 155 160

Pro Ser Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu
 165 170 175

Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala
 180 185 190

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Pro
 195 200 205

Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr His Arg Ser Arg Lys
 210 215 220

Arg Val Cys Lys Cys Pro Arg Pro Leu Val Arg Gln Glu Gly Lys Pro
 225 230 235 240

Arg Pro Ser Glu Lys Ile Val
245

<210> 88
<211> 69
<212> PRT
<213> Mus musculus

<400> 88
Ser Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His Pro
1 5 10 15

Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly
20 25 30

Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
35 40 45

Ala Pro Leu Ala Gly Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile
50 55 60

Thr Leu Ile Cys Tyr
65

<210> 89
<211> 207
<212> DNA
<213> Mus musculus

<400> 89
tctactacta ccaagccagt gctgcgaact ccctcacctg tgcaccctac cgggacatct 60
cagccccaga gaccagaaga ttgtcggccc cgtggctcag tgaaggggac cggattggac 120
ttgcctgtg atatttacat ctgggcaccc ttggccggaa tctgcgtggc ctttctgctg 180
tccttgatca tcactctcat ctgctac 207

<210> 90
<211> 220

<212> PRT

<213> Homo sapiens

<400> 90

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15

Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

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

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115 120 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145 150 155 160

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

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met

180

185

190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 195 200 205

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

<210> 91
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 91
 ttttgggtgc tgggtgggtg tgggtggagtc ctggcttgct atagcttgct agtaacagtg 60
 gcctttatta ttttctgggt g 81

<210> 92
 <211> 27
 <212> PRT
 <213> Homo sapiens

<400> 92
 Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
 1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 20 25

<210> 93
 <211> 81
 <212> DNA
 <213> Homo sapiens

<400> 93
 ttttgggtgc tgggtgggtg tgggtggagtc ctggcttgct atagcttgct agtaacagtg 60
 gcctttatta ttttctgggt g 81

<210> 94
 <211> 164

<212> PRT

<213> Homo sapiens

<400> 94

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

Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
20 25 30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
35 40 45

Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
50 55 60

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65 70 75 80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
85 90 95

Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
100 105 110

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
115 120 125

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
130 135 140

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
145 150 155 160

Leu Pro Pro Arg

<210> 95

<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 95
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 96
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 96
agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc	120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat	180
gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc	240
cggagggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc	300
tacgacgccc ttcacatgca ggccctgccc cctcgc	336

<210> 97
 <211> 218
 <212> PRT
 <213> Mus musculus

<400> 97
 Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
 1 5 10 15

Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
 20 25 30

Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
 35 40 45

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
 50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
 65 70 75 80

Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
 85 90 95

Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
 100 105 110

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
 115 120 125

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

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
 145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
 165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Ser Asp Tyr Met Asn Met
 180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
 195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
 210 215

<210> 98
 <211> 123
 <212> DNA
 <213> Mus musculus

<400> 98
 aatagtagaa ggaacagact ccttcaaagt gactacatga acatgactcc ccggaggcct 60
 gggctcactc gaaagcctta ccagccctac gcccctgccag gagactttgc agcgtaccgc 120
 ccc 123

<210> 99
 <211> 41
 <212> PRT
 <213> Mus musculus

<400> 99
 Asn Ser Arg Arg Asn Arg Leu Leu Gln Ser Asp Tyr Met Asn Met Thr
 1 5 10 15

Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro
 20 25 30

Ala Arg Asp Phe Ala Ala Tyr Arg Pro
 35 40

<210> 100
 <211> 123
 <212> DNA
 <213> Mus musculus

<400> 100
 aatagtagaa ggaacagact ccttcaaagt gactacatga acatgactcc ccggaggcct 60
 gggctcactc gaaagcctta ccagccctac gcccctgcca gagactttgc agcgtaccgc 120
 ccc 123

<210> 101
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 101
 Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
 1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 35 40

<210> 102
 <211> 123
 <212> DNA
 <213> Mus musculus

<400> 102
 aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60
 gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
 tcc 123

<210> 103
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 103

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
 1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
 20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
 35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
 50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
 65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
 85 90 95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
 100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
 115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
 130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
 145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
 165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
180 185 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
245 250 255

<210> 104
<211> 42
<212> PRT
<213> Homo sapiens

<400> 104
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 105
<211> 126
<212> DNA
<213> Homo sapiens

<400> 105
aaacgggggca gaaagaaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg

126

<210> 106

<211> 277

<212> PRT

<213> Homo sapiens

<400> 106

Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro Cys Ala Ala Leu
1 5 10 15

Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val
20 25 30

Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
35 40 45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
85 90 95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
100 105 110

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
145 150 155 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
165 170 175

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

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
195 200 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
210 215 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
225 230 235 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
245 250 255

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
260 265 270

Thr Leu Ala Lys Ile
275

<210> 107

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 107

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 108
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 108
Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Lys
35 40

<210> 109
<211> 39
<212> PRT
<213> Homo sapiens

<400> 109
Asn Gln Leu Glu Arg Thr Val Asn Ser Leu Asn Val Pro Ala Ile Ser
1 5 10 15

Ile Pro Glu His Asp Glu Ala Asp Glu Ile Ser Asp Glu Asn Arg Glu
20 25 30

Lys Val Asn Asp Gln Ala Lys
35

<210> 110
<211> 42
<212> PRT
<213> Homo sapiens

<400> 110
Ala Ala Ala Asn Gln Leu Glu Arg Thr Val Asn Ser Leu Asn Val Ser

1	5	10	15
Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp Glu Ile Ser Asp Glu	20	25	30

Asn Arg Glu Lys Val Asn Asp Gln Ala Lys	35	40
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<210> 111
 <211> 48
 <212> PRT
 <213> Homo sapiens

<400> 111			
Pro Glu His Asp Glu Ala Asp Glu Ile Ser Asp Glu Asn Arg Glu Lys	5	10	15
1			

Val Asn Asp Gln Ala Lys Leu Ile Val Gly Ile Val Val Gly Leu Leu	20	25	30
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Leu Ala Ala Leu Val Ala Gly Val Val Tyr Trp Leu Tyr Met Lys Lys	35	40	45
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<210> 112
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 112			
Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu Ile Val Gly Ile	5	10	15
1			

Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly Val Val Tyr Trp	20	25	30
---	----	----	----

Leu Tyr Met Lys Lys	35
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<210> 113
 <211> 65

<212> PRT

<213> Homo sapiens

<400> 113

Asn Gln Leu Glu Arg Thr Val Asn Ser Leu Asn Val Pro Ala Ile Ser
1 5 10 15

Ile Pro Glu His Asp Glu Ala Asp Glu Ile Ser Asp Glu Asn Arg Glu
20 25 30

Lys Val Asn Asp Gln Ala Lys Leu Ile Val Gly Ile Val Val Gly Leu
35 40 45

Leu Leu Ala Ala Leu Val Ala Gly Val Val Tyr Trp Leu Tyr Met Lys
50 55 60

Lys
65

<210> 114

<211> 66

<212> PRT

<213> Homo sapiens

<400> 114

Thr Cys Thr Ala Glu Asn Gln Leu Glu Arg Thr Val Asn Ser Leu Asn
1 5 10 15

Val Ser Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp Glu Ile Ser
20 25 30

Asp Glu Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu Ile Val Gly
35 40 45

Ile Val Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly Val Val Tyr
50 55 60

Trp Leu
65

<210> 115
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 115
 Pro Glu His Asp Glu Ala Asp Glu Ile Ser Asp Glu Asn Arg Glu Lys
 1 5 10 15

Val Asn Asp Gln Ala Lys Leu Ile Val Gly Ile Val Val Gly Leu Leu
 20 25 30

Leu Ala Ala Leu Val Ala Gly Val Val Tyr Trp Leu
 35 40

<210> 116
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 116
 Asn Gln Leu Glu Arg Thr Val Asn Ser Leu Asn Val Ser Ala Ile Ser
 1 5 10 15

Ile Pro Glu His Asp Glu Ala Asp Glu Ile Ser Asp Glu Asn Arg Glu
 20 25 30

Lys Val Asn Asp Gln Ala Lys Leu Ile Val Gly Ile Val Val Gly Leu
 35 40 45

Leu Leu Ala Ala Leu Val Ala Gly Val Val Tyr Trp Leu
 50 55 60

<210> 117
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 117
 Ala Ala Ala Asn Gln Leu Glu Arg Thr Val Asn Ser Leu Asn Val Ser
 1 5 10 15

Ala Ile Ser Ile Pro Glu His Asp Glu Ala Asp Glu Ile Ser Asp Glu
20 25 30

Asn Arg Glu Lys Val Asn Asp Gln Ala Lys Leu Ile Val Gly Ile Val
35 40 45

Val Gly Leu Leu Leu Ala Ala Leu Val Ala Gly Val Val Tyr Trp Leu
50 55 60

Tyr Met Lys Lys
65

<210> 118
<211> 4
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD28 motif sequence

<400> 118
Tyr Met Asn Met
1

<210> 119
<211> 4
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD28 motif sequence

<400> 119
Pro Tyr Ala Pro
1