

SEQUENCE LISTING

<110> Yang, Wen

<120> Composition and Method for Adoptive Immunotherapy

<130> 180423.00200

<150> 62/877,331

<151> 2019-07-23

<150> 63/044,059

<151> 2020-06-25

<160> 73

<170> PatentIn version 3.5

<210> 1

<211> 275

<212> PRT

<213> Homo sapiens

<400> 1

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
1 5 10 15

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

Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
35 40 45

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

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65 70 75 80

Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
85 90 95

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

Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser

115

120

125

Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
 130 135 140

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
 145 150 155 160

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
 165 170 175

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
 180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
 195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
 210 215 220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
 225 230 235 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
 245 250 255

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
 260 265 270

Ser Ser Arg
 275

<210> 2
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
290 295 300

Lys Arg Lys Asp Ser Arg Gly
305 310

<210> 3
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 3

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

Pro Gly Pro

<210> 4
<211> 227
<212> PRT
<213> Homo sapiens

<400> 4

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
1 5 10 15

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

Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
35 40 45

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

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65 70 75 80

Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
85 90 95

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

Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser
115 120 125

Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
130 135 140

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
145 150 155 160

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
165 170 175

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
210 215 220

Glu Ser Ser
225

<210> 5

<211> 262
<212> PRT
<213> Homo sapiens

<400> 5

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp
260

<210> 6
<211> 68
<212> PRT
<213> Homo sapiens

<400> 6

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 Arg Ser Lys Arg Ser
20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
50 55 60

Ala Tyr Arg Ser
65

<210> 7
<211> 112
<212> PRT
<213> Homo sapiens

<400> 7

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> 8
<211> 55
<212> PRT
<213> Homo sapiens

<400> 8

Lys Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala
1 5 10 15

Gly Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro
20 25 30

Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr Ser
35 40 45

Gly Leu Asn Gln Arg Arg Ile
50 55

<210> 9
<211> 612
<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 9

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
1 5 10 15

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

Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
35 40 45

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

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65 70 75 80

Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
85 90 95

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

Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser
115 120 125

Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
130 135 140

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
145 150 155 160

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
165 170 175

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
210 215 220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
225 230 235 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
245 250 255

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
260 265 270

Ser Ser Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu
275 280 285

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser Ile
290 295 300

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

Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
325 330 335

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
340 345 350

Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
355 360 365

Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro Asn Gly Tyr
370 375 380

Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
385 390 395 400

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Tyr Val

405

410

415

Gly Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val
 420 425 430

Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
 435 440 445

Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
 450 455 460

Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val
 465 470 475 480

Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu
 485 490 495

Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser Ser Arg
 500 505 510

Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His Phe Arg
 515 520 525

Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln
 530 535 540

Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly
 545 550 555 560

Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu
 565 570 575

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
 580 585 590

Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys
 595 600 605

Asp Ser Arg Gly
 610

<210> 10
<211> 883
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 10

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Phe Trp Val Leu Val Val
260 265 270

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
275 280 285

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
290 295 300

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
305 310 315 320

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
325 330 335

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
340 345 350

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
355 360 365

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
370 375 380

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys

385		390		395		400									
Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg
				405					410					415	
Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys
			420					425					430		
Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Ala	Lys
		435					440					445			
Arg	Ser	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly
	450					455					460				
Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Thr	Leu	Leu	Gly	Leu	Leu
465					470					475					480
Ile	Leu	Trp	Leu	Gln	Leu	Gln	Trp	Val	Ser	Ser	Lys	Gln	Glu	Val	Thr
				485					490					495	
Gln	Ile	Pro	Ala	Ala	Leu	Ser	Val	Pro	Glu	Gly	Glu	Asn	Leu	Val	Leu
			500					505					510		
Asn	Cys	Ser	Phe	Thr	Asp	Ser	Ala	Ile	Tyr	Asn	Leu	Gln	Trp	Phe	Arg
		515					520					525			
Gln	Asp	Pro	Gly	Lys	Gly	Leu	Thr	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Ser
	530					535					540				
Gln	Arg	Glu	Gln	Thr	Ser	Gly	Arg	Leu	Asn	Ala	Ser	Leu	Asp	Lys	Ser
545					550					555					560
Ser	Gly	Arg	Ser	Thr	Leu	Tyr	Ile	Ala	Ala	Ser	Gln	Pro	Gly	Asp	Ser
				565					570					575	
Ala	Thr	Tyr	Leu	Cys	Ala	Val	Arg	Pro	Leu	Tyr	Gly	Gly	Ser	Tyr	Ile
			580					585					590		
Pro	Thr	Phe	Gly	Arg	Gly	Thr	Ser	Leu	Ile	Val	His	Pro	Tyr	Ile	Gln
		595					600					605			

Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp
610 615 620

Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser
625 630 635 640

Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp
645 650 655

Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn
660 665 670

Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro
675 680 685

Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Gly Ser Pro Lys Phe
690 695 700

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
705 710 715 720

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
725 730 735

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
740 745 750

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
755 760 765

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
770 775 780

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
785 790 795 800

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
805 810 815

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu

820

825

830

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 835 840 845

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 850 855 860

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 865 870 875 880

Pro Pro Arg

<210> 11

<211> 769

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 11

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
 50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
 65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
 85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser

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

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Asn
325 330 335

Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly Gly
340 345 350

Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro Asn Pro
355 360 365

Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu
370 375 380

Asn Gln Arg Arg Ile Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe
385 390 395 400

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met
405 410 415

Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp Val
420 425 430

Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro
435 440 445

Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile
450 455 460

Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser
465 470 475 480

Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu
485 490 495

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

Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Pro
515 520 525

Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser Leu

530

535

540

Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu
 545 550 555 560

Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe
 565 570 575

Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile
 580 585 590

Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn
 595 600 605

Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala
 610 615 620

Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu
 625 630 635 640

Ser Ser Gly Ser Pro Lys Phe Trp Val Leu Val Val Val Gly Gly Val
 645 650 655

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
 660 665 670

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
 675 680 685

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
 690 695 700

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Asn Arg Lys Ala Lys
 705 710 715 720

Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly
 725 730 735

Gln Asn Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro
 740 745 750

Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Arg
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Ile

<210> 12
 <211> 1839
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 12

atggagacc	tcttgggcct	gcttatcctt	tggtgcagc	tgcaatgggt	gagcagcaaa	60
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aactgcagtt	tcactgatag	cgctattttac	aacctccagt	ggtttaggca	ggaccctggg	180
aaaggtctca	catctctgtt	gcttattcag	tcaagtcaga	gagagcaaac	aagtggaaga	240
cttaatgcct	cgctggataa	atcatcagga	cgtagtactt	tatacattgc	agcttctcag	300
cctggtgact	cagccaccta	cctctgtgct	gtgaggcccc	tgtacggagg	aagctacata	360
cctacatttg	gaagaggaac	cagccttatt	gttcatccgt	atatccagaa	ccctgaccct	420
gccgtgtacc	agctgagaga	ctctaaatcc	agtgacaagt	ctgtctgcct	attcacccgat	480
tttgattctc	aaacaaatgt	gtcacaaagt	aaggattctg	atgtgtatat	cacagacaaa	540
actgtgctag	acatgaggtc	tatggacttc	aagagcaaca	gtgctgtggc	ctggagcaac	600
aaatctgact	ttgcatgtgc	aaacgccttc	aacaacagca	ttattccaga	agacaccttc	660
ttccccagcc	cagaaagtcc	ctgtgatgtc	aagctggtcg	agaaaagctt	tgaaacagat	720
acgaacctaa	actttcaaaa	cctgtcagtg	attgggttcc	gaatcctcct	cctgaaagtg	780
gccgggttta	atctgctcat	gacgctgcgg	ctgtggtcca	gccgggccaa	gcggtctggg	840
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<210> 13
 <211> 2652
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

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<210> 14
 <211> 2310
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

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cagtgtgccc aggatatgaa ccatgaatac atgtcctggt atcgacaaga cccaggcatg	180
gggctgaggc tgattcatta ctcagttggt gctggtatca ctgaccaagg agaagtcccc	240
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gctccctccc agacatctgt gtacttctgt gccagcagtt acgtcgggaa caccggggag	360
ctgttttttg gagaaggctc taggctgacc gtactggagg acctgaaaaa cgtgttccca	420
cccgaggctg ctgtgtttga gccatcagaa gcagagatct cccacacca aaaggccaca	480
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ctcaatgact ccagatacgc tctgagcagc cgcctgaggg tctcggccac cttctggcag	660
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ttacattccg attatatgaa tatgacacct aggagacctg gcccgactag gaaacactat	960
caaccttacg cacctcccag agattttgct gcttacagga gtaaaaaccg caaagctaaa	1020
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gccaagcctg tgacacgagg agcgggtgct ggcggcaggc aaaggggaca aaacaaggag	2220
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<211> 141
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 15

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
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Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
20 25 30

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
35 40 45

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
50 55 60

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
65 70 75 80

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
85 90 95

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
100 105 110

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
115 120 125

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
130 135 140

<210> 16
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 16

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aacatgactc cccgccgccc cgggcccacc cgcaagcatt accagcccta tgccccacca	180
cgcgacttcg cagcctatcg ctccagagtg aagttcagca ggagcgcaga cgcccccgcg	240
taccagcagg gccagaacca gctctataac gagctcaatc taggacgaag agaggagtac	300
gatgttttgg acaagagacg tggccgggac cctgagatgg ggggaaagcc gagaaggaag	360
aaccctcagg aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt	420
gagattggga tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggt	480
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<210> 17
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 17	
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aacatgactc cccgccgccc cgggcccacc cgcaagcatt accagcccta tgccccacca	180
cgcgacttcg cagcctatcg ctcc	204

<210> 18
 <211> 204
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 18	
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gctttcataa tcttttgggt ccgctcaaaa cgctctcgtc tgttacattc cgattatatg	120
aatatgacac ctaggagacc tggcccgact aggaaacact atcaacctta cgcacctccc	180
agagattttg ctgcttacag gagt	204

<210> 19
 <211> 336

<212> DNA
<213> Homo sapiens

<400> 19
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120
cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
gaactgcaga aagataagat ggcgagggcc tacagtgaga ttgggatgaa aggcgagcgc 240
cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300
tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 20
<211> 336
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 20
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tacaatgaat tgaacttggg tagaaggga gaatatgacg tgctcgataa acggaggggg 120
agagatccag aaatgggcgg taaaccacgg cgcaaaaatc cacaagaggg attgtataac 180
gagctccaaa aggacaaaat ggcagaagct tattcagaaa taggaatgaa gggggaaagg 240
agacgaggta aaggatcatga cggattgtat caaggattgt caaccgctac taaagataca 300
tatgatgctt tgcatatgca agctttgcct cccaga 336

<210> 21
<211> 540
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 21
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gctttcataa tcttttgggt ccgctcaaaa cgctctcgtc tgttacattc cgattatatg 120
aatatgacac ctaggagacc tggcccgact aggaaacact atcaacctta cgcacctccc 180

agagattttg ctgcttacag gagtcgggtc aaattttcac gctccgctga tgctcctgcc	240
tatcaacaag ggcaaaatca attgtacaat gaattgaact tgggtagaag ggaagaatat	300
gacgtgctcg ataaacggag ggggagagat ccagaaatgg gcggtaaacc acggcgcaaa	360
aatccacaag agggtattgta taacgagctc caaaaggaca aaatggcaga agcttattca	420
gaaataggaa tgaaggggga aaggagacga ggtaaaggtc atgacggatt gtatcaagga	480
ttgtcaaccg ctactaaaga tacatatgat gctttgcata tgcaagcttt gcctcccaga	540

<210> 22
 <211> 165
 <212> DNA
 <213> Homo sapiens

<400> 22	
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aggggacaaa acaaggagag gccaccacct gttcccaacc cagactatga gcccatccgg	120
aaaggccagc gggacctgta ttctggcctg aatcagagac gcatc	165

<210> 23
 <211> 165
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 23	
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aggggacaaa acaaggagag gccaccacct gttcccaacc cagactatga gcccatccgc	120
aaaggccagc gggacctgta ttctggcctg aatcagagac gcatc	165

<210> 24
 <211> 165
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 24	
aaaaaccgca aagctaaagc taaaccgctc actagggggg ccggagcagg agggcgccag	60
cgcggtcaga ataaagaacg ccctcctccc gtccctaadc ctgattacga accgattaga	120

aaggggcaaa gagatctcta cagcggactc aaccaacgga gaatt

165

<210> 25
<211> 9
<212> PRT
<213> Homo sapiens

<400> 25

Ser Leu Leu Met Trp Ile Thr Gln Cys
1 5

<210> 26
<211> 40
<212> PRT
<213> Homo sapiens

<400> 26

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

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

Leu Phe Pro Gly Pro Ser Lys Pro
35 40

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

<400> 27

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> 28
<211> 41
<212> PRT
<213> Homo sapiens

<400> 28

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> 29

<211> 42

<212> PRT

<213> Homo sapiens

<400> 29

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> 30

<211> 46

<212> PRT

<213> Homo sapiens

<400> 30

Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
1 5 10 15

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
20 25 30

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
35 40 45

<210> 31

<211> 26

<212> PRT
<213> Homo sapiens

<400> 31

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
1 5 10 15

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
20 25

<210> 32
<211> 883
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 32

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Cys Asp Ile Tyr Ile Trp
260 265 270

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
275 280 285

Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys
290 295 300

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
305 310 315 320

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

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn

340

345

350

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 355 360 365

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 370 375 380

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

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 405 410 415

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 420 425 430

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys
 435 440 445

Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu Gly Leu Leu
 465 470 475 480

Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys Gln Glu Val Thr
 485 490 495

Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu Asn Leu Val Leu
 500 505 510

Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu Gln Trp Phe Arg
 515 520 525

Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu Ile Gln Ser Ser
 530 535 540

Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser Leu Asp Lys Ser
 545 550 555 560

Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln Pro Gly Asp Ser
565 570 575

Ala Thr Tyr Leu Cys Ala Val Arg Pro Leu Tyr Gly Gly Ser Tyr Ile
580 585 590

Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His Pro Tyr Ile Gln
595 600 605

Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp
610 615 620

Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser
625 630 635 640

Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp
645 650 655

Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn
660 665 670

Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro
675 680 685

Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Gly Ser Pro Lys Cys
690 695 700

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
705 710 715 720

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
725 730 735

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
740 745 750

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
755 760 765

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr

770

775

780

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 785 790 795 800

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 805 810 815

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 820 825 830

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 835 840 845

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 850 855 860

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 865 870 875 880

Pro Pro Arg

<210> 33

<211> 885

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 33

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu

50

55

60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Phe Trp Val Leu Val Val
260 265 270

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
275 280 285

Ile Ile Phe Trp Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
290 295 300

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
305 310 315 320

Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg
325 330 335

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
340 345 350

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
355 360 365

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
370 375 380

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

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
405 410 415

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
420 425 430

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
435 440 445

Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
450 455 460

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu Gly Leu
465 470 475 480

Leu Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys Gln Glu Val

485

490

495

Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu Asn Leu Val
 500 505 510

Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu Gln Trp Phe
 515 520 525

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

Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser Leu Asp Lys
 545 550 555 560

Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln Pro Gly Asp
 565 570 575

Ser Ala Thr Tyr Leu Cys Ala Val Arg Pro Leu Tyr Gly Gly Ser Tyr
 580 585 590

Ile Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His Pro Tyr Ile
 595 600 605

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
 610 615 620

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
 625 630 635 640

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
 645 650 655

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
 660 665 670

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
 675 680 685

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Gly Ser Pro Lys
 690 695 700

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
705 710 715 720

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Lys Arg Gly Arg Lys
725 730 735

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
740 745 750

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
755 760 765

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
770 775 780

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
785 790 795 800

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
805 810 815

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
820 825 830

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
835 840 845

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
850 855 860

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
865 870 875 880

Ala Leu Pro Pro Arg
885

<210> 34
<211> 967
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic

<400> 34

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu

195

200

205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
 210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
 225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
 245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Phe Trp Val Leu Val Val
 260 265 270

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
 275 280 285

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 290 295 300

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
 305 310 315 320

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg
 325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
 340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
 355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
 370 375 380

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

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

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

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

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

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

His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Ala
485 490 495

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
500 505 510

Gly Pro Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu
515 520 525

Gln Trp Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu
530 535 540

Ser Val Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp
545 550 555 560

Ser Ala Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly
565 570 575

Leu Thr Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser
580 585 590

Gly Arg Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu
595 600 605

Tyr Ile Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala
610 615 620

Val Arg Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly

625		630		635		640
Thr Ser Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val						
		645		650		655
Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe						
		660		665		670
Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp						
		675		680		685
Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe						
		690		695		700
Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys						
705		710		715		720
Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro						
		725		730		735
Ser Pro Glu Ser Ser Gly Ser Pro Lys Phe Trp Val Leu Val Val Val						
		740		745		750
Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile						
		755		760		765
Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr						
		770		775		780
Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln						
785		790		795		800
Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly						
		805		810		815
Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val						
		820		825		830
Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu						
		835		840		845

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
850 855 860

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
865 870 875 880

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
885 890 895

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
900 905 910

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
915 920 925

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
930 935 940

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
945 950 955 960

Met Gln Ala Leu Pro Pro Arg
965

<210> 35
<211> 883
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 35

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Phe Trp Val Leu Val Val

260

265

270

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
 275 280 285

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 290 295 300

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
 305 310 315 320

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
 325 330 335

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 340 345 350

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 355 360 365

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 370 375 380

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

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 405 410 415

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 420 425 430

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys
 435 440 445

Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu Gly Leu Leu
 465 470 475 480

Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys Gln Glu Val Thr
485 490 495

Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu Asn Leu Val Leu
500 505 510

Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu Gln Trp Phe Arg
515 520 525

Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu Ile Gln Ser Ser
530 535 540

Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser Leu Asp Lys Ser
545 550 555 560

Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln Pro Gly Asp Ser
565 570 575

Ala Thr Tyr Leu Cys Ala Val Arg Pro Leu Tyr Gly Gly Ser Tyr Ile
580 585 590

Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His Pro Tyr Ile Gln
595 600 605

Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp
610 615 620

Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser
625 630 635 640

Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp
645 650 655

Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn
660 665 670

Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro
675 680 685

Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Gly Ser Pro Lys Cys

690

695

700

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
 705 710 715 720

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
 725 730 735

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 740 745 750

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
 755 760 765

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 770 775 780

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 785 790 795 800

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 805 810 815

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
 820 825 830

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 835 840 845

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 850 855 860

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 865 870 875 880

Pro Pro Arg

<210> 36

<211> 771

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 36

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Phe Trp Val Leu Val Val
260 265 270

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
275 280 285

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
290 295 300

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
305 310 315 320

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
325 330 335

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
340 345 350

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
355 360 365

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
370 375 380

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

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg

405

410

415

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 420 425 430

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys
 435 440 445

Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu Gly Leu Leu
 465 470 475 480

Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys Gln Glu Val Thr
 485 490 495

Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu Asn Leu Val Leu
 500 505 510

Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu Gln Trp Phe Arg
 515 520 525

Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu Ile Gln Ser Ser
 530 535 540

Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser Leu Asp Lys Ser
 545 550 555 560

Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln Pro Gly Asp Ser
 565 570 575

Ala Thr Tyr Leu Cys Ala Val Arg Pro Leu Tyr Gly Gly Ser Tyr Ile
 580 585 590

Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His Pro Tyr Ile Gln
 595 600 605

Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp
 610 615 620

Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser
625 630 635 640

Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp
645 650 655

Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn
660 665 670

Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro
675 680 685

Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Gly Ser Pro Lys Cys
690 695 700

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
705 710 715 720

Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
725 730 735

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
740 745 750

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
755 760 765

Cys Glu Leu
770

<210> 37
<211> 884
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 37

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu

225		230		235		240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu						
		245		250		255
Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Phe Trp Val Leu Val Val						
		260		265		270
Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe						
		275		280		285
Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp						
		290		295		300
Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr						
305		310		315		320
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val						
		325		330		335
Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn						
		340		345		350
Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val						
		355		360		365
Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg						
		370		375		380
Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys						
385		390		395		400
Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg						
		405		410		415
Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys						
		420		425		430
Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys						
		435		440		445

Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
450 455 460

Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu Gly Leu Leu
465 470 475 480

Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys Gln Glu Val Thr
485 490 495

Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu Asn Leu Val Leu
500 505 510

Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu Gln Trp Phe Arg
515 520 525

Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu Ile Gln Ser Ser
530 535 540

Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser Leu Asp Lys Ser
545 550 555 560

Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln Pro Gly Asp Ser
565 570 575

Ala Thr Tyr Leu Cys Ala Val Arg Pro Leu Tyr Gly Gly Ser Tyr Ile
580 585 590

Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His Pro Tyr Ile Gln
595 600 605

Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp
610 615 620

Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser
625 630 635 640

Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp
645 650 655

Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn

660

665

670

Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro
 675 680 685

Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Gly Ser Pro Lys Phe
 690 695 700

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
 705 710 715 720

Val Thr Val Ala Phe Ile Ile Phe Trp Val Lys Arg Gly Arg Lys Lys
 725 730 735

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
 740 745 750

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly
 755 760 765

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 770 775 780

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 785 790 795 800

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 805 810 815

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 820 825 830

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 835 840 845

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 850 855 860

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 865 870 875 880

Leu Pro Pro Arg

<210> 38

<211> 882

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 38

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Cys Asp Ile Tyr Ile Trp
260 265 270

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
275 280 285

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
290 295 300

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
305 310 315 320

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
325 330 335

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
340 345 350

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
355 360 365

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg

370

375

380

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
 385 390 395 400

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
 405 410 415

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 420 425 430

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Lys Arg
 435 440 445

Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp
 450 455 460

Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu Leu Gly Leu Leu Ile
 465 470 475 480

Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys Gln Glu Val Thr Gln
 485 490 495

Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu Asn Leu Val Leu Asn
 500 505 510

Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu Gln Trp Phe Arg Gln
 515 520 525

Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu Ile Gln Ser Ser Gln
 530 535 540

Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser Leu Asp Lys Ser Ser
 545 550 555 560

Gly Arg Ser Thr Leu Tyr Ile Ala Ala Ser Gln Pro Gly Asp Ser Ala
 565 570 575

Thr Tyr Leu Cys Ala Val Arg Pro Leu Tyr Gly Gly Ser Tyr Ile Pro
 580 585 590

Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His Pro Tyr Ile Gln Asn
595 600 605

Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys
610 615 620

Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln
625 630 635 640

Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met
645 650 655

Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys
660 665 670

Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu
675 680 685

Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Gly Ser Pro Lys Cys Asp
690 695 700

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
705 710 715 720

Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu
725 730 735

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
740 745 750

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
755 760 765

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
770 775 780

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
785 790 795 800

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

805

810

815

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 820 825 830

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 835 840 845

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 850 855 860

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 865 870 875 880

Pro Arg

<210> 39

<211> 965

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 39

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
 50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
 65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg

85

90

95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
 130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
 145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
 165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
 180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
 195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
 210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
 225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
 245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Cys Asp Ile Tyr Ile Trp
 260 265 270

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
 275 280 285

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
 290 295 300

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
305 310 315 320

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Ser Lys
325 330 335

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

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

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

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

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

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

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

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

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

Gln Ala Leu Pro Pro Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn
485 490 495

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
500 505 510

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp

515

520

525

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

Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
 545 550 555 560

Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
 565 570 575

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
 580 585 590

Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
 595 600 605

Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg
 610 615 620

Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser
 625 630 635 640

Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
 645 650 655

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
 660 665 670

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
 675 680 685

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
 690 695 700

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
 705 710 715 720

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
 725 730 735

Glu Ser Ser Gly Ser Pro Lys Cys Asp Ile Tyr Ile Trp Ala Pro Leu
740 745 750

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
755 760 765

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
770 775 780

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
785 790 795 800

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Lys Arg Gly Arg Lys
805 810 815

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
820 825 830

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
835 840 845

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
850 855 860

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
865 870 875 880

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
885 890 895

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
900 905 910

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
915 920 925

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
930 935 940

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

945	950	955	960
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Ala Leu Pro Pro Arg
965

<210> 40
 <211> 1059
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic

<400> 40

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
 50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
 65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
 85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
 130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr

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

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
370 375 380

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
385 390 395 400

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

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
420 425 430

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
435 440 445

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
450 455 460

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

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
485 490 495

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
500 505 510

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
515 520 525

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

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
545 550 555 560

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
565 570 575

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

580

585

590

Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala
 595 600 605

Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
 610 615 620

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
 625 630 635 640

Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
 645 650 655

Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg
 660 665 670

Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser
 675 680 685

Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
 690 695 700

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
 705 710 715 720

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
 725 730 735

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
 740 745 750

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
 755 760 765

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
 770 775 780

Glu Ser Ser Gly Ser Pro Lys Ala Lys Pro Thr Thr Thr Pro Ala Pro
 785 790 795 800

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
805 810 815

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
820 825 830

Gly Leu Asp Phe Ala Pro Arg Lys Ile Glu Val Met Tyr Pro Pro Pro
835 840 845

Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
850 855 860

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
865 870 875 880

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
885 890 895

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
900 905 910

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
915 920 925

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
930 935 940

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
945 950 955 960

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
965 970 975

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
980 985 990

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
995 1000 1005

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met

1010

1015

1020

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 1025 1030 1035

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
 1040 1045 1050

Gln Ala Leu Pro Pro Arg
 1055

<210> 41

<211> 859

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 41

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
 50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
 65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
 85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 100 105 110

Ser Tyr Val Gly Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg

115

120

125

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
 130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
 145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
 165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
 180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
 195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
 210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
 225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
 245 250 255

Ala Trp Gly Arg Ala Asp Gly Ser Pro Lys Ala Lys Pro Thr Thr Thr
 260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
 275 280 285

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
 290 295 300

His Thr Arg Gly Leu Asp Phe Ala Pro Arg Lys Ile Glu Val Met Tyr
 305 310 315 320

Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His
 325 330 335

Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser
340 345 350

Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
355 360 365

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
370 375 380

Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg
385 390 395 400

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

Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
420 425 430

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
435 440 445

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
450 455 460

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

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
485 490 495

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
500 505 510

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
515 520 525

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

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro

545		550		555		560									
Met	Glu	Thr	Leu	Leu	Gly	Leu	Leu	Ile	Leu	Trp	Leu	Gln	Leu	Gln	Trp
			565					570					575		
Val	Ser	Ser	Lys	Gln	Glu	Val	Thr	Gln	Ile	Pro	Ala	Ala	Leu	Ser	Val
			580					585					590		
Pro	Glu	Gly	Glu	Asn	Leu	Val	Leu	Asn	Cys	Ser	Phe	Thr	Asp	Ser	Ala
		595					600					605			
Ile	Tyr	Asn	Leu	Gln	Trp	Phe	Arg	Gln	Asp	Pro	Gly	Lys	Gly	Leu	Thr
	610					615					620				
Ser	Leu	Leu	Leu	Ile	Gln	Ser	Ser	Gln	Arg	Glu	Gln	Thr	Ser	Gly	Arg
625					630					635					640
Leu	Asn	Ala	Ser	Leu	Asp	Lys	Ser	Ser	Gly	Arg	Ser	Thr	Leu	Tyr	Ile
				645					650					655	
Ala	Ala	Ser	Gln	Pro	Gly	Asp	Ser	Ala	Thr	Tyr	Leu	Cys	Ala	Val	Arg
			660					665					670		
Pro	Leu	Tyr	Gly	Gly	Ser	Tyr	Ile	Pro	Thr	Phe	Gly	Arg	Gly	Thr	Ser
		675					680					685			
Leu	Ile	Val	His	Pro	Tyr	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln
	690					695					700				
Leu	Arg	Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp
705					710					715					720
Phe	Asp	Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr
			725					730						735	
Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser
		740						745					750		
Asn	Ser	Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn
		755					760					765			

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
770 775 780

Glu Ser Ser Gly Ser Pro Lys Cys Asp Ile Tyr Ile Trp Ala Pro Leu
785 790 795 800

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
805 810 815

Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
820 825 830

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
835 840 845

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
850 855

<210> 42
<211> 120
<212> DNA
<213> Homo sapiens

<400> 42
aaaattgaag ttatgtatcc tcctccttac ctagacaatg agaagagcaa tggaaccatt 60
atccatgtga aagggaaca cttttgtcca agtcccctat tccccggacc ttctaagccc 120

<210> 43
<211> 120
<212> DNA
<213> Homo sapiens

<400> 43
aagatcgagg taatgtaccc accgccctat cttgataacg aaaaatctaa cggtacaata 60
attcacgtca agggcaagca tttgtgccct tccccgttgt tccccggccc aagcaaaccg 120

<210> 44
<211> 81
<212> DNA
<213> Homo sapiens

<400> 44
ttttgggtgc tggtggtggt tggtggagtc ctggcttgct atagcttgct agtaacagtg 60

gcctttatta ttttctgggt g 81

<210> 45
<211> 81
<212> DNA
<213> Homo sapiens

<400> 45
ttctgggttc tcgtcgtcgt gggaggtgtg ttagcatgtt actctctctt ggttactgtc 60
gctttcataa tcttttgggt c 81

<210> 46
<211> 123
<212> DNA
<213> Homo sapiens

<400> 46
aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60
gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
tcc 123

<210> 47
<211> 123
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 47
cgctcaaaac gctctcgctt gttacattcc gattatatga atatgacacc taggagacct 60
ggcccgacta ggaaacacta tcaaccttac gcacctcca gagattttgc tgcttacagg 120
agt 123

<210> 48
<211> 126
<212> DNA
<213> Homo sapiens

<400> 48
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 49
<211> 126
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic

<400> 49
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tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa	2220
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$\langle 210 \rangle$	64
$\langle 211 \rangle$	612
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial sequence

<220>
<223> Synthetic

<400> 64

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
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Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
20 25 30

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
290 295 300

Lys Arg Lys Asp Ser Arg Gly Ala Lys Arg Ser Gly Ser Gly Ala Thr
305 310 315 320

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
325 330 335

Pro Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln
340 345 350

Trp Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser

355

360

365

Val Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser
 370 375 380

Ala Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu
 385 390 395 400

Thr Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly
 405 410 415

Arg Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr
 420 425 430

Ile Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val
 435 440 445

Arg Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr
 450 455 460

Ser Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr
 465 470 475 480

Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
 485 490 495

Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
 500 505 510

Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys
 515 520 525

Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
 530 535 540

Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
 545 550 555 560

Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
 565 570 575

Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile
580 585 590

Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
595 600 605

Trp Ser Ser Arg
610

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<211> 1839
<212> DNA
<213> Artificial sequence

<220>
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<400> 65
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cagtgtgccc aggatatgaa ccatgaatac atgtcctggt atcgacaaga cccaggcatg 180
gggctgaggc tgattcatta ctgagttggt gctggtatca ctgaccaagg agaagtcccc 240
aatggctaca atgtctccag atcaaccaca gaggatttcc cgctcaggct gctgtcggct 300
gctccctccc agacatctgt gtacttctgt gccagcagtt acgtcgggaa caccggggag 360
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cccgaggctg ctgtgtttga gccatcagaa gcagagatct cccacacca aaaggccaca 480
ctggtgtgcc tggccacagg cttctacccc gaccacgtgg agctgagctg gtgggtgaat 540
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aactttcaaa acctgtcagt gattgggttc cgaatcctcc tcctgaaagt ggccgggttt 1800
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<210> 66
<211> 48
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 66

Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu
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Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys
20 25 30

Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Arg
35 40 45

<210> 67

<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 67

Ala Lys Arg Ser Gly Ser Gly
1 5

<210> 68
<211> 49
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 68

Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr
1 5 10 15

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
20 25 30

Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg
35 40 45

Gly

<210> 69
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 69

Gly Ser Pro Lys
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<210> 70

<211> 2
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 70

Pro Arg
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<210> 71
<211> 6
<212> DNA
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<220>
<223> Synthetic

<400> 71

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6

<210> 72
<211> 14
<212> DNA
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<220>
<223> Synthetic

<400> 72

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14

<210> 73
<211> 8
<212> DNA
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<220>
<223> Synthetic

<400> 73

gcggccgc

8