

SEQUENCE LISTING

<110> The Regents of the University of California

<120> Notch Receptors With Hinge Domain

<130> 048536-654001WO

<140> Herewith

<141> Herewith

<150> US 62/905,251

<151> 2019-09-24

<150> US 62/905,263

<151> 2019-09-24

<160> 80

<170> PatentIn version 3.5

<210> 1

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 1

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	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asp
			20					25					30		

Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp
		35					40					45			

Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr	Leu
	50					55					60				

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

His	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
				85					90					95	

Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu
			100					105					110		

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
180 185 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
195 200 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
210 215 220

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

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
245 250 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
260 265 270

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

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
290 295 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Met
305 310 315 320

Tyr Val Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly
325 330 335

Val Leu Leu Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser Ser Ile

340	345	350
Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys		
355	360	365
Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg		
370	375	380
Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr		
385	390	395
Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile		
405	410	415
Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln		
420	425	430
Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn		
435	440	445
Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro		
450	455	460
Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu		
465	470	475
Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly		
485	490	495
Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu		
500	505	510
Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu		
515	520	525
Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp		
530	535	540
Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser		
545	550	555

<210> 2
 <211> 538
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 2

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
50 55 60

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

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
85 90 95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
100 105 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
180 185 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
195 200 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
 210 215 220

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

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
 245 250 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 260 265 270

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

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Phe Met Tyr Val
 290 295 300

Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu
 305 310 315 320

Leu Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser Ser Ile Glu Gln
 325 330 335

Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys Glu Lys
 340 345 350

Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg Tyr Ser
 355 360 365

Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr Glu Val
 370 375 380

Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro
 385 390 395 400

Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile
 405 410 415

Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp
 420 425 430

Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr

435 440 445
 Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser
 450 455 460
 Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser
 465 470 475 480
 Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
 485 490 495
 Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
 500 505 510
 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
 515 520 525
 Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
 530 535

 <210> 3
 <211> 550
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic construct

 <400> 3

 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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
 20 25 30

 Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
 35 40 45

 Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
 50 55 60

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

 His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

85

90

95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
100 105 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
180 185 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
195 200 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
210 215 220

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

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
245 250 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
260 265 270

Ser Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
275 280 285

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
290 295 300

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

Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser Arg Lys
325 330 335

Arg Arg Arg Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile
340 345 350

Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala
355 360 365

Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys
370 375 380

Arg Ser Pro Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu
385 390 395 400

Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu
405 410 415

Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu
420 425 430

Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp
435 440 445

Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His
450 455 460

Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln
465 470 475 480

Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser Gly Gly Ser Gly
485 490 495

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp
500 505 510

Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp
515 520 525

Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp
530 535 540

Leu Asp Met Leu Gly Ser

545

550

<210> 4
 <211> 538
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 4

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
 20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
 35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
 50 55 60

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

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 85 90 95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
 100 105 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
 115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
 145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
 165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln

180	185	190
Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu		
195	200	205
Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys		
210	215	220
Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr		
225	230	235
Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly		
	245	250
		255
Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser		
	260	265
		270
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		
	275	280
		285
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Phe Met Tyr Val		
290	295	300
Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu		
305	310	315
Leu Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser Ser Ile Glu Gln		
	325	330
		335
Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys Glu Lys		
	340	345
		350
Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg Tyr Ser		
	355	360
		365
Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr Glu Val		
370	375	380
Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro		
385	390	395
		400
Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile		
	405	410
		415

Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp
420 425 430

Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr
435 440 445

Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser
450 455 460

Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser
465 470 475 480

Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
485 490 495

Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
500 505 510

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
515 520 525

Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535

<210> 5
<211> 697
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
50 55 60

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

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
85 90 95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
100 105 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
180 185 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
195 200 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
210 215 220

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

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
245 250 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
260 265 270

Ser Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys
275 280 285

His Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser

290					295					300					
Gln	Asn	Thr	Val	Cys	Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val
305					310					315					320
Val	Ser	Ser	Lys	Pro	Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser
				325					330					335	
Gly	Ser	Glu	Arg	Lys	Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	Thr	Val	Cys
			340					345					350		
Arg	Cys	Arg	Ala	Gly	Thr	Gln	Pro	Leu	Asp	Ser	Tyr	Lys	Pro	Gly	Val
		355					360					365			
Asp	Cys	Ala	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Asp	Asn	Gln
	370						375				380				
Ala	Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu	Ala	Gly	Lys	His	Thr	Leu
385						390					395				400
Gln	Pro	Ala	Ser	Asn	Ser	Ser	Asp	Ala	Ile	Cys	Glu	Asp	Arg	Asp	Pro
				405					410					415	
Pro	Ala	Thr	Gln	Pro	Gln	Glu	Thr	Gln	Gly	Pro	Pro	Ala	Arg	Pro	Ile
			420					425					430		
Thr	Val	Gln	Pro	Thr	Glu	Ala	Trp	Pro	Arg	Thr	Ser	Gln	Gly	Pro	Ser
		435					440					445			
Thr	Arg	Pro	Val	Glu	Val	Pro	Gly	Gly	Arg	Ala	Phe	Met	Tyr	Val	Ala
	450					455					460				
Ala	Ala	Ala	Phe	Val	Leu	Leu	Phe	Phe	Val	Gly	Cys	Gly	Val	Leu	Leu
465						470					475				480
Ser	Arg	Lys	Arg	Arg	Arg	Met	Lys	Leu	Leu	Ser	Ser	Ile	Glu	Gln	Ala
				485					490					495	
Cys	Asp	Ile	Cys	Arg	Leu	Lys	Lys	Leu	Lys	Cys	Ser	Lys	Glu	Lys	Pro
			500					505					510		
Lys	Cys	Ala	Lys	Cys	Leu	Lys	Asn	Asn	Trp	Glu	Cys	Arg	Tyr	Ser	Pro
		515					520					525			

Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr Glu Val Glu
530 535 540

Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg
545 550 555 560

Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile Lys
565 570 575

Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp Ala
580 585 590

Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr Leu
595 600 605

Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn
610 615 620

Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser Gly
625 630 635 640

Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
645 650 655

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp
660 665 670

Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp
675 680 685

Asp Phe Asp Leu Asp Met Leu Gly Ser
690 695

<210> 6
<211> 539
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 6

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

His Ala Ala Arg Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
 20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
 35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
 50 55 60

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

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 85 90 95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
 100 105 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
 115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
 145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
 165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
 180 185 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
 195 200 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
 210 215 220

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

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly

245								250				255				
Ser	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	
			260						265				270			
Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	
			275				280					285				
Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Phe	Met	Tyr	Val	
	290					295					300					
Ala	Ala	Ala	Ala	Phe	Val	Leu	Leu	Phe	Phe	Val	Gly	Cys	Gly	Val	Leu	
305					310					315					320	
Leu	Ser	Lys	Arg	Lys	Arg	Lys	His	Met	Lys	Leu	Leu	Ser	Ser	Ile	Glu	
				325					330					335		
Gln	Ala	Cys	Asp	Ile	Cys	Arg	Leu	Lys	Lys	Leu	Lys	Cys	Ser	Lys	Glu	
			340						345				350			
Lys	Pro	Lys	Cys	Ala	Lys	Cys	Leu	Lys	Asn	Asn	Trp	Glu	Cys	Arg	Tyr	
		355					360					365				
Ser	Pro	Lys	Thr	Lys	Arg	Ser	Pro	Leu	Thr	Arg	Ala	His	Leu	Thr	Glu	
	370					375					380					
Val	Glu	Ser	Arg	Leu	Glu	Arg	Leu	Glu	Gln	Leu	Phe	Leu	Leu	Ile	Phe	
385					390					395					400	
Pro	Arg	Glu	Asp	Leu	Asp	Met	Ile	Leu	Lys	Met	Asp	Ser	Leu	Gln	Asp	
				405					410					415		
Ile	Lys	Ala	Leu	Leu	Thr	Gly	Leu	Phe	Val	Gln	Asp	Asn	Val	Asn	Lys	
			420						425				430			
Asp	Ala	Val	Thr	Asp	Arg	Leu	Ala	Ser	Val	Glu	Thr	Asp	Met	Pro	Leu	
		435					440					445				
Thr	Leu	Arg	Gln	His	Arg	Ile	Ser	Ala	Thr	Ser	Ser	Ser	Glu	Glu	Ser	
	450					455					460					
Ser	Asn	Lys	Gly	Gln	Arg	Gln	Leu	Thr	Val	Ser	Ala	Ala	Ala	Gly	Gly	
465					470					475					480	

Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp
485 490 495

Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly
500 505 510

Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala
515 520 525

Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535

<210> 7
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 7

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gln
20 25 30

Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
35 40 45

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
50 55 60

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
65 70 75 80

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
85 90 95

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
100 105 110

Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
115 120 125

Lys Glu Gly Asp Ser Ser Arg Trp Ser Tyr Asp Leu Trp Gly Arg Gly
130 135 140

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

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

Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser
180 185 190

Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro
195 200 205

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

Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
225 230 235 240

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
245 250 255

Ser Ser Tyr Thr Ile Ala Ser Thr Leu Val Val Phe Gly Gly Gly Thr
260 265 270

Lys Leu Thr Val Leu Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
305 310 315 320

Cys Gly Val Leu Leu Ser Arg Lys Arg Arg Met Lys Leu Leu Ser
325 330 335

Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys
340 345 350

Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu

355		360		365											
Cys	Arg	Tyr	Ser	Pro	Lys	Thr	Lys	Arg	Ser	Pro	Leu	Thr	Arg	Ala	His
370						375					380				
Leu	Thr	Glu	Val	Glu	Ser	Arg	Leu	Glu	Arg	Leu	Glu	Gln	Leu	Phe	Leu
385					390					395					400
Leu	Ile	Phe	Pro	Arg	Glu	Asp	Leu	Asp	Met	Ile	Leu	Lys	Met	Asp	Ser
				405					410					415	
Leu	Gln	Asp	Ile	Lys	Ala	Leu	Leu	Thr	Gly	Leu	Phe	Val	Gln	Asp	Asn
			420					425					430		
Val	Asn	Lys	Asp	Ala	Val	Thr	Asp	Arg	Leu	Ala	Ser	Val	Glu	Thr	Asp
		435					440					445			
Met	Pro	Leu	Thr	Leu	Arg	Gln	His	Arg	Ile	Ser	Ala	Thr	Ser	Ser	Ser
450						455					460				
Glu	Glu	Ser	Ser	Asn	Lys	Gly	Gln	Arg	Gln	Leu	Thr	Val	Ser	Ala	Ala
465					470					475					480
Ala	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Asp	Ala	Leu	Asp	Asp	Phe
				485					490					495	
Asp	Leu	Asp	Met	Leu	Gly	Ser	Asp	Ala	Leu	Asp	Asp	Phe	Asp	Leu	Asp
			500					505					510		
Met	Leu	Gly	Ser	Asp	Ala	Leu	Asp	Asp	Phe	Asp	Leu	Asp	Met	Leu	Gly
		515					520					525			
Ser	Asp	Ala	Leu	Asp	Asp	Phe	Asp	Leu	Asp	Met	Leu	Gly	Ser		
530						535					540				
<210>	8														
<211>	525														
<212>	PRT														
<213>	Artificial Sequence														
<220>															
<223>	Synthetic construct														
<400>	8														
Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro

1		5		10		15										
Gly	Ser	Thr	Gly	Asp	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	
			20					25					30			
Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	
		35					40					45				
Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	
	50					55					60					
Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	
65					70					75					80	
Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	
				85					90					95		
Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	
			100					105					110			
Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	
		115					120					125				
Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	
	130					135					140					
Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	
145					150					155					160	
His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	
				165					170					175		
Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	
			180					185					190			
Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	
		195					200					205				
Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	
	210					215					220					
Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	
225					230					235					240	

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 245 250 255

Glu Leu Tyr Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala
 260 265 270

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Phe
 275 280 285

Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys
 290 295 300

Gly Val Leu Leu Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser Ser
 305 310 315 320

Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser
 325 330 335

Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys
 340 345 350

Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu
 355 360 365

Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu
 370 375 380

Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu
 385 390 395 400

Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val
 405 410 415

Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met
 420 425 430

Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu
 435 440 445

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

Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp

130		135		140
Gly 145	Gly 145	Gly 145	Ser 145	Gly 145
		Gly 150	Gly 150	Gly 150
			Ser 155	Glu 155
			Val 155	Lys 155
			Leu 160	Gln 160
			Glu 160	Ser 160
Gly 165	Pro 165	Gly 165	Leu 165	Val 165
		Ala 170	Pro 170	Ser 170
			Gln 170	Ser 170
			Leu 175	Ser 175
			Val 175	Thr 175
			Cys 175	Thr 175
Val 180	Ser 180	Gly 180	Val 180	Ser 180
		Leu 185	Pro 185	Asp 185
			Tyr 185	Gly 185
			Val 190	Ser 190
			Trp 190	Ile 190
			Arg 190	Gln 190
Pro 195	Pro 195	Arg 195	Lys 195	Gly 195
			Leu 200	Glu 200
			Trp 200	Leu 200
			Gly 205	Val 205
			Ile 205	Trp 205
			Gly 210	Ser 210
			Glu 210	Leu 210
			Thr 210	Ile 210
			Lys 210	
Asp 225	Asn 225	Ser 225	Lys 225	Ser 225
		Gln 230	Val 230	Phe 230
			Leu 235	Lys 235
			Met 235	Asn 235
			Ser 240	Leu 240
			Gln 240	Thr 240
Asp 245	Asp 245	Thr 245	Ala 245	Ile 245
			Tyr 250	Tyr 250
			Cys 250	Ala 250
			Lys 250	His 250
			Tyr 255	Tyr 255
			Tyr 255	Gly 255
			Gly 255	
Ser 260	Tyr 260	Ala 260	Met 260	Asp 260
			Tyr 265	Trp 265
			Gly 265	Gln 265
			Gly 270	Thr 270
			Ser 270	Val 270
			Thr 270	Val 270
			Ser 270	

Ser

<210> 10
 <211> 277
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 10

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

His 20	Ala 20	Ala 20	Arg 20	Pro 20	Glu 25	Gln 25	Lys 25	Leu 25	Ile 25	Ser 30	Glu 30	Glu 30	Asp 30	Leu 30	Gln 30
--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------

Val 30	Gln 30	Leu 30	Gln 30	Gln 30	Ser 30	Gly 30	Gly 30	Gly 30	Leu 30	Val 30	Lys 30	Pro 30	Gly 30	Gly 30	Ser 30
--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------

35					40					45					
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ala
50					55					60					
Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala
65					70					75					80
Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
				85					90					95	
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu
			100					105					110		
Gln	Met	Asp	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
		115					120					125			
Lys	Glu	Gly	Asp	Ser	Ser	Arg	Trp	Ser	Tyr	Asp	Leu	Trp	Gly	Arg	Gly
	130					135					140				
Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
145					150					155					160
Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ser	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val
				165					170					175	
Ser	Gly	Ser	Pro	Gly	Gln	Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser
			180					185					190		
Ser	Asp	Val	Gly	Gly	Tyr	Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro
		195					200					205			
Gly	Lys	Ala	Pro	Lys	Val	Met	Ile	Tyr	Asp	Val	Thr	Asn	Arg	Pro	Ser
	210					215					220				
Gly	Val	Ser	Asn	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser
225					230					235					240
Leu	Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
				245					250					255	
Ser	Ser	Tyr	Thr	Ile	Ala	Ser	Thr	Leu	Val	Val	Phe	Gly	Gly	Gly	Thr
			260					265					270		

Lys Leu Thr Val Leu
275

<210> 11
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 11

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

Gly Ser Thr Gly Asp Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly
20 25 30

Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
35 40 45

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

Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
65 70 75 80

Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr
85 90 95

Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
100 105 110

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

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

Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
145 150 155 160

His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
165 170 175

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

Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
195 200 205

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
210 215 220

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
225 230 235 240

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
245 250 255

Glu Leu Tyr Lys
260

<210> 12
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 12

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

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

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

<210> 13
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 13

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala

1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
20 25

<210> 14
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 14

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> 15
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 15

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
20 25

<210> 16
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 16

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His

1	5	10	15
Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln	20	25	30
Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val	35	40	45
Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly	50	55	60
Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg	65	70	75
Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp	85	90	95
Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala	100	105	110
Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln	115	120	125
Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro	130	135	140
Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr	145	150	155
Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr	165	170	175
Arg Pro Val Glu Val Pro Gly Gly Arg Ala	180	185	

<210> 17
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 17

Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly

1 5 10 15

Cys Gly Val Leu Leu Ser
20

<210> 18
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 18

Arg Lys Arg Arg Arg
1 5

<210> 19
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 19

Lys Arg Lys Arg Lys His
1 5

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

<220>
<223> Synthetic construct

<400> 20

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
1 5 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu

50		55		60
Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile				
65		70		75 80
Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu				
	85		90	95
Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala				
	100		105	110
Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser				
	115		120	125
Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu				
	130		135	140
Thr Val Ser Ala Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp				
	145		150	155 160
Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp				
	165		170	175
Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp				
	180		185	190
Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met				
	195		200	205
Leu Gly Ser				
	210			

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

<220>
 <223> Synthetic construct

<400> 21

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

<210> 22
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 22

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 23
 ggagcactgt cctccgaacg
 20

<210> 24
 <211> 537
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 24

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
 20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
 35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
 50 55 60

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

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

Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu
 305 310 315 320

Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser Ser Ile Glu Gln Ala
 325 330 335

Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro
 340 345 350

Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro
 355 360 365

Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr Glu Val Glu
 370 375 380

Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg
 385 390 395 400

Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile Lys
 405 410 415

Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp Ala
 420 425 430

Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr Leu
 435 440 445

Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn
 450 455 460

Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser Gly
 465 470 475 480

Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
 485 490 495

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp
 500 505 510

Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp
 515 520 525

Asp Phe Asp Leu Asp Met Leu Gly Ser
 530 535

<210> 25
 <211> 529
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 25

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
 20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
 35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
 50 55 60

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

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 85 90 95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
 100 105 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
 115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
 145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
 165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
 180 185 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
 195 200 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
 210 215 220

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

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
 245 250 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 260 265 270

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

Ala Cys Asp Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe
 290 295 300

Phe Val Gly Cys Gly Val Leu Leu Ser Arg Lys Arg Arg Arg Met Lys
 305 310 315 320

Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys
 325 330 335

Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn
 340 345 350

Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr
 355 360 365

Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln
 370 375 380

Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys
 385 390 395 400

Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val
 405 410 415

Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val
420 425 430

Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr
435 440 445

Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val
450 455 460

Ser Ala Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu
465 470 475 480

Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe
485 490 495

Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp
500 505 510

Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly
515 520 525

Ser

<210> 26
<211> 530
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 26

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
50 55 60

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

Phe Phe Val Gly Cys Gly Val Leu Leu Ser Arg Lys Arg Arg Arg Met
 305 310 315 320

Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys
 325 330 335

Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys
 340 345 350

Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu
 355 360 365

Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu
 370 375 380

Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu
 385 390 395 400

Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe
 405 410 415

Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser
 420 425 430

Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala
 435 440 445

Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr
 450 455 460

Val Ser Ala Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala
 465 470 475 480

Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp
 485 490 495

Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
 500 505 510

Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
 515 520 525

Gly Ser
530

<210> 27
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 27

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gln
20 25 30

Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
35 40 45

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
50 55 60

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
65 70 75 80

Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
85 90 95

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
100 105 110

Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
115 120 125

Lys Glu Gly Asp Ser Ser Arg Trp Ser Tyr Asp Leu Trp Gly Arg Gly
130 135 140

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

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

Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser
180 185 190

Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro
195 200 205

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

Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser
225 230 235 240

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
245 250 255

Ser Ser Tyr Thr Ile Ala Ser Thr Leu Val Val Phe Gly Gly Gly Thr
260 265 270

Lys Leu Thr Val Leu Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
305 310 315 320

Cys Gly Val Leu Leu Ser Lys Arg Lys Arg Lys His Met Lys Leu Leu
325 330 335

Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys
340 345 350

Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp
355 360 365

Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala
370 375 380

His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe
385 390 395 400

Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp
405 410 415

Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp
420 425 430

Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr
435 440 445

Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser
450 455 460

Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala
465 470 475 480

Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp
485 490 495

Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
500 505 510

Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
515 520 525

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535 540

<210> 28
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 28

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

His Ala Ala Arg Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gln
20 25 30

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
35 40 45

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Pro Asp Tyr Tyr
50 55 60

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

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 290 295 300

Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
 305 310 315 320

Cys Gly Val Leu Leu Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser
 325 330 335

Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys
 340 345 350

Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu
 355 360 365

Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His
 370 375 380

Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu
 385 390 395 400

Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser
 405 410 415

Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn
 420 425 430

Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp
 435 440 445

Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser
 450 455 460

Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala
 465 470 475 480

Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe
 485 490 495

Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp
 500 505 510

Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly
 515 520 525

Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535 540

<210> 29
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 29

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gln
20 25 30

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
35 40 45

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Pro Asp Tyr Tyr
50 55 60

Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
65 70 75 80

Trp Ile Tyr Phe Ala Ser Gly Asn Ser Glu Tyr Asn Gln Lys Phe Thr
85 90 95

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr Met
100 105 110

Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala
115 120 125

Ser Leu Tyr Asp Tyr Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
130 135 140

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu
165 170 175

Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln
180 185 190

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
195 200 205

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg
210 215 220

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

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

Tyr Cys Ser Gln Ser Ser Ile Tyr Pro Trp Thr Phe Gly Gln Gly Thr
260 265 270

Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
275 280 285

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
305 310 315 320

Cys Gly Val Leu Leu Ser Lys Arg Lys Arg Lys His Met Lys Leu Leu
325 330 335

Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys
340 345 350

Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp
355 360 365

Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala
370 375 380

His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe
385 390 395 400

Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp
405 410 415

Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp
420 425 430

Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr
435 440 445

Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser
450 455 460

Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala
465 470 475 480

Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp
485 490 495

Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
500 505 510

Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
515 520 525

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535 540

<210> 30
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 30

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

His Ala Ala Arg Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
35 40 45

Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala	Val
50						55					60				
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
65					70					75					80
Ser	Ala	Ser	Phe	Leu	Tyr	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
				85					90					95	
Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu
			100					105					110		
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro	Thr
		115					120					125			
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Gly	Ser	Thr	Ser
	130					135					140				
Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Glu	Val	Gln	Leu	Val
145					150					155				160	
Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser
				165					170					175	
Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	Ile	His	Trp	Val
			180					185					190		
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Arg	Ile	Tyr	Pro
		195					200					205			
Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr
	210					215					220				
Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser
225					230					235					240
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly
				245					250					255	
Asp	Gly	Phe	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
			260					265					270		
Val	Ser	Ser	Gly	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro
		275					280					285			

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 290 295 300

Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
 305 310 315 320

Cys Gly Val Leu Leu Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser
 325 330 335

Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys
 340 345 350

Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu
 355 360 365

Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His
 370 375 380

Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu
 385 390 395 400

Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser
 405 410 415

Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn
 420 425 430

Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp
 435 440 445

Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser
 450 455 460

Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala
 465 470 475 480

Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe
 485 490 495

Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp
 500 505 510

Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly
515 520 525

Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535 540

<210> 31
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 31

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
35 40 45

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

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
65 70 75 80

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
85 90 95

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
100 105 110

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
115 120 125

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly Ser Thr Ser
130 135 140

Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Glu Val Gln Leu Val
145 150 155 160

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
165 170 175

Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val
180 185 190

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro
195 200 205

Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
210 215 220

Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser
225 230 235 240

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

Asp Gly Phe Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr
260 265 270

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

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Phe Met Tyr Val Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
305 310 315 320

Cys Gly Val Leu Leu Ser Lys Arg Lys Arg Lys His Met Lys Leu Leu
325 330 335

Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys
340 345 350

Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp
355 360 365

Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala
370 375 380

His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe
385 390 395 400

Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp
405 410 415

Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp
420 425 430

Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr
435 440 445

Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser
450 455 460

Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala
465 470 475 480

Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp
485 490 495

Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
500 505 510

Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
515 520 525

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535 540

<210> 32
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 32

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
35 40 45

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

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 290 295 300

Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
 305 310 315 320

Cys Gly Val Leu Leu Ser Arg Lys Arg Arg Arg Met Lys Leu Leu Ser
 325 330 335

Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys
 340 345 350

Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu
 355 360 365

Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His
 370 375 380

Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu
 385 390 395 400

Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser
 405 410 415

Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn
 420 425 430

Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp
 435 440 445

Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser
 450 455 460

Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala
 465 470 475 480

Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe
 485 490 495

Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp
 500 505 510

Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly
515 520 525

Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535 540

<210> 33
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 33

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
35 40 45

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

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
65 70 75 80

Ser Ala Ser Phe Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
85 90 95

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
100 105 110

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
115 120 125

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly Ser Thr Ser
130 135 140

Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Glu Val Gln Leu Val
145 150 155 160

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
165 170 175

Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val
180 185 190

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro
195 200 205

Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
210 215 220

Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser
225 230 235 240

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

Asp Gly Phe Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr
260 265 270

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

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
290 295 300

Phe Met Tyr Val Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly
305 310 315 320

Cys Gly Val Leu Leu Ser Lys Arg Lys Arg Lys His Met Lys Leu Leu
325 330 335

Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys
340 345 350

Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp
355 360 365

Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala
370 375 380

His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe
 385 390 395 400

Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp
 405 410 415

Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp
 420 425 430

Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr
 435 440 445

Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser
 450 455 460

Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala
 465 470 475 480

Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp
 485 490 495

Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu
 500 505 510

Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
 515 520 525

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
 530 535 540

<210> 34
 <211> 416
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 34

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 Asp Tyr Lys Asp Asp Asp Asp Lys Glu Val Gln
 20 25 30

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 35 40 45

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
 50 55 60

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
 65 70 75 80

Ser Gly Ser Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg
 85 90 95

Phe Thr Ile Ser Arg Asp Ile Ser Lys Asn Thr Leu Tyr Leu Gln Met
 100 105 110

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Glu
 115 120 125

Gly Thr Gly Ala Asn Ser Ser Leu Ala Asp Tyr Arg Gly Gln Gly Thr
 130 135 140

Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
 145 150 155 160

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
 165 170 175

Cys Phe Met Tyr Val Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val
 180 185 190

Gly Cys Gly Val Leu Leu Ser Lys Arg Lys Arg Lys His Met Lys Leu
 195 200 205

Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu
 210 215 220

Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn
 225 230 235 240

Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg
 245 250 255

Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu
 260 265 270

Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met
275 280 285

Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln
290 295 300

Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu
305 310 315 320

Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser
325 330 335

Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser
340 345 350

Ala Ala Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp
355 360 365

Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp
370 375 380

Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
385 390 395 400

Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
405 410 415

<210> 35
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 35

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 Asp Tyr Lys Asp Asp Asp Asp Lys Glu Val Gln
20 25 30

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
35 40 45

59

Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro
 275 280 285

Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile
 290 295 300

Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp
 305 310 315 320

Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr
 325 330 335

Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser
 340 345 350

Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser
 355 360 365

Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
 370 375 380

Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
 385 390 395 400

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu
 405 410 415

Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
 420 425

<210> 36
 <211> 277
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 36

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gln
 20 25 30

Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	
		35					40					45				
Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Pro	Asp	Tyr	Tyr	
	50					55					60					
Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	
65					70					75					80	
Trp	Ile	Tyr	Phe	Ala	Ser	Gly	Asn	Ser	Glu	Tyr	Asn	Gln	Lys	Phe	Thr	
				85					90					95		
Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Asn	Thr	Ala	Tyr	Met	
			100					105					110			
Glu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Ala	
		115					120					125				
Ser	Leu	Tyr	Asp	Tyr	Asp	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	
	130					135					140					
Met	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
145					150					155					160	
Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	
				165					170					175		
Ser	Val	Thr	Pro	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	
			180					185					190			
Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	
		195					200					205				
Lys	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	
	210					215					220					
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
225					230					235					240	
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Ile	Tyr	
				245					250					255		
Tyr	Cys	Ser	Gln	Ser	Ser	Ile	Tyr	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	
			260					265					270			

Lys Leu Glu Ile Lys
275

<210> 37
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 37

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
35 40 45

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

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
65 70 75 80

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
85 90 95

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
100 105 110

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
115 120 125

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly Ser Thr Ser
130 135 140

Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Glu Val Gln Leu Val
145 150 155 160

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
165 170 175

Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val
180 185 190

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro
195 200 205

Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
210 215 220

Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser
225 230 235 240

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

Asp Gly Phe Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr
260 265 270

Val Ser Ser Gly Ser
275

<210> 38
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 38

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 Asp Tyr Lys Asp Asp Asp Asp Lys Glu Val Gln
20 25 30

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
35 40 45

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
50 55 60

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
65 70 75 80

Ser Gly Ser Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg
85 90 95

Phe Thr Ile Ser Arg Asp Ile Ser Lys Asn Thr Leu Tyr Leu Gln Met
100 105 110

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Glu
115 120 125

Gly Thr Gly Ala Asn Ser Ser Leu Ala Asp Tyr Arg Gly Gln Gly Thr
130 135 140

Leu Val Thr Val Ser Ser
145 150

<210> 39
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 39

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

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
20 25

<210> 40
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 40

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
1 5 10 15

Cys Asp

<210> 41
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 41

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
1 5 10 15

Ala Cys Asp

<210> 42
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 42

Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro
1 5 10 15

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

Arg Pro Glu Ala Cys
35

<210> 43
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 43

Arg Arg Arg Arg Glu His
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 44

Lys Tyr Lys Gln Lys Pro Lys
1 5

<210> 45
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 45

Lys Arg Arg Arg
1

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 46

Arg Lys Lys Arg Lys Gly Lys
1 5

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 47

Lys Gln Gln Arg Ile Lys
1 5

<210> 48
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 48

Lys Arg Lys Arg Thr His
1 5

<210> 49

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 49

Arg Arg Gln Arg Arg
1 5

<210> 50

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 50

Lys Lys Gly Arg Arg Ser Tyr Lys
1 5

<210> 51

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 51

Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg
1 5 10

<210> 52

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 52

Lys Arg Lys Arg Arg Thr Lys Thr Ile Arg Arg
1 5 10

<210> 53

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 53

Arg Lys Arg Arg Lys Glu Arg Glu Arg Ser Arg Leu Pro Arg
1 5 10

<210> 54

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 54

Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys
1 5 10

<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 55

Arg Ser Arg Lys Val Asp Lys Arg
1 5

<210> 56

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 56

Lys Arg Arg Asp Lys Glu Arg Gln Ala Lys
1 5 10

<210> 57
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 57

Lys Thr Lys Lys Gln Arg Lys Gln Met His Asn His Leu Arg
1 5 10

<210> 58
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 58

Lys Lys Ser Lys Leu Ala Lys Lys Arg Lys
1 5 10

<210> 59
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 59

His Pro Leu Arg Lys Arg Arg Lys Arg Lys Lys Lys
1 5 10

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 60

Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys
1 5 10

<210> 61
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 61

His	Arg	Arg	Cys	Lys	His	Arg	Thr	Gly	Lys
1				5					10

<210> 62
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 62

Lys	Lys	Arg	Lys	Leu	Ala	Lys	Lys	Arg	Lys
1				5					10

<210> 63
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 63

Arg	Arg	Lys	Arg	Glu	His
1				5	

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> X can be any amino acid residue

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X represents a hydrophobic residue such as Leu, Ile, Val, Phe,
 Trp, Tyr, Val, Met, and Pro

<400> 64

Pro Xaa Xaa Xaa
 1

<210> 65
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>
 <221> MISC_FEATURE
 <222> (2)..(3)
 <223> X can be any amino acid residue

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X represents a hydrophobic residue such as Leu, Ile, Val, Phe,
 Trp, Tyr, Val, Met, and Pro

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> X is either Ser or Thr

<400> 65

Pro Xaa Xaa Xaa Xaa
 1 5

<210> 66
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> X is either Leu or Gln

<400> 66

Pro Xaa Gly Met Thr Ser
1 5

<210> 67
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X is either Leu or Gln

<400> 67

Pro Xaa Gly Met Thr
1 5

<210> 68
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 68

Val Gly Arg
1

<210> 69
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 69

Glu Asn Leu Tyr Thr Gln Ser
1 5

<210> 70
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 70

Asp Asp Asp Asp Lys
1 5

<210> 71
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 71

Leu Val Pro Arg
1

<210> 72
<211> 277
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic construct

<400> 72

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
20 25 30

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
35 40 45

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

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
65 70 75 80

Ser Ala Ser Phe Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
85 90 95

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu

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

<210> 73
 <211> 543
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic construct

<400> 73

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	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asp	
			20					25					30			
Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	
		35					40					45				
Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr	Leu	
	50					55					60					
Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr	
65					70					75				80		
His	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	
				85					90					95		
Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu	
			100					105					110			
Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr	
		115					120					125				
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Thr	Gly	Gly	Gly	Gly	Ser	Gly	
	130					135					140					
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Lys	Leu	Gln	Glu	Ser	
145					150					155					160	
Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser	Gln	Ser	Leu	Ser	Val	Thr	Cys	Thr	
				165					170					175		
Val	Ser	Gly	Val	Ser	Leu	Pro	Asp	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	
			180					185					190			
Pro	Pro	Arg	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Ser	Glu	
		195					200					205				
Thr	Thr	Tyr	Tyr	Asn	Ser	Ala	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ile	Lys	
	210					215					220					
Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys	Met	Asn	Ser	Leu	Gln	Thr	
225					230					235					240	

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
 245 250 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 260 265 270

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

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Ala Thr Val Val
 290 295 300

Ile Val Val Cys Val Ser Phe Leu Val Phe Met Ile Ile Leu Gly Val
 305 310 315 320

Phe Arg Ile Arg Ala Ala His Arg Arg Thr Met Arg Met Lys Leu Leu
 325 330 335

Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys
 340 345 350

Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp
 355 360 365

Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala
 370 375 380

His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe
 385 390 395 400

Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp
 405 410 415

Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp
 420 425 430

Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr
 435 440 445

Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser
 450 455 460

Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala

115																
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Thr	Gly	Gly	Gly	Gly	Ser	Gly	
130						135					140					
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Lys	Leu	Gln	Glu	Ser	
145					150					155					160	
Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser	Gln	Ser	Leu	Ser	Val	Thr	Cys	Thr	
				165					170					175		
Val	Ser	Gly	Val	Ser	Leu	Pro	Asp	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln	
			180					185					190			
Pro	Pro	Arg	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Ser	Glu	
		195					200					205				
Thr	Thr	Tyr	Tyr	Asn	Ser	Ala	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ile	Lys	
210						215					220					
Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys	Met	Asn	Ser	Leu	Gln	Thr	
225					230					235					240	
Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Lys	His	Tyr	Tyr	Tyr	Gly	Gly	
				245					250					255		
Ser	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	
			260					265					270			
Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	
			275				280					285				
Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Ile	Ala	Thr	Val	
						295					300					
Val	Ile	Ile	Ile	Ser	Val	Cys	Met	Leu	Val	Phe	Val	Val	Ala	Met	Gly	
305					310					315					320	
Val	Tyr	Arg	Val	Arg	Ile	Ala	His	Gln	His	Met	Lys	Leu	Leu	Ser	Ser	
				325					330					335		
Ile	Glu	Gln	Ala	Cys	Asp	Ile	Cys	Arg	Leu	Lys	Lys	Leu	Lys	Cys	Ser	
			340					345					350			

Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys
355 360 365

Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu
370 375 380

Thr Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu
385 390 395 400

Ile Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu
405 410 415

Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val
420 425 430

Asn Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met
435 440 445

Pro Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu
450 455 460

Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala
465 470 475 480

Gly Gly Ser Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp
485 490 495

Leu Asp Met Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met
500 505 510

Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
515 520 525

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser
530 535 540

<210> 75
<211> 537
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic construct

<400> 75

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	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asp		
			20					25					30				
Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp		
		35					40					45					
Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Lys	Tyr	Leu		
	50					55					60						
Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr		
65					70					75				80			
His	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser		
				85					90					95			
Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu		
			100					105					110				
Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr	Thr		
		115					120					125					
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Thr	Gly	Gly	Gly	Gly	Ser	Gly		
	130					135					140						
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Lys	Leu	Gln	Glu	Ser		
145					150					155					160		
Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser	Gln	Ser	Leu	Ser	Val	Thr	Cys	Thr		
				165					170					175			
Val	Ser	Gly	Val	Ser	Leu	Pro	Asp	Tyr	Gly	Val	Ser	Trp	Ile	Arg	Gln		
			180					185					190				
Pro	Pro	Arg	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Ser	Glu		
		195					200					205					
Thr	Thr	Tyr	Tyr	Asn	Ser	Ala	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ile	Lys		
	210					215					220						
Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys	Met	Asn	Ser	Leu	Gln	Thr		

225					230						235				240
Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Lys	His	Tyr	Tyr	Tyr	Gly	Gly
				245					250					255	
Ser	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser
			260					265					270		
Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile
			275				280					285			
Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Ala	Thr	Val	Val
	290					295					300				
Ile	Val	Val	Cys	Val	Ser	Phe	Leu	Val	Phe	Met	Ile	Ile	Leu	Gly	Val
305					310					315					320
Phe	Arg	Lys	Arg	Arg	Arg	Met	Lys	Leu	Leu	Ser	Ser	Ile	Glu	Gln	Ala
				325					330					335	
Cys	Asp	Ile	Cys	Arg	Leu	Lys	Lys	Leu	Lys	Cys	Ser	Lys	Glu	Lys	Pro
			340					345					350		
Lys	Cys	Ala	Lys	Cys	Leu	Lys	Asn	Asn	Trp	Glu	Cys	Arg	Tyr	Ser	Pro
		355					360					365			
Lys	Thr	Lys	Arg	Ser	Pro	Leu	Thr	Arg	Ala	His	Leu	Thr	Glu	Val	Glu
	370					375					380				
Ser	Arg	Leu	Glu	Arg	Leu	Glu	Gln	Leu	Phe	Leu	Leu	Ile	Phe	Pro	Arg
385					390				395						400
Glu	Asp	Leu	Asp	Met	Ile	Leu	Lys	Met	Asp	Ser	Leu	Gln	Asp	Ile	Lys
				405					410					415	
Ala	Leu	Leu	Thr	Gly	Leu	Phe	Val	Gln	Asp	Asn	Val	Asn	Lys	Asp	Ala
			420					425					430		
Val	Thr	Asp	Arg	Leu	Ala	Ser	Val	Glu	Thr	Asp	Met	Pro	Leu	Thr	Leu
		435					440					445			
Arg	Gln	His	Arg	Ile	Ser	Ala	Thr	Ser	Ser	Ser	Glu	Glu	Ser	Ser	Asn
450						455					460				

Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser Gly
 465 470 475 480

Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
 485 490 495

Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp
 500 505 510

Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu Asp
 515 520 525

Asp Phe Asp Leu Asp Met Leu Gly Ser
 530 535

<210> 76
 <211> 538
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic construct

<400> 76

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 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
 20 25 30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
 35 40 45

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
 50 55 60

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

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 85 90 95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
 100 105 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
 115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
 145 150 155 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
 165 170 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
 180 185 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
 195 200 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
 210 215 220

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

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
 245 250 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 260 265 270

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

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Ile Ala Thr Val
 290 295 300

Val Ile Ile Ile Ser Val Cys Met Leu Val Phe Val Val Ala Met Gly
 305 310 315 320

Val Tyr Arg Lys Arg Arg Arg Met Lys Leu Leu Ser Ser Ile Glu Gln
 325 330 335

Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys Glu Lys

340	345	350
Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg Tyr Ser		
355	360	365
Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr Glu Val		
370	375	380
Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile Phe Pro		
385	390	395
Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln Asp Ile		
405	410	415
Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn Lys Asp		
420	425	430
Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro Leu Thr		
435	440	445
Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu Ser Ser		
450	455	460
Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Ala Ala Ala Gly Gly Ser		
465	470	475
Gly Gly Ser Gly Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met		
485	490	495
Leu Gly Ser Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser		
500	505	510
Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu Gly Ser Asp Ala Leu		
515	520	525
Asp Asp Phe Asp Leu Asp Met Leu Gly Ser		
530	535	

<210> 77
 <211> 21
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic construct

<400> 77

Ala Thr Val Val Ile Val Val Cys Val Ser Phe Leu Val Phe Met Ile
1 5 10 15

Ile Leu Gly Val Phe
20

<210> 78

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic construct

<400> 78

Ile Ala Thr Val Val Ile Ile Ile Ser Val Cys Met Leu Val Phe Val
1 5 10 15

Val Ala Met Gly Val Tyr
20

<210> 79

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic construct

<400> 79

Arg Ile Arg Ala Ala His Arg Arg Thr Met Arg
1 5 10

<210> 80

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic construct

<400> 80

Arg Val Arg Ile Ala His Gln His
1 5