

SEQUENCE LISTING

<110> Janssen Pharmaceutica NV
 Zheng, Songmao
 Kimko, Holly
 Hermann, Robert
 Fabbrini, Elisa
 Stojanovic-Susulic, Vedrana
 Rothenberg, Paul

<120> [0001] GDF15 analogs and methods for use in the treatment of obesity and associated comorbidities

<130> PRD3476

<160> 128

<170> PatentIn version 3.5

<210> 1
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HSA variant

<400> 1

Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu
1				5					10					15	

Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln
			20					25					30		

Gln	Cys	Pro	Phe	Glu	Asp	His	Val	Lys	Leu	Val	Asn	Glu	Val	Thr	Glu
		35					40				45				

Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys
	50					55					60				

Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu
65					70					75					80

Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	Pro
				85					90					95	

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

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

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 2
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> HSA variant

<400> 2

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

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

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 3
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> HSA variant

<400> 3

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 4
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 4

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

Gly Gly Gly Ser
20

<210> 5
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 5

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

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

35

40

45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
 580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
 595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
 610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
 625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
 645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
 660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 6
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 6

Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg
1 5 10 15

Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp
20 25 30

Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys
35 40 45

Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser
50 55 60

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

Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val
85 90 95

Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105 110

<210> 7
<211> 109
<212> PRT

<213> Artificial Sequence

<220>

<223> GDF15 variant

<400> 7

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

Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser
20 25 30

Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln
35 40 45

Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg
50 55 60

Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr
65 70 75 80

Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln
85 90 95

Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105

<210> 8

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> GDF15 variant

<400> 8

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

Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro
20 25 30

Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe
35 40 45

Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu
50 55 60

Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn
65 70 75 80

Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr
85 90 95

Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105

<210> 9
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 9

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

Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg
20 25 30

Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg
35 40 45

Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys
50 55 60

Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro
65 70 75 80

Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr
85 90 95

Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105

<210> 10
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 10

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

Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu
20 25 30

Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala
35 40 45

Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro
50 55 60

Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met
65 70 75 80

Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp
85 90 95

Asp Leu Leu Ala Lys Asp Cys His Cys Ile
100 105

<210> 11
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 11

Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala
 1 5 10 15

Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly
 20 25 30

Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys
 35 40 45

Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys
 50 55 60

Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr
 65 70 75 80

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

Cys Ile

<210> 12
 <211> 42
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker

<400> 12

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 35 40

<210> 13
 <211> 42
 <212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 13

Gly Ala Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Gly Gly Gly Gly
1 5 10 15

Ala Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala
20 25 30

Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala
35 40

<210> 14

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 14

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro
20

<210> 15

<211> 24

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 15

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro Ala Pro Ala Pro
20

<210> 16
<211> 48
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 16

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

Thr Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu
20 25 30

Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Ser
35 40 45

<210> 17
<211> 42
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 17

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

Ser Pro Gly Gly Gly Ser Pro Gly Gly Gly Ser Pro Gly Gly Gly Ser
20 25 30

Pro Gly Gly Gly Ser Pro Gly Gly Gly Ser
35 40

<210> 18
<211> 42
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 18

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

Ser Ala Gly Gly Gly Ser Ala Gly Gly Gly Ser Ala Gly Gly Gly Ser
20 25 30

Ala Gly Gly Gly Ser Ala Gly Gly Gly Ser
35 40

<210> 19

<211> 34

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 19

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

Thr Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gly
20 25 30

Gly Ser

<210> 20

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 20

Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Thr
1 5 10

<210> 21

<211> 44

<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 21

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Thr
35 40

<210> 22
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 22

Ala Ser Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gly Thr
1 5 10

<210> 23
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 23

Ala Ser Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro Ala Pro Gly Thr
20

<210> 24

<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 24

Ala Ser Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
1 5 10 15

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
20 25 30

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gly Thr
35 40

<210> 25
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 25

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Thr Ala Arg Asn Gly Asp His Cys Pro Leu
595 600 605

Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu
610 615 620

Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val
625 630 635 640

Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met
645 650 655

His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val
660 665 670

Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile
675 680 685

Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu
690 695 700

Ala Lys Asp Cys His Cys Ile
705 710

<210> 26

<211> 741
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 26

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Gly Thr Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro
625 630 635 640

Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu
645 650 655

Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met
660 665 670

Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala
675 680 685

Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala
690 695 700

Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys
705 710 715 720

Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys
725 730 735

Asp Cys His Cys Ile
740

<210> 27
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 27

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

20

25

30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Ser Ala Pro Ala Pro Ala
580 585 590

Pro Ala Pro Ala Pro Gly Thr Ala Arg Asn Gly Asp His Cys Pro Leu
595 600 605

Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu
610 615 620

Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val
625 630 635 640

Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met
645 650 655

His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val
660 665 670

Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile
675 680 685

Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu
690 695 700

Ala Lys Asp Cys His Cys Ile
705 710

<210> 28

<211> 721

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 28

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu

530

535

540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Ser Ala Pro Ala Pro Ala
 580 585 590

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gly
 595 600 605

Thr Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys
 610 615 620

Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp
 625 630 635 640

Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala
 645 650 655

Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr
 660 665 670

Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val
 675 680 685

Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly
 690 695 700

Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys
 705 710 715 720

Ile

<210> 29

<211> 741

<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 29

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Ser Ala Pro Ala Pro Ala
580 585 590

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
595 600 605

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
610 615 620

Pro Ala Pro Gly Thr Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro
625 630 635 640

Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu
645 650 655

Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met
660 665 670

Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala
675 680 685

Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala
690 695 700

Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys
705 710 715 720

Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys
725 730 735

Asp Cys His Cys Ile
740

<210> 30
<211> 721
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 30

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Ser Glu Ala Ala Ala Lys
580 585 590

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly
595 600 605

Thr Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys
610 615 620

Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp
625 630 635 640

Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala
645 650 655

Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr

660

665

670

Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val
 675 680 685

Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly
 690 695 700

Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys
 705 710 715 720

Ile

<210> 31

<211> 741

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 31

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

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

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Ser Glu Ala Ala Ala Lys
580 585 590

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
595 600 605

Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala
610 615 620

Ala Ala Lys Gly Thr Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro
625 630 635 640

Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu
645 650 655

Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met
660 665 670

Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala
675 680 685

Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala
690 695 700

Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys
705 710 715 720

Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys
725 730 735

Asp Cys His Cys Ile
740

<210> 32
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 32

Ala Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
1 5 10 15

Lys Glu Ala Ala Ala Lys Gly Thr
20

<210> 33
<211> 44
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 33

Ala Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
1 5 10 15

Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
20 25 30

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Gly Thr
35 40

<210> 34
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 34

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

<210> 35

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 35

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

<210> 36

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 36

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala

515

520

525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
 580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys
 595 600 605

Ser Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala
 610 615 620

Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly
 625 630 635 640

Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys
 645 650 655

Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys
 660 665 670

Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr
 675 680 685

Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His
 690 695 700

Cys Ile
 705

<210> 37
 <211> 705

<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 37

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys
595 600 605

Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp
610 615 620

Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala
625 630 635 640

Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr
645 650 655

Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val
660 665 670

Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly
675 680 685

Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys
690 695 700

Ile
705

<210> 38
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 38

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

Gly Gly Gly Ser
20

<210> 39
<211> 25
<212> PRT
<213> Artificial sequence

<220>

<223> linker

<400> 39

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 40

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 40

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys

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

<210> 41
 <211> 30
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> linker

 <400> 41

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

<210> 42
<211> 35
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 42

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser
35

<210> 43
<211> 40
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 43

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser
35 40

<210> 44

<211> 45
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 44

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
35 40 45

<210> 45
<211> 50
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 45

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser
50

<210> 46
<211> 55
<212> PRT
<213> Artificial sequence

<220>

<223> linker

<400> 46

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser
50 55

<210> 47

<211> 60

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 47

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

<210> 48

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 48

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
 625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
 645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
 660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
 675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
 690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 705 710 715

<210> 49
 <211> 65
 <212> PRT
 <213> Artificial sequence

<220>
 <223> linker

<400> 49

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 50 55 60

Ser
 65

<210> 50
<211> 70
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 50

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser
65 70

<210> 51
<211> 75
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 51

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75

<210> 52
<211> 80
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 52

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

<210> 53
<211> 85
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 53

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

20

25

30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 65 70 75 80

Gly Gly Gly Gly Ser
 85

<210> 54

<211> 90

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 54

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 85 90

<210> 55
 <211> 739
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein

<400> 55

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
 580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

595

600

605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg
 625 630 635 640

Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp
 645 650 655

Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile
 660 665 670

Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile
 675 680 685

Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys
 690 695 700

Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp
 705 710 715 720

Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys
 725 730 735

His Cys Ile

<210> 56

<211> 717

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 56

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys

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

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Ala Pro Ala Pro Ala
580 585 590

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Arg Asn
595 600 605

Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr
610 615 620

Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser
625 630 635 640

Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln
645 650 655

Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg
660 665 670

Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr
675 680 685

Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln
690 695 700

Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 57
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 57

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 58
<211> 719
<212> PRT
<213> Artificial Sequence

<220>

<223> fusion protein

<400> 58

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ala Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro

415

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 59
<211> 717
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 59

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu

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

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Ala Pro Ala Pro Ala
580 585 590

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Arg Asn
595 600 605

Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr
610 615 620

Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser
625 630 635 640

Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln
645 650 655

Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg
660 665 670

Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr
675 680 685

Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln
690 695 700

Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 705 710 715

<210> 60
 <211> 739
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein

<400> 60

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser

580

585

590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Ala Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg
 625 630 635 640

Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp
 645 650 655

Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile
 660 665 670

Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile
 675 680 685

Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys
 690 695 700

Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp
 705 710 715 720

Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys
 725 730 735

His Cys Ile

<210> 61

<211> 95

<212> PRT

<213> Artificial sequence

<220>

<223> linker

<400> 61

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
85 90 95

<210> 62
<211> 100
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 62

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
85 90 95

Gly Gly Gly Ser
100

<210> 63
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> linker

<400> 63

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10

<210> 64
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 64

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser

290

295

300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

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

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 65
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 65

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
 580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
 595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
 610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
 625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
 645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
 660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
 675 680 685

Ser Tyr Asn Pro Met Val Leu Trp Gln Lys Thr Asp Thr Gly Val Ser
 690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 705 710 715

<210> 66
 <211> 719
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein

<400> 66

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465		470		475		480
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr						
		485		490		495
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp						
		500		505		510
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala						
		515		520		525
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu						
		530		535		540
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys						
545			550		555	560
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val						
		565		570		575
Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser						
		580		585		590
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala						
		595		600		605
Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu						
		610		615		620
His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val						
625			630		635	640
Ala Ala Pro Ala Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro						
		645		650		655
Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu						
		660		665		670
His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala						
		675		680		685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 67
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 67

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130

135

140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

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

Ala Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 68
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 68

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Ala Ala Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro

645

650

655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

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

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 69

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 69

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala

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

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

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

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 70
<211> 719
<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 70

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Trp Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 71
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 71

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485

490

495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
 580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
 595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
 610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Ala Val
 625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
 645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
 660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
 675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
 690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 72
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 72

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg

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

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Ala Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 73
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 73

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Ala Ile Lys Thr Ala Leu

660

665

670

His Ala Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
 675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
 690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
 705 710 715

<210> 74

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 74

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg

325

330

335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Ala Ala Asp Trp Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Ala Ala Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 75

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 75

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
595 600 605

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
610 615 620

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Ala Ala Asp Ala Val
625 630 635 640

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
645 650 655

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
660 665 670

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
675 680 685

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
690 695 700

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
705 710 715

<210> 76
<211> 2157
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 76
gacgcccaca agagcgaggt ggcccaccgg ttcaaggacc tgggcgagga gaacttcaag 60
gccctggtgc tgatgcctt cgcccagtac ctgcagcagt cccccttcga ggaccacgtg 120
aagctggtga acgaggtgac cgagttcgcc aagacctgcg tggccgacga gagcgccgag 180
aactgcgaca agagcctgca caccctgttc ggcgacaagc tgtgcaccgt ggccaccctg 240
cgggagacct acggcgagat ggccgactgc tgcgccaagc aggagcccga gcggaacgag 300
tgcttcctgc agcacaagga cgacaacccc aacctgcccc ggctggtgcg gcccagagtg 360
gacgtgatgt gcaccgcctt ccacgacaac gaggagacct tcctgaagaa gtacctgtac 420
gagatcgccc ggcgggcacc ctacttctac gccccgagc tgctgttctt cgccaagcgg 480
tacaaggccg ccttcaccga gtgctgccag gccgccgaca aggccgcctg cctgctgccc 540
aagctggacg agctgcggga cgagggcaag gccagcagcg ccaagcagcg gctgaagtgc 600

gccagcctgc agaagttcgg cgagcgggcc ttcaaggcct gggccgtggc ccggctgagc	660
cagcggttcc ccaaggccga gttcgccgag gtgagcaagc tggtgaccga cctgaccaag	720
gtgcacaccg agtgctgcca cggcgacctg ctggagtgcg ccgacgaccg ggccgacctg	780
gccaagtaca tctgcgagaa ccaggacagc atcagcagca agctgaagga gtgctgcgag	840
aagcccctgc tggagaagag ccactgcatc gccgaggtgg agaacgacga gatgcccgcc	900
gacctgcccc gcctggccgc cgacttcgtg gagagcaagg acgtgtgcaa gaactacgcc	960
gaggccaagg acgtgttcct gggcatgttc ctgtacgagt acgcccggcg gcaccccgac	1020
tacagcgtgg tgctgctgct gcggctggcc aagacctacg agaccaccct ggagaagtgc	1080
tgcgccgccg ccgaccccc aagtgctac gccaaaggtgt tcgacgagtt caagcccctg	1140
gtggaggagc cccagaacct gatcaagcag aactgcgagc tgttcgagca gctgggagcag	1200
tacaagttcc agaacgccct gctggtgcgg tacaccaaga aggtgcccc ggtgagcacc	1260
cccaccctgg tggaggtgag ccggaacctg ggcaaggtgg gcagcaagtg ctgcaagcac	1320
cccgaggcca agcggatgcc ctgcgccgag gactacctga gcgtggtgct gaaccagctg	1380
tgctgctgc acgagaagac ccccgtgagc gaccgggtga ccaagtgtg caccgagagc	1440
ctggtgaacc ggcgccctg cttcagcgcc ctggaggtgg acgagacct cgtgccccag	1500
gagttcaacg ccgagacctt caccttcac gccgacatct gcaccctgag cgagaaggag	1560
cggcagatca agaagcagac cgccctggtg gagctggtga agcacaagcc caaggccacc	1620
aaggagcagc tgaaggccgt gatggacgac ttcgccgcct tcgtggagaa gtgctgcaag	1680
gccgacgaca aggagacctg cttcgccgag gagggaaga agctggtggc cgccagccag	1740
gccgcccctg gcctgggag cggcgccggc ggagcgggc gcggcgatc tgggtggaggt	1800
ggcagtgag gagggggatc cgctcgcaac ggtgaccact gccctctggg tcctggtcgc	1860
tgctgccgcc tgcacaccgt tcgcgcttct ctggaagacc tgggttgggc tgactgggtt	1920
ctgtctctc gcgaagttca gggtaccatg tgcacggtg cttgcccttc tcagttccgc	1980
gctgctaaca tgcacgctca gatcaaaacc tctctgcacc gcctgaaacc tgacaccgtt	2040
cctgtctctt gctgcgttcc tgcttcttac aaccctatgg ttctgatcca gaaaaccgac	2100
accggtgttt ctctgcagac ctacgacgac ctgctggcta aagactgcca ctgcatc	2157

<210> 77
 <211> 2133
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion protein coding sequence

<400> 77
 gatgtcata agtccgaagt cgcccacaga ttcaaggacc tcggagaaga aaattttaag 60
 gccctcgtgc ttatcgctt cgccaatac ctccagcagt ccccggtcga ggaccacgtg 120
 aagctcgtga acgaagtac cgagtttgcc aagacttggtg tggcggatga atccgccgag 180
 aactgcgaca agagcctcca cacgctgttc ggcgacaagc tgtgcaccgt cgccacgctg 240
 agagaaactt acggagagat ggccgactgc tgcgcaaagc aggagccgga acggaacgaa 300
 tgcttcctgc aacataagga cgataaccct aacttgcttc gcctggtccg ccctgaggtc 360
 gacgtgatgt gcaccgcgtt ccacgacaac gaggaaacct ttcttaagaa gtacctgtac 420
 gagattgcgc ggaggcacc ttatttctac gccccgaac tgttggttctt cgccaagcgg 480
 tacaaggctg cttttaccga atgctgccag gccgccgata aggcggcttg cctgctgccg 540
 aagctcgacg agttgcgcga tgaggggaag gcgtcctccg ctaagcagcg gctgaaatgt 600
 gcgagcctcc agaagtccgg ggagcgcgcc ttcaaggcct gggccgtggc gcgcctgtct 660
 caacggttcc cgaaggccga gttcgccgaa gtgtcgaagc tggtcaccga cctgacgaaa 720
 gtgcacaccg aatgttgtca cggcgatctg ctggaatgcg ccgatgacag agccgatttg 780
 gccaagtaca tctgcgaaaa ccaggacagc atttcgtcaa agctgaagga atgctgcgaa 840
 aagcccttgc tggaaaagtc cactgcatc gcggaagtgg agaacgacga gatgcccgcc 900
 gacctcccgt ccctggccgc cgatttcgtg gagtgcgaagg atgtgtgcaa gaactacgca 960
 gaagccaagg acgtgttcct gggaatgttt ctgtatgagt acgcccgcg ccacccggac 1020
 tactcggctg tgctcctgct gcgactggca aagacctacg aaaccactct ggagaagtgc 1080
 tgcgccgccg cggacccgca cgagtgtac gcaaaggtgt tcgacgagtt caagccactt 1140
 gtcgaggagc ctcagaacct gatcaagcag aactgcgaac tgttcgagca gctgggagag 1200
 taaaaattcc agaacgcgct tctcgtgcgc tacaccaaga aggtcccca ggtgtccact 1260
 ccgaccctgg tggaagtgtc caggaacctg ggaaaggtcg gtcctaagtg ttgcaagcat 1320

cccgaggcta agcgcacatgcc ctgcgccgag gactacttgt ccgtggtgct gaatcagctg	1380
tgcgtgctcc atgaaaagac cccagtgtcc gacagagtga ccaagtgtg taccgaatcg	1440
ctcgtgaacc ggcggccgtg cttttccgca ctggaggtgg acgaaaccta cgtgccgaag	1500
gagttcaacg cagaaacctt cactttccac gccgacatct gcactctgtc cgagaaggag	1560
cggcagatta agaagcagac tgccctggtg gagcttgtga aacacaagcc taaggccacc	1620
aaagagcagc tgaaggccgt catggatgat ttcgcggcct tcgtggaaaa gtgttgtaaa	1680
gcggacgaca aggagacttg cttcgccgaa gaaggaaaga agctcgtggc agcgtcacag	1740
gccgctctgg gcctcgctag cgggtggagg ggacgcggtg gtggaggatc cggtagccgc	1800
cgcaacgggg accactgtcc gctcggggccc gggcggttgc gccgtctgca caccgtccgc	1860
gcgtcgctgg aagacctggg ctgggcccgt tgggtgctgt cgccacggga ggtgcaagt	1920
accatgtgca tcggcgctg cccgagccag ttccgggcgg caaacatgca cgcgcagatc	1980
aagacgagcc tgcaccgcct gaagcccgac acggtgccag cgccctgctg cgtgcccgcc	2040
agctacaatc ccatggtgct cattcaaaag accgacaccg ggggtgtcgt ccagacctat	2100
gatgacttgt tagccaaaga ctgccactgc ata	2133

<210> 78

<211> 2223

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 78

gatgctcata agtccgaagt cgcccacaga ttcaaggacc tcggagaaga aaattttaag	60
gccctcgtgc ttatcgctt cgcccaatac ctccagcagt ccccgttcga ggaccacgtg	120
aagctcgtga acgaagtac cgagtttgcc aagacttgtg tggcggatga atccgccgag	180
aactgcgaca agagcctcca cacgctgttc ggcgacaagc tgtgcaccgt cgccacgctg	240
agagaaactt acggagagat ggccgactgc tgcgcaaagc aggagccgga acggaacgaa	300
tgcttcctgc aacataagga cgataaccct aacttgcttc gcctgggtccg ccctgaggtc	360
gacgtgatgt gcaccgcgtt ccacgacaac gaggaaacct ttcttaagaa gtacctgtac	420
gagattgcgc ggaggcacc ttatttctac gccccgaac tgttggttctt cgccaagcgg	480

tacaaggctg cctttaccga atgctgccag gccgccgata aggcggcttg cctgctgccg	540
aagctcgacg agttgcgcga tgaggggaag gcgtcctccg ctaagcagcg gctgaaatgt	600
gcgagcctcc agaagttcgg ggagcgcgcc ttcaaggcct gggccgtggc gcgcctgtct	660
caacggttcc cgaaggccga gttcgccgaa gtgtcgaagc tggtcaccga cctgacgaaa	720
gtgcacaccg aatgtttgtca cggcgatctg ctggaatgcg ccgatgacag agccgatttg	780
gccaagtaca tctgcgaaaa ccaggacagc atttcgtcaa agctgaagga atgctgcgaa	840
aagcccttgc tggaaaagtc ccactgcatc gcggaagtgg agaacgacga gatgcccgcc	900
gacctcccgt ccctggccgc cgatttcgtg gagtcgaagg atgtgtgcaa gaactacgca	960
gaagccaagg acgtgttcct gggaatgttt ctgtatgagt acgcccgccg ccacccggac	1020
tactcggtcg tgctcctgct gcgactggca aagacctacg aaaccactct ggagaagtgc	1080
tgcgccgccg cggacccgca cgagtgtctac gcaaagggtgt tcgacgagtt caagccactt	1140
gtcgaggagc ctcagaacct gatcaagcag aactgcgaac tgttcgagca gctgggagag	1200
tacaaattcc agaacgcgct tctcgtgcgc tacaccaaga aggtcccca ggtgtccact	1260
ccgaccctgg tggaagtgtc caggaacctg ggaaaggctg gctccaagtg ttgcaagcat	1320
cccgaggcta agcgcatgcc ctgcgccgag gactacttgt ccgtggtgct gaatcagctg	1380
tgctgtctcc atgaaaagac cccagtgtcc gacagagtga ccaagtgtg taccgaatcg	1440
ctcgtgaacc ggcgccgtg cttttccgca ctggaggtgg acgaaacctc cgtgccgaag	1500
gagttcaacg cagaaacctt cactttccac gccgacatct gcactctgtc cgagaaggag	1560
cggcagatta agaagcagac tgccctggtg gagcttgtga aacacaagcc taaggccacc	1620
aaagagcagc tgaaggccgt catggatgat ttcgcggcct tcgtggaaaa gtgttgtaaa	1680
gcggacgaca aggagacttg cttcgccgaa gaaggaaaga agctcgtggc agcgtcacag	1740
gccgctctgg gcctcgctag cggaggtggc ggatcaggtg gcggaggtag cggaggaggc	1800
ggctctggcg gaggtggatc aggcggagga ggttccggtg gaggaggctc aggaggagga	1860
ggaagtggag gagggggatc cggtagccgc cgcaacgggg accactgtcc gctcggggcc	1920
gggcgttgct gccgtctgca cacggtccgc gcgtcgctgg aagacctggg ctgggccgat	1980
tgggtgctgt cgccacggga ggtgcaagtg accatgtgca tcggcgcgtg cccgagccag	2040

ttccggg	cgg	caa	catgca	cgcgcagatc	aagacgagcc	tgcaccgcct	gaagccc	gac	2100
acggtg	ccag	cgccctg	ctg	cgtgccc	gcc	agctacaatc	ccatgggtg	ct	2160
acgacac	cgg	gggtgtc	gct	ccagacctat	gatgactt	gt	tagccaa	aga	2220
ctgcc	actgc								2223

<210> 79
 <211> 2133
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion protein coding sequence

gatgctcata	agtccgaagt	cgccacaga	ttcaaggacc	tcggagaaga	aaattttaag		60
gccctcgtgc	ttatcgcctt	cgccaatac	ctccagcagt	ccccgttcga	ggaccacgtg		120
aagctcgtga	acgaagtgac	cgagtttgcc	aagacttgtg	tggcggatga	atccgccgag		180
aactgcgaca	agagcctcca	cacgctgttc	ggcgacaagc	tgtgcaccgt	cgccacgctg		240
agagaaactt	acggagagat	ggccgactgc	tgcgcaaagc	aggagccgga	acggaacgaa		300
tgcttcctgc	aacataagga	cgataaccct	aacttgcctc	gcctgggtccg	ccctgaggtc		360
gacgtgatgt	gcaccgcgtt	ccacgacaac	gaggaaacct	ttcttaagaa	gtacctgtac		420
gagattgcgc	ggaggcacc	ttatttctac	gccccgaac	tgttggttctt	cgccaagcgg		480
tacaagggtg	cctttaccga	atgctgccag	gccgccgata	aggcggcttg	cctgctgccg		540
aagctcgacg	agttgcgcga	tgaggggaag	gcgtcctccg	ctaagcagcg	gctgaaatgt		600
gcgagcctcc	agaagttcgg	ggagcgcgcc	ttcaaggcct	gggccgtggc	gcgcctgtct		660
caacggttcc	cgaaggccga	gttcgccgaa	gtgtcgaagc	tggtcaccga	cctgacgaaa		720
gtgcacaccg	aatgttgtca	cggcgatctg	ctggaatgcg	ccgatgacag	agccgatttg		780
gccaaagtaca	tctgcgaaaa	ccaggacagc	atttcgtcaa	agctgaagga	atgctgcgaa		840
aagcccttgc	tggaaaagtc	ccactgcata	gcggaagtgg	agaacgacga	gatgcccgcc		900
gacctcccgt	ccctggccgc	cgatttcgtg	gagtcgaagg	atgtgtgcaa	gaactacgca		960
gaagccaagg	acgtgttcct	gggaatgttt	ctgtatgagt	acgcccgccg	ccacccggac		1020
tactcggtcg	tgctcctgct	gcgactggca	aagacctacg	aaaccactct	ggagaagtgc		1080

tgcgccgccc	cggacccgca	cgagtgttac	gcaaaggtgt	tcgacgagtt	caagccactt	1140
gtcgaaggagc	ctcagaacct	gatcaagcag	aactgcgaac	tgttcgagca	gctgggagag	1200
tacaaattcc	agaacgcgct	tctcgtgctc	tacaccaaga	aggtcccca	ggtgtccact	1260
ccgaccctgg	tggaagtgtc	caggaacctg	ggaaaggtcg	gctccaagtg	ttgcaagcat	1320
cccgaaggcta	agcgcatgcc	ctgcgccgag	gactacttgt	ccgtggtgct	gaatcagctg	1380
tgcgtgctcc	atgaaaagac	cccagtgtcc	gacagagtga	ccaagtgtg	taccgaatcg	1440
ctcgtgaacc	ggcggccgtg	cttttccgca	ctggaggtgg	acgaaacct	cgtgccgaag	1500
gagttcaacg	cagaaacctt	cactttccac	gccgacatct	gcactctgtc	cgagaaggag	1560
cggcagatta	agaagcagac	tgccctggtg	gagcttgtga	aacacaagcc	taaggccacc	1620
aaagagcagc	tgaaggccgt	catggatgat	ttcgcggcct	tcgtggaaaa	gtgttgtaaa	1680
gcggacgaca	aggagacttg	cttcgccgaa	gaaggaaaga	agctcgtggc	agcgtcacag	1740
gccgctctgg	gcctcgctag	cgcacctgcc	cccgtccag	ctcctgcacc	aggtaccgcg	1800
cgcaacgggg	accactgtcc	gctcggggcc	ggcgcttgct	gccgtctgca	cacggtccgc	1860
gcgtcgctgg	aagacctggg	ctgggccgat	tgggtgctgt	cgccacggga	ggtgcaagtg	1920
accatgtgca	tcggcgctg	cccagaccag	ttccgggcgg	caaacatgca	cgcgcagatc	1980
aagacgagcc	tgcaccgcct	gaagcccgac	acggtgccag	cgccctgctg	cgtgcccgcc	2040
agctacaatc	ccatggtgct	cattcaaaag	accgacaccg	gggtgtcgct	ccagacctat	2100
gatgacttgt	tagccaaaga	ctgccactgc	ata			2133

<210> 80

<211> 2163

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 80

gatgctcata	agtccgaagt	cgccacaga	ttcaaggacc	tcggagaaga	aaattttaag	60
------------	------------	-----------	------------	------------	------------	----

gccctcgtgc	ttatcgctt	cgccaatac	ctccagcagt	ccccgttcga	ggaccacgtg	120
------------	-----------	-----------	------------	------------	------------	-----

aagctcgtga	acgaagtgc	cgagtttgcc	aagacttgtg	tggcggatga	atccgccgag	180
------------	-----------	------------	------------	------------	------------	-----

aactgcgaca agagcctcca cacgctgttc ggcgacaagc tgtgcaccgt cgccacgctg	240
agagaaactt acggagagat ggccgactgc tgcgcaaagc aggagccgga acggaacgaa	300
tgcttcctgc aacataagga cgataaccct aacttgcttc gcctgggtccg ccctgaggtc	360
gacgtgatgt gcaccgcgtt ccacgacaac gaggaacct ttcttaagaa gtacctgtac	420
gagattgcgc ggaggcacc ttattttctac gccccgaac tgttggttctt cgccaagcgg	480
tacaaggctg cttttaccga atgctgccag gccgccgata aggcggcttg cctgctgccg	540
aagctcgacg agttgcgcga tgaggggaag gcgtcctccg ctaagcagcg gctgaaatgt	600
gcgagcctcc agaagttcgg ggagcgcgcc ttcaaggcct gggccgtggc gcgcctgtct	660
caacggttcc cgaaggccga gttcgccgaa gtgtcgaagc tggtcaccga cctgacgaaa	720
gtgcacaccg aatgttgtca cggcgatctg ctggaatgcg ccgatgacag agccgatttg	780
gccaagtaca tctgcgaaaa ccaggacagc atttcgtcaa agctgaagga atgctgcgaa	840
aagcccttgc tggaaaagtc ccactgcatc gcggaagtgg agaacgacga gatgcccgcc	900
gacctcccgt ccctggccgc cgatttcgtg gagtcgaagg atgtgtgcaa gaactacgca	960
gaagccaagg acgtgttcct gggaatgttt ctgtatgagt acgcccgcg ccacccggac	1020
tactcggctg tgctcctgct gcgactggca aagacctacg aaaccactct ggagaagtgc	1080
tgcgccgccg cggacccgca cgagtgtac gcaaaggtgt tcgacgagtt caagccactt	1140
gtcgaggagc ctcaaacct gatcaagcag aactgcgaac tgttcgagca gctgggagag	1200
tacaaattcc agaacgcgct tctcgtgcgc tacaccaaga aggtcccca ggtgtccact	1260
ccgaccctgg tggaagtgtc caggaacctg ggaaaggtcg gctccaagtg ttgcaagcat	1320
cccgaggcta agcgcgatgcc ctgcgccgag gactacttgt ccgtgggtgct gaatcagctg	1380
tgcgtgctcc atgaaaagac cccagtgtcc gacagagtga ccaagtgtg taccgaatcg	1440
ctcgtgaacc ggcgggccgtg cttttccgca ctggaggtgg acgaaacctt cgtgccgaag	1500
gagttcaacg cagaaacctt cactttccac gccgacatct gcactctgtc cgagaaggag	1560
cggcagatta agaagcagac tgccctgggtg gagcttgtga aacacaagcc taaggccacc	1620
aaagagcagc tgaaggccgt catggatgat ttcgggcct tcgtggaaaa gtgttgtaaa	1680
gcggacgaca aggagacttg cttcgccgaa gaaggaaaga agctcgtggc agcgtcacag	1740
gccgctctgg gcctcgctag cgcacctgcc cccgctccag caccgcccc agcccctgct	1800

cccgaccag ctcctgcacc aggtaccgct cgcaacggtg accactgccc tctgggtcct	1860
ggtcgtgct gccgcctgca caccgttcgc gcttctctgg aagacctggg ttgggctgac	1920
tgggttctgt ctctcgcga agttcaggtt accatgtgca tcggtgcttg cccttctcag	1980
ttccgcgtg ctaacatgca cgctcagatc aaaacctctc tgcaccgcct gaaacctgac	2040
accgttcctg ctcttgctg cgttcctgct tcttacaacc ctatggttct gatccagaaa	2100
accgacaccg gtgtttctct gcagacctac gacgacctgc tggctaaaga ctgccactgc	2160
atc	2163

<210> 81

<211> 2223

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 81

gatgctcata agtccgaagt cgccacaga ttcaaggacc tcggagaaga aaattttaag	60
gccctcgtgc ttatcgctt cgccaatac ctccagcagt ccccgttcga ggaccacgtg	120
aagctcgtga acgaagtgc cgagtttgcc aagacttggtg tggcggatga atccgccgag	180
aactgcgaca agagcctcca cacgctgttc ggcgacaagc tgtgcaccgt cgccacgctg	240
agagaaactt acggagagat ggccgactgc tgcgcaaagc aggagccgga acggaacgaa	300
tgcttcctgc aacataagga cgataaccct aacttgcttc gcctgggtccg ccctgaggtc	360
gacgtgatgt gcaccgcgtt ccacgacaac gaggaaacct ttcttaagaa gtacctgtac	420
gagattgcgc ggaggcacc ttatttctac gccccgaac tgttgttctt cgccaagcgg	480
tacaaggctg cttttaccga atgctgccag gccgccgata aggcggcttg cctgctgccg	540
aagctcgacg agttgcgcga tgaggggaag gcgtcctccg ctaagcagcg gctgaaatgt	600
gcgagcctcc agaagttcgg ggagcgcgcc ttcaaggcct gggccgtggc gcgcctgtct	660
caacggttcc cgaaggccga gttcgccgaa gtgtcgaagc tggtcaccga cctgacgaaa	720
gtgcacaccg aatgttgtca cggcgatctg ctggaatgcg ccgatgacag agccgatttg	780
gccaagtaca tctgcgaaaa ccaggacagc atttcgtcaa agctgaagga atgctgcgaa	840

aagcccttgc tggaaaagtc ccactgcatc gcggaagtgg agaacgacga gatgcccgcc	900
gacctcccggt ccctggccgc cgatttcgtg gagtgcgaagg atgtgtgcaa gaactacgca	960
gaagccaagg acgtgttcct gggaatgttt ctgtatgagt acgcccgccg ccacccggac	1020
tactcggtcg tgctcctgct gcgactggca aagacctacg aaaccactct ggagaagtgc	1080
tgcgccgccg cggacccgca cgagtgtctac gcaaaggtgt tcgacgagtt caagccactt	1140
gtcgaggagc ctcagaacct gatcaagcag aactgcgaac tgttcgagca gctgggagag	1200
tacaaattcc agaacgcgct tctcgtgcgc tacaccaaga aggtcccca ggtgtccact	1260
ccgaccttg tggaagtgtc caggaacctg ggaaaggtcg gctccaagtg ttgcaagcat	1320
cccgaggcta agcgcctgcc ctgcgccgag gactacttgt ccgtggtgct gaatcagctg	1380
tgcgtgctcc atgaaaagac ccagtgctcc gacagagtga ccaagtgtg taccgaatcg	1440
ctcgtgaacc ggcggccgtg cttttccgca ctggaggtgg acgaaaccta cgtgccgaag	1500
gagttcaacg cagaaacctt cactttccac gccgacatct gcactctgtc cgagaaggag	1560
cggcagatta agaagcagac tgccctggtg gagcttgtga aacacaagcc taaggccacc	1620
aaagagcagc tgaaggccgt catggatgat ttcgcggcct tcgtggaaaa gtgttgtaaa	1680
gcggacgaca aggagacttg cttcgccgaa gaaggaaaga agctcgtggc agcgtcacag	1740
gccgctctgg gcctcgctag cgcacctgcc ccgctccag cccagctcc tgcacctgct	1800
ccagcaccag ctctgcacc agctccagcc cctgcacctg caccgctcc agccccagct	1860
cctgcacctg ctccagcacc aggtaccgcg cgcaacgggg accactgtcc gctcgggccc	1920
gggcgttgct gccgtctgca cacggtccgc gcgtcgtgg aagacctggg ctgggccgat	1980
tgggtgctgt cgccacggga ggtgcaagt accatgtgca tcggcgctg cccgagccag	2040
ttccgggcgg caaacatgca cgcgcagatc aagacgagcc tgcaccgcct gaagcccagc	2100
acggtgccag cgccctgctg cgtgcccgc agctacaatc ccatggtgct cattcaaaag	2160
accgacaccg ggggtgtcgt ccagacctat gatgacttgt tagccaaaga ctgccactgc	2220
ata	2223

<210> 82
 <211> 2163
 <212> DNA
 <213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 82

gatgctcata agtccgaagt cgccacaga ttcaaggacc tcggagaaga aaattttaag	60
gccctcgtgc ttatcgctt cgccaatac ctccagcagt ccccgttcga ggaccacgtg	120
aagctcgtga acgaagtac cgagtttgcc aagacttgtg tggcggatga atccgccgag	180
aactgcgaca agagcctcca cacgctgttc ggcgacaagc tgtgcaccgt cgccacgctg	240
agagaaactt acggagagat ggccgactgc tgcgcaaagc aggagccgga acggaacgaa	300
tgcttcctgc aacataagga cgataaccct aacttgcctc gcctgggtccg ccctgaggtc	360
gacgtgatgt gcaccgcgtt ccacgacaac gaggaaacct ttcttaagaa gtacctgtac	420
gagattgcgc ggaggcacc ttatttctac gccccgaac tgttgttctt cgccaagcgg	480
tacaaggctg cttttaccga atgctgccag gccgccgata aggcggcttg cctgctgccg	540
aagctcgacg agttgcgcga tgaggggaag gcgtcctccg ctaagcagcg gctgaaatgt	600
gcgagcctcc agaagttcgg ggagcgcgcc ttcaaggcct gggccgtggc gcgcctgtct	660
caacggttcc cgaaggccga gttcgccgaa gtgtcgaagc tggtcaccga cctgacgaaa	720
gtgcacaccg aatgttgtca cggcgatctg ctggaatgcg ccgatgacag agccgatttg	780
gccaagtaca tctgcgaaaa ccaggacagc atttcgtcaa agctgaagga atgctgcgaa	840
aagcccttgc tggaaaagtc cactgcatc gcggaagtgg agaacgacga gatgcccgcc	900
gacctccgt ccctggccgc cgatttcgtg gagtccaagg atgtgtgcaa gaactacgca	960
gaagccaagg acgtgttcct gggaatgttt ctgtatgagt acgcccgcg ccacccggac	1020
tactcggctg tgctcctgct gcgactggca aagacctacg aaaccactct ggagaagtgc	1080
tgcgccgccg cggacccgca cgagtgtac gcaaagggtg tcgacgagtt caagccactt	1140
gtcgaggagc ctcagaacct gatcaagcag aactgcgaac tgttcgagca gctgggagag	1200
tacaaattcc agaacgcgt tctcgtgcgc tacaccaaga aggtcccca ggtgtccact	1260
ccgaccctgg tggaagtgtc caggaacctg ggaaaggctg gctccaagtg ttgcaagcat	1320
ccgaggcta agcgcgtgcc ctgcgccgag gactacttgt ccgtggtgct gaatcagctg	1380
tgctgtctcc atgaaaagac ccagtgctc gacagagtga ccaagtgtg taccgaatcg	1440

ctcgtgaacc ggcggccgtg cttttccgca ctggaggtgg acgaaaccta cgtgccgaag	1500
gagttcaacg cagaaacctt cactttccac gccgacatct gcactctgtc cgagaaggag	1560
cggcagatta agaagcagac tgccctgggtg gagcttgtga aacacaagcc taaggccacc	1620
aaagagcagc tgaaggccgt catggatgat ttcgcggcct tcgtggaaaa gtgttgtaaa	1680
gcggacgaca aggagacttg cttcgccgaa gaaggaaaga agctcgtggc agcgtcacag	1740
gccgctctgg gcctcgctag cgaagcagca gccaaagaag cagccgcaaa agaagcagcc	1800
gctaaggagg ccgcagcaaa ggggtaccgcg cgcaacgggg accactgtcc gctcgggccc	1860
gggcgttgct gccgtctgca cacgggtccgc gcgtcgtgg aagacctggg ctgggcccgat	1920
tgggtgctgt cgccacggga ggtgcaagt accatgtgca tcggcgctg cccgagccag	1980
ttccgggcgg caaacatgca cgcgcagatc aagacgagcc tgcaccgcct gaagcccgcac	2040
acggtgccag cgccctgctg cgtgcccgcc agctacaatc ccatggtgct cattcaaaag	2100
accgacaccg ggggtgtcgt ccagacctat gatgacttgt tagccaaaga ctgccactgc	2160
ata	2163

<210> 83

<211> 2157

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 83

gacgcccaca agagcgaggt ggcccaccgg ttcaaggacc tgggcgagga gaacttcaag	60
gccctgggtgc tgatcgctt cgcccagtac ctgcagcagt cccccttcga ggaccacgtg	120
aagctgggtga acgaggtgac cgagttcgcc aagacctgcg tggccgacga gagcgccgag	180
aactgcgaca agagcctgca caccctgttc ggcgacaagc tgtgcaccgt ggccaccctg	240
cgggagacct acggcgagat ggccgactgc tgcgccaagc aggagcccga gcggaacgag	300
tgcttcctgc agcacaagga cgacaacccc aacctgcccc ggctgggtgcg gcccgagggtg	360
gacgtgatgt gcaccgcctt ccacgacaac gaggagacct tcctgaagaa gtacctgtac	420
gagatcgccc ggcggcacc ctacttctac gccccgagc tgctgttctt cgccaagcgg	480
tacaaggccg ccttcaccga gtgctgccag gccgccgaca aggccgcctg cctgctgccc	540

aagctggacg agctgcggga cgagggcaag gccagcagcg ccaagcagcg gctgaagtgc	600
gccagcctgc agaagttcgg cgagcgggcc ttcaaggcct gggccgtggc ccggctgagc	660
cagcggttcc ccaaggccga gttcgccgag gtgagcaagc tggtagaccga cctgaccaag	720
gtgcacaccg agtgctgcca cggcgacctg ctggagtgcg ccgacgaccg ggccgacctg	780
gccaagtaca tctgcgagaa ccaggacagc atcagcagca agctgaagga gtgctgcgag	840
aagcccctgc tggagaagag ccactgcatc gccgaggtgg agaacgacga gatgcccgcc	900
gacctgcca gcctggccgc cgacttcgtg gagagcaagg acgtgtgcaa gaactacgcc	960
gaggccaagg acgtgttcct gggcatgttc ctgtacgagt acgcccggcg gcaccccgac	1020
tacagcgtgg tgctgctgct gcggctggcc aagacctacg agaccaccct ggagaagtgc	1080
tgcgccgccg ccgaccccca cgagtgtac gccaaaggtgt tcgacgagtt caagcccctg	1140
gtggaggagc cccagaacct gatcaagcag aactgcgagc tgttcgagca gctgggcgag	1200
tacaagttcc agaacgccct gctggtgcgg tacaccaaga aggtgccccca ggtgagcacc	1260
cccaccctgg tggaggtgag ccggaacctg ggcaaggtgg gcagcaagtg ctgcaagcac	1320
cccgaggcca agcggatgcc ctgcgccgag gactacctga gcgtggtgct gaaccagctg	1380
tgctgtgctg acgagaagac ccccgtagc gaccgggtga ccaagtgtg caccgagagc	1440
ctggtgaacc ggcggccctg cttcagcgcc ctggaggtgg acgagacctg cgtgccccaa	1500
gagttcaacg ccgagacctt caccttcac gccgacatct gcaccctgag cgagaaggag	1560
cggcagatca agaagcagac cgccctggtg gagctggtga agcacaagcc caaggccacc	1620
aaggagcagc tgaaggccgt gatggacgac ttcgccgcct tcgtggagaa gtgctgcaag	1680
gccgacgaca aggagacctg cttcgccgag gagggaaga agctggtggc cgccagccag	1740
gccgccctgg gcctgggcag cggcggcgcc ggagcggcg gcggcggatc tggtaggagt	1800
ggcagtggag gagggggatc cgcgcgcaac ggggaccact gtccgctcgg gcccgggcgt	1860
tgctgccgtc tgcacacggt ccgcgctcg ctggaagacc tgggctgggc cgattgggtg	1920
ctgtcgccac gggaggtgca agtgaccatg tgcacggcg cgtgcccag ccagttccgg	1980
gcggcaaaca tgcacgcga gatcaagacg agcctgcacc gcctgaagcc cgacacggtg	2040
ccagcgccct gctgcgtgcc cgccagctac aatcccatgg tgctcattca aaagaccgac	2100

accggggtgt cgctccagac ctatgatgac ttgttagcca aagactgcca ctgcata 2157

<210> 84

<211> 2217

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 84

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagg cccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180

aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300

tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt 360

gatgtgatgt gactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600

gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660

cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa 720

gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840

aaacctctgt tggaaaaatc cactgcatt gccgaagtgg aaaatgatga gatgcctgct 900

gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960

gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080

tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag 1200

tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gcagcaaatag ttgtaaacaat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatagtg cacagaatcc	1440
ttggtgaaca ggcgacctg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttggtgc tgcaagtcaa	1740
gctgccttag gcttaggcag cggcggcggc ggagcggcg gcggcggatc tgggtggaggt	1800
ggcagtgagg gagggggatc cggcggcggc ggagcggcg gcggcggatc tgggtggaggt	1860
ggcagtgagg gagggggatc cgcgcgcaac ggggaccact gtccgctcgg gcccgggcgt	1920
tgctgccgtc tgcacacggt ccgcgcgtcg ctggaagacc tgggctgggc cgattgggtg	1980
ctgtcgccac gggaggtgca agtgacctg tgcacggcg cgtgcccagag ccagttccgg	2040
gcggcaaaac tgcacgcga gatcaagacg agcctgcacc gcctgaagcc cgacacggtg	2100
ccagcgccct gctgcgtgcc cgccagctac aatcccatgg tgctcattca aaagaccgac	2160
accgggggtg cgctccagac ctatgatgac ttgttagcca aagactgcca ctgcata	2217

<210> 85

<211> 2151

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 85

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa	60
gccttggtgt tgattgcctt tgctcagtat cttcagcagg cccatttga agatcatgta	120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300

tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt	360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacattatat	420
gaaattgccca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgccca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcacccctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaagtg ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc	1440
ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa	1740
gctgccttag gcttagcacc tgccccgct ccagcacccg cccagcccc tgctcccga	1800
ccagctcctg caccagcgcg caacggggac cactgtccgc tcgggcccgg gcgttgctgc	1860
cgtctgcaca cgggtccgcg gtcgctggaa gacctgggct gggccgattg ggtgctgtcg	1920

ccacgggagg tgcaagtac catgtgcatc ggcgctgcc cgagccagtt ccgggcggca	1980
aacatgcacg cgcagatcaa gacgagcctg caccgcctga agcccgacac ggtgccagcg	2040
ccctgctgcg tgcccgccag ctacaatccc atgggtgctca ttcaaaagac cgacaccggg	2100
gtgtcgtccc agacctatga tgacttgcta gccaaagact gccactgcat a	2151

<210> 86

<211> 2157

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 86

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa	60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt cccatttga agatcatgta	120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aatttgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt	360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat	420
gaaattgccca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgccca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcacacctgat	1020

tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaag ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc	1440
ttggtgaaca ggcgacctg cttttcagct ctggaagtcg atgaaacata cgttcccaa	1500
gagttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttggtgc tgcaagtcaa	1740
gctgccttag gcttaggcag cggcggcggc ggagcggcg gcggcggatc tggaggaggt	1800
ggcagtgag gagggggatc cgcgcgcaac ggggaccact gtccgctcgg gcccgggcgt	1860
tgctgccgtc tgcacacggt ccgcgcgtcg ctggaagacc tgggctgggc cgattgggtg	1920
ctgtcgccac gggagggtga agtgacctg tgcacggcg cgtgcccag ccagttccgg	1980
gcggcaaaca tgcacgcga gatcaagac agcctgcacc gcctgaagcc cgacacgggtg	2040
ccagcgccct gctgcgtgcc cgccagctac aatcccatgg tgctcattca aaagaccgac	2100
accgggggtg cgctccagac ctatgatgac ttgttagcca aagactgcca ctgcata	2157

<210> 87

<211> 2157

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 87

gacgcccaca agagcgaggt ggcccacaga ttcaaggacc tgggcgagga aaacttcaag	60
gccctggtgc tgatgcctt cgcccagtac ctgcagcaga gcccttcga ggaccacgtg	120
aagctggtca acgaagtgc cgagttcgcc aagacctgcg tggccgacga gagcgccgag	180

aactgcgaca agagcctgca caccctgttc ggcgacaagc tgtgcaccgt ggccaccctg	240
cgggaaacct acggcgagat ggccgactgc tgcgccaagc aggaacccga gcggaacgag	300
tgcttcctgc agcacaagga cgacaacccc aacctgcccc gactcgtgcg gcccgagggtg	360
gacgtgatgt gcaccgcctt ccacgacaac gaggaaacct tcctgaagaa gtacctgtac	420
gagatcgcca gacggcacc ctactttctac gcccccgagc tgctgttctt cgccaagcgg	480
tacaaggccg ctttcaccga gtgctgccag gccgccgata aggccgcctg cctgctgccc	540
aagctggacg agctgagaga tgagggcaag gccagctccg ccaagcagcg gctgaagtgc	600
gccagcctgc agaagttcgg cgagcgggcc tttaaggctt gggctgtggc ccggctgagc	660
cagagattcc ccaaggccga gtttgccgag gtgtccaagc tggtcaccga cctgaccaag	720
gtgcacaccg agtgttgtca cggcgacctg ctggaatgcg ccgacgacag agccgacctg	780
gccaagtaca tctgcgagaa ccaggacagc atcagcagca agctgaaaga gtgctgcgag	840
aagcccctgc tggaaaagag ccactgtatc gccgaggtgg aaaacgacga gatgcccgt	900
gacctgcccc gcctggccgc cgacttcgtg gaaagcaagg acgtgtgcaa gaactacgcc	960
gaggccaagg atgtgttcct gggcatgttc ctgtatgagt acgcccgcag acaccccgac	1020
tacagcgtgg tgctgctgct gcggctggcc aagacctacg agacaaccct ggaaaagtgc	1080
tgcgccgctg ccgaccccc aagtgctac gccaaaggtgt tcgacgagtt caagcctctg	1140
gtggaagaac ccagaacct gatcaagcag aactgcgagc tgttcgagca gctgggcgag	1200
tacaagttcc agaacgccct gctcgtgcgg tacaccaaga aagtgcccc ggtgtccacc	1260
cccaccctgg tcgaagtgtc ccggaacctg ggcaaagtgg gcagcaagtg ctgcaagcac	1320
cctgaggcca agcggatgcc ctgcgccgag gactacctgt ccgtggtgct gaaccagctg	1380
tgctgctgc acgagaaaac ccccggtgtcc gacagagtga ccaagtgtg taccgagagc	1440
ctggtcaaca gacggccctg cttcagcgcc ctggaagtgg acgagacata cgtgccccaa	1500
gagttcaacg ccgagacatt caccttcac gccgacatct gcaccctgag cgagaaagag	1560
cggcagatca agaagcagac cgccctggtc gagctggtca agcacaagcc caaggccacc	1620
aaagaacagc tgaaggccgt gatggacgac ttcgccgcct tcgtcgagaa gtgttgcaag	1680
gccgacgaca aagagacatg cttcgccgaa gagggcaaga aactggtggc cgcctctcag	1740

gccgccctgg gactgggatac tggcggcgga ggaagcggag gcggaggatac tgggggaggc	1800
ggctctggcg gagggggatac cgccagaaat ggcgaccact gtcccctggg ccctggccgg	1860
tgttgacagac tgcacacagt gcggggccagc ctggaagatac tgggctgggc cgattgggtg	1920
ctgagcccca gagaagtga ggtcacaaat tgcatacggc cctgccccag ccagttcaga	1980
gccgccaaca tgcacgcccc gatcaagacc agcctgcacc ggctgaagcc cgacaccgtg	2040
cctgccccctt gttgcgtgcc cgccagctac aaccccatgg tgctgattca gaaaaccgac	2100
accggcgtgt ccctgcagac ctacgacgat ctgctggcca aggactgcca ctgcatac	2157

<210> 88

<211> 2157

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 88

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaattttcaaa	60
gccttggtgt tgattgcctt tgctcagtat cttcagcagg cccattttga agatcatgta	120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt	360
gatgtgatgt gactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat	420
gaaattgcca gaagacatcc ttactttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900

gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcagaatth aatcaaaca aattgtgagc tttttgagca gcttggagag	1200
tacaaattcc agaatgctgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaacctt ggaaaagtgg gcagcaaatt ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaattgctg cacagaatcc	1440
ttggtgaaca ggcgacctg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttggtgc tgcaagtcaa	1740
gctgccttag gcttaggcag cggcggcggc ggagcggcg gcggcggatc tgggtggaggt	1800
ggcagtgagg gagggggatc cgcgcgcaac ggggaccact gtccgctcgg gcccgggcgt	1860
tgctgccgtc tgcacacggt ccgcgcgtcg ctggaagacc tgggctgggc cgattgggtg	1920
ctgtcgccac gggaggtgca agtgacctg tgcacggcg cgtgcccag ccagttccgg	1980
gcggcaaaca tgcacgcga gatcaagacg agcctgcacc gcctgaagcc cgacacggtg	2040
ccagcgccct gctgcgtgcc cgccagctac aatcccatgg tgctcattca aaagaccgac	2100
accggggtgt cgctccagac ctatgatgac ttgttagcca aagactgcca ctgcata	2157

<210> 89

<211> 2151

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 89

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa	60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt ccccatTTga agatcatgta	120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aattgtgaca aatcacttca taccctTTTT ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt	360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat	420
gaaattgcca gaagacatcc ttactTTTTat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgagaa gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttctt gggcatgttt ttgtatgaat atgcaagaag gcacctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagtctgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaag ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggctct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc	1440
ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa	1740
gctgccttag gcttagcacc tgcccccgct ccagcacccg cccagcccc tgctcccga	1800
ccagctcctg caccagcgcg caacggggac cactgtccgc tcggggcccg gcgttgctgc	1860
cgtctgcaca cgggtccgcgc gtcgctggaa gacctgggct gggccgattg ggtgctgtcg	1920
ccacggggagg tgcaagtgc catgtgcatc ggcgctgcc cgagccagtt ccgggcggca	1980
aacatgcacg cgagatcaa gacgagcctg caccgcctga agcccagac ggtgccagcg	2040
ccctgctgcg tgccccccag ctacaatccc atgggtgctca ttcaaaagac cgacaccggg	2100
gtgtcgctcc agacctatga tgacttgta gccaaagact gccactgcat a	2151

<210> 90
 <211> 2217
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion protein coding sequence

<400> 90	
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa	60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt cccatttga agatcatgta	120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aatttgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt	360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat	420
gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa	720

gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatacctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcaagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaag ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc	1440
ttggtgaaca ggcgacctg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttggttc tgcaagtcaa	1740
gctgccttag gcttaggcag cggcggcggc ggcagcggcg gcggcggatc tgggtggaggt	1800
ggcagtggag gagggggatc cggcggcggc ggcagcggcg gcggcggatc tgggtggaggt	1860
ggcagtggag gagggggatc cgcgcgcaac ggggaccact gtccgctcgg gcccgggcgt	1920
tgctgccgtc tgcacacggt ccgcgctcg ctggaagacc tgggctgggc cgattgggtg	1980
ctgtcgccac gggaggtgca agtgacctg tgcacggcg cgtgcccag ccagttccgg	2040
gcggcaaaca tgcacgcga gatcaagac agcctgcacc gcctgaagcc cgacacggtg	2100
ccagcgccct gctgcgtgcc cgccagctac aatcccatgg tgctcattca aaagaccgac	2160
accggggtgt cgctccagac ctatgatgac ttgttagcca aagactgcca ctgcata	2217

<210> 91

<211> 2157

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 91

gacgcccaca agagcgaggt ggcccaccgg ttcaaggacc tgggcgagga gaacttcaag	60
gccctggtgc tgatcgctt cgcccagtac ctgcagcagt ccccttcga ggaccacgtg	120
aagctggtga acgaggtgac cgagttcgcc aagacctgcg tggccgacga gagcgccgag	180
aactgcgaca agagcctgca caccctgttc ggcgacaagc tgtgcaccgt ggccaccctg	240
cgggagacct acggcgagat ggccgactgc tgcgccaagc aggagcccga gcggaacgag	300
tgcttcctgc agcacaagga cgacaacccc aacctgcccc ggctggtgcg gcccgaggtg	360
gacgtgatgt gcaccgcctt ccacgacaac gaggagacct tcctgaagaa gtacctgtac	420
gagatcgccc ggcggcaccc ctactttctac gccccgagc tgctgttctt cgccaagcgg	480
tacaaggccg ccttcaccga gtgctgccag gccgccgaca aggccgcctg cctgctgccc	540
aagctggacg agctgcggga cgagggcaag gccagcagcg ccaagcagcg gctgaagtgc	600
gccagcctgc agaagttcgg cgagcgggcc ttcaaggcct gggccgtggc ccggctgagc	660
cagcggttcc ccaaggccga gttcgccgag gtgagcaagc tggtgaccga cctgaccaag	720
gtgcacaccg agtgctgcca cggcgacctg ctggagtgcg ccgacgaccg ggccgacctg	780
gccaagtaca tctgcgagaa ccaggacagc atcagcagca agctgaagga gtgctgcgag	840
aagcccctgc tggagaagag ccaactgcac gccgaggtgg agaacgacga gatgcccgcc	900
gacctgcccga gcctggccgc cgacttcgtg gagagcaagg acgtgtgcaa gaactacgcc	960
gaggccaagg acgtgttcct gggcatgttc ctgtacgagt acgcccggcg gcaccccgac	1020
tacagcgtgg tgctgctgct gcggctggcc aagacctacg agaccaccct ggagaagtgc	1080
tgcgccgccg ccgaccccca cgagtgtac gccaaagtggt tcgacgagtt caagcccctg	1140
gtggaggagc cccagaacct gatcaagcag aactgcgagc tgttcgagca gctgggcgag	1200
tacaagttcc agaacgccct gctggtgcgg tacaccaaga aggtgccccca ggtgagcacc	1260
cccaccctgg tggaggtgag ccggaacctg ggcaaggtgg gcagcaagtg ctgcaagcac	1320
cccgaggcca agcggtatgcc ctgcgccgag gactacctga gcgtggtgct gaaccagctg	1380

tgcgtgctgc acgagaagac ccccgtgagc gaccgggtga ccaagtgctg caccgagagc 1440
 ctggtgaacc ggcgggccctg cttcagcgcc ctggaggtgg acgagacctt cgtgcccagg 1500
 gagttcaacg ccgagacctt caccttcac gccgacatct gcaccctgag cgagaaggag 1560
 cggcagatca agaagcagac cgccctggtg gagctggtga agcacaagcc caaggccacc 1620
 aaggagcagc tgaaggccgt gatggacgac ttccgcccct tcgtggagaa gtgctgcaag 1680
 gccgacgaca aggagacctg cttcgccgag gagggaaga agctggtggc cgccagccag 1740
 gccgcccctg gcctggggcag cggcggcggc ggcagcggcg gcggcggtatc tgggtggaggt 1800
 ggcatggtgag gagggggatc cgctcgcaac ggtgaccact gccctctggg tcctggtcgc 1860
 tgctgccgcc tgcacaccgt tcgcgcttct ctggaagacc tgggttgggc tgactgggtt 1920
 ctgtctcctc gcgaagttca gggtaccatg tgcacgggtg cttgcccttc tcagttccgc 1980
 gctgctaaca tgcacgcttg gatcaaac tctctgcacc gcctgaaacc tgacaccgtt 2040
 cctgctcctt gctgcgttcc tgcttcttac aaccctatgg ttctgatcca gaaaaccgac 2100
 accggtgttt ctctgcagac ctacgacgac ctgctggcta aagactgcca ctgcac 2157

<210> 92

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 92

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His

275

280

285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
625 630 635 640

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
645 650 655

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
660 665 670

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
675 680 685

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
690 695 700

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
705 710 715 720

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
725 730 735

<210> 93

<211> 734

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 93

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His
625 630 635 640

Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu
645 650 655

Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser
660 665 670

Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His
675 680 685

Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser
690 695 700

Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu
705 710 715 720

Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
725 730

<210> 94

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 94

Glu Phe His His His His His His Asp Ala His Lys Ser Glu Val Ala
1 5 10 15

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

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Ser Pro Phe Glu Asp His Val
35 40 45

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
50 55 60

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
65 70 75 80

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

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
100 105 110

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
115 120 125

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
130 135 140

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
145 150 155 160

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
165 170 175

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
180 185 190

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
195 200 205

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
210 215 220

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
225 230 235 240

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
245 250 255

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
260 265 270

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
275 280 285

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
290 295 300

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
305 310 315 320

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
325 330 335

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
340 345 350

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
355 360 365

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
370 375 380

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
385 390 395 400

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
405 410 415

Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val

420

425

430

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
 435 440 445

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
 450 455 460

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
 465 470 475 480

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
 485 490 495

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

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
 515 520 525

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
 530 535 540

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
 545 550 555 560

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
 565 570 575

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
 580 585 590

Leu Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 595 600 605

Gly Ser Gly Gly Gly Gly Ser Leu Glu Val Leu Phe Gln Gly Pro Ala
 610 615 620

Arg Asn Gly Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
 625 630 635 640

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
645 650 655

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
660 665 670

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
675 680 685

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
690 695 700

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
705 710 715 720

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
725 730 735

<210> 95
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 95
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt ccccatattga agatcatgta 120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
tgcttcttgc aacacaaaaga tgacaacca aacctcccc gattggtgag accagaggtt 360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420
gaaattgccca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540

aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcaagaattt aatcaaaca aattgtgagc tttttgagca gcttggagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaattg ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc	1440
ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa	1740
gctgccttag ggcttggaag cggcggaggg gggagtggcg gcggtggctc cggggggggc	1800
ggatccggcg gagggggcag cgggggtgga gggagtggcg ggggaggatc agggggagga	1860
ggatcaggag ggggcggaag tgatcattgc cctctcgggc ccggacggtg ttgccgcctc	1920
cacactgtga gggcttcact tgaagacctt ggatgggccg actgggtgct gtccccaaga	1980
gaggtacaag tcacaatgtg tattggcgcc tgccccagcc agtttcgcgc cgctaacatg	2040
cacgcccaga taaaaaccag cctgcaccgc ctgaagcccg acacggtgcc agcgccctgc	2100
tgctgccccg ccagctacaa tcccatggtg ctcatcctaaa agaccgacac cggggtgtcg	2160

ctccagacct atgatgactt gttagccaaa gactgccact gcata 2205

<210> 96
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 96
ggggaccact gtccgctcgg gcccgggcgt tgctgccgtc tgcacacggt ccgcgcgtcg 60
ctggaagacc tgggctgggc cgattgggtg ctgtcgccac gggaggtgca agtgaccatg 120
tgcatcggcg cgtgcccag ccagttccgg gcggcaaaca tgcacgcgca gatcaagacg 180
agcctgcacc gcctgaagcc cgacacggtg ccagcgccct gctgcgtgcc cgccagctac 240
aatcccatgg tgctcattca aaagaccgac accgggggtgt cgctccagac ctatgatgac 300
ttgtagcca aagactgcca ctgcata 327

<210> 97
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 97
gaccactgtc cgctcgggcc cgggcgttgc tgccgtctgc acacggtccg cgcgtcgtcg 60
gaagacctgg gctgggccga ttgggtgctg tcgccacggg aggtgcaagt gaccatgtgc 120
atcggcgcgt gcccagacca gttccgggcg gcaaacatgc acgcgcagat caagacgagc 180
ctgcaccgcc tgaagcccga cacggtgcca gcgccctgct gcgtgcccgc cagctacaat 240
cccatggtgc tcattcaaaa gaccgacacc ggggtgtcgc tccagaccta tgatgacttg 300
ttagccaaag actgccactg cata 324

<210> 98
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> GDF15 variant

<400> 98

gatcattgcc ctctcgggcc cggacgggtgt tgccgcctcc acactgtgag ggcttcactt	60
gaagaccttg gatgggccga ctgggtgctg tccccaaagag aggtacaagt cacaatgtgt	120
attggcgcct gccccagcca gtttcgcgcc gctaacaatgc acgcccagat aaaaaccagc	180
ctgcaccgcc tgaagcccga cacggtgcca gcgccctgct gcgtgcccgc cagctacaat	240
cccatgggtgc tcattcaaaa gaccgacacc ggggtgtcgc tccagaccta tgatgacttg	300
ttagccaaag actgccactg cata	324

<210> 99

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> GDF15 variant

<400> 99

gatcattgtc cccttggacc gggtagatgc tgtcgcctgc acactgtgcg ggcttcactg	60
gaggacctcg gctgggctga ctgggtgctg tccccacggg aggtgcaagt gaccatgtgc	120
atcggcgcct gtccttcgca attccgggcc gcgaatatgc acgcccagat caagacctcc	180
ctgcatcgcc tcaagcccga cactgtgcct gctccatgct gtgtgccggc ctcctataac	240
cccatgggtgc tgatccagaa aaccgatacc ggcgtcagcc tgcagacgta tgatgatctg	300
ctggccaagg actgccattg catc	324

<210> 100

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> GDF15 variant

<400> 100

cactgtccgc tcgggcccg gcttgctgc cgtctgcaca cgggccgcgc gtcgctggaa	60
gacctgggct gggccgattg ggtgctgtcg ccacgggagg tgcaagtgac catgtgcatc	120
ggcgcgtgcc cgagccagtt ccgggcggca aacatgcacg cgcagatcaa gacgagcctg	180

caccgcctga agcccgacac ggtgccagcg ccctgctgcg tgcccgccag ctacaatccc	240
atggtgctca ttcaaaagac cgacaccggg gtgtcgctcc agacctatga tgacttgta	300
gccaaagact gccactgcat a	321

<210> 101
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GDF15 variant

<400> 101	
cattgccctc tcgggcccgg acggtgttgc cgcctccaca ctgtgagggc ttcacttgaa	60
gaccttggaat gggccgactg ggtgctgtcc ccaagagagg tacaagtcac aatgtgtatt	120
ggcgcctgcc ccagccagtt tcgcgccgct aacatgcacg cccagataaa aaccagcctg	180
caccgcctga agcccgacac ggtgccagcg ccctgctgcg tgcccgccag ctacaatccc	240
atggtgctca ttcaaaagac cgacaccggg gtgtcgctcc agacctatga tgacttgta	300
gccaaagact gccactgcat a	321

<210> 102
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GDF15 variant

<400> 102	
cattgtcccc ttggaccggg tagatgctgt cgcctgcaca ctgtgcgggc ttcactggag	60
gacctcggct gggctgactg ggtgctgtcc ccacgggagg tgcaagtga catgtgcatc	120
ggcgcctgtc cttcgcaatt ccgggcccgc aatatgcacg cccagatcaa gacctccctg	180
catcgctca agcccgacac tgtgcctgct ccatgctgtg tgccggcctc ctataacccc	240
atggtgctga tccagaaaac cgataccggc gtcagcctgc agacgtatga tgatctgctg	300
gccaaaggact gccattgcat c	321

<210> 103

<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 103
tgtccgctcg ggcccgggcg ttgctgccgt ctgcacacgg tccgcgcgtc gctggaagac 60
ctgggctggg ccgattgggt gctgtcgcca cgggaggtgc aagtgaccat gtgcatcggc 120
gcgtgcccga gccagttccg ggcggaac atgcacgcgc agatcaagac gagcctgcac 180
cgcctgaagc ccgacacggt gccagcggc tgctgcgtgc ccgccagcta caatcccatg 240
gtgctcattc aaaagaccga caccggggtg tcgctccaga cctatgatga cttgttagcc 300
aaagactgcc actgcata 318

<210> 104
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 104
tgccctctcg ggcccggacg gtgttgccgc ctccacactg tgagggcttc acttgaagac 60
cttgatggg ccgactgggt gctgtcccca agagaggtac aagtcacaat gtgtattggc 120
gcctgcccc gccagtttcg cgccgctaac atgcacgccc agataaaaac cagcctgcac 180
cgcctgaagc ccgacacggt gccagcggc tgctgcgtgc ccgccagcta caatcccatg 240
gtgctcattc aaaagaccga caccggggtg tcgctccaga cctatgatga cttgttagcc 300
aaagactgcc actgcata 318

<210> 105
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 105
tgtcccttg gaccgggtag atgctgtcgc ctgcacactg tgcgggcttc actggaggac 60

ctcggctggg ctgactgggt gctgtcccca cgggaggtgc aagtgaccat gtgcatcggc	120
gcctgtcctt cgcaattccg ggccgcgaat atgcacgccc agatcaagac ctccctgcat	180
cgcctcaagc ccgacactgt gcctgctcca tgctgtgtgc cggcctccta taaccccatg	240
gtgctgatcc agaaaaccga taccggcgtc agcctgcaga cgtatgatga tctgctggcc	300
aaggactgcc attgcatc	318

<210> 106
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GDF15 variant

<400> 106	
tgccgtctgc acacggtccg cgcgtcgtg gaagacctgg gctgggccga ttgggtgctg	60
tgccacggg aggtgcaagt gaccatgtgc atcggcgcgt gcccagacca gttccgggcg	120
gcaaacatgc acgcgcagat caagacgagc ctgcaccgcc tgaagcccga cacggtgcc	180
gcgccctgct gcgtgcccgc cagctacaat cccatggtgc tcattcaaaa gaccgacacc	240
ggggtgtcgc tccagaccta tgatgacttg ttagccaaag actgccactg cata	294

<210> 107
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GDF15 variant

<400> 107	
tgccgcctcc aactgtgag ggcttcactt gaagaccttg gatgggccga ctgggtgctg	60
tcccaagag aggtacaagt cacaatgtgt attggcgcct gcccagacca gtttcgcgcc	120
gctaacatgc acgcccagat aaaaaccagc ctgcaccgcc tgaagcccga cacggtgcc	180
gcgccctgct gcgtgcccgc cagctacaat cccatggtgc tcattcaaaa gaccgacacc	240
ggggtgtcgc tccagaccta tgatgacttg ttagccaaag actgccactg cata	294

<210> 108

<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> GDF15 variant

<400> 108
tgtcgcctgc acactgtgcg ggcttcactg gaggacctcg gctgggctga ctgggtgctg 60
tccccacggg aggtgcaagt gaccatgtgc atcggcgcct gtccttcgca attccgggcc 120
gcgaatatgc acgcccagat caagacctcc ctgcatcgcc tcaagcccga cactgtgcct 180
gctccatgct gtgtgccggc ctctataac cccatgggtgc tgatccagaa aaccgatacc 240
ggcgtcagcc tgcagacgta tgatgatctg ctggccaagg actgccattg catc 294

<210> 109
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 109
gatgcgcaca agtcggaagt ggcccatcgc tttaaggacc tgggagaaga gaacttcaag 60
gccctgggtcc tgatcgcgtt cgcccagtac ctccagcagt ccccgtttga ggaccacgtc 120
aagcttgtga acgaagtgc cgagttcgca aagacttgtg tggccgatga gtccgccgaa 180
aactgcgaca agtccctgca caccttgttc ggagacaagc tgtgcaccgt cgcgactttg 240
cgggagactt acggcgaaat ggcggactgc tgcgcaaagc aggagcccga aaggaacgag 300
tgcttcctgc aacacaagga cgacaacccg aaccttccga gactcgtgcg gcctgaggtc 360
gacgtgatgt gactgcatt ccatgataac gaagaaacat tcctgaagaa gtacctgtat 420
gaaattgcc aacgcccacc gtacttctac gccccgaac tgctgttctt cgccaagaga 480
tacaaggccg cctttaccga atgttgtaaa gccgccgata aggcagcgtg cctgctgccg 540
aagttggacg agctcaggga cgaaggaaag gcctcgtccg ccaagcagag gctgaagtgc 600
gcgtcgctcc agaagtttgg agagcgggct tttaaggcct gggcagtggc taggttgagc 660
cagaggttcc ccaaggcgga gtttgccgaa gtgtccaagc tcgtgactga cctgactaaa 720
gtccataacc aatgctgcc cggcgatctg ctcaatgcg cagatgaccg ggcggatttg 780

gccaagtaca tttgcgaaaa ccaagactcc ataagctcca agctgaagga gtgctgtgaa	840
aagcctctgc tcgagaagtc ccactgtatc gccgaggtgg agaacgacga aatgccggca	900
gacctcccta gcctggcagc cgacttcgtc gaatccaagg acgtgtgcaa gaactacgcc	960
gaagcgaagg acgtgttcct gggaatgttc ctgtacgagt acgccagacg gcatccagac	1020
tactccgtgg tgcttctctt gcggctggcc aagacttatg aaacgaccct ggagaaatgt	1080
tgcgctgctg ctgaccaca cgagtgtac gccaaagtgt tcgacgagtt taagcctctc	1140
gtggaggaac cccagaacct catcaagcag aactgcgaac ttttcgagca gctcggggag	1200
tacaagttcc aaaacgcgct gcttgtccgc tacaccaaga aagtgccgca agtgtccaca	1260
ccgaccctcg tggaagtgtc caggaacctg ggcaaagtcg gaagcaaagtg ttgcaagcac	1320
cccgaagcca agcgcgtgcc gtgcgcagag gactaccttt cgggtggtgtt gaaccagctc	1380
tgcgctcctg acgaaaagac cccggtgtca gaccgcgtga ccaagtgtg taccgaaagc	1440
ctcgtgaatc ggcgcccctg cttctcggcc ctggaggtgg acgaaactta cgtgccgaaa	1500
gagttcaacg cggaacaccc cacctttcat gccgatatct gcaccctgtc cgagaaggag	1560
cggcagatca agaagcagac cgccctggtg gagcttgtga aacacaagcc gaaggccact	1620
aaggaacagc tgaaggccgt catggacgat ttcgctgcct tcgtcgagaa gtgctgcaag	1680
gccgacgaca aggagacttg cttcgtgaa gaagggaaga agcttgtggc cgctagccag	1740
gctgcactgg gactgggtag cgggtggaggg ggatcagggg gtggtggatc gggaggagga	1800
ggatcaggag gtggcggctc aggaggaggc ggatcaggcg gtggaggatc cggaggcgga	1860
ggatcgggtg gaggaggctc agcgaggaac ggggatcatt gtccccttg accgggtaga	1920
tgctgtcgcc tgcacactgt gcgggcttca ctggaggacc tcggctgggc tgactgggtg	1980
ctgtccccac gggagggtgca agtgaccatg tgcatcggcg cctgtccttc gcaattccgg	2040
gccgcgaata tgcacgcca gatcaagacc tccctgcatc gcctcaagcc cgacactgtg	2100
cctgtcccat gctgtgtgcc ggcctcctat aaccccatgg tgctgatcca gaaaaccgat	2160
accggcgtca gcctgcagac gtatgatgat ctgctggcca aggactgcca ttgcatc	2217

<210> 110
 <211> 2205
 <212> DNA

<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 110

gatgcgcaca agtcggaagt ggcccatcgc ttttaaggacc tgggagaaga gaacttcaag	60
gccctggtcc tgatcgcgtt cgcccagtac ctccagcagt ccccgtttga ggaccacgtc	120
aagcttgtga acgaagtgac cgagttcgca aagacttgtg tggccgatga gtccgccgaa	180
aactgcgaca agtccctgca caccttgttc ggagacaagc tgtgcaccgt cgcgactttg	240
cgggagactt acggcgaaat ggcggaactgc tgcgcaaagc aggagcccga aaggaacgag	300
tgcttcctgc aacacaagga cgacaacccg aaccttccga gactcgtgcg gcctgaggtc	360
gacgtgatgt gactgcatt ccatgataac gaagaaacat tcctgaagaa gtacctgtat	420
gaaattgcc aacgcccacc gtacttctac gccccgaac tgctgttctt cgccaagaga	480
tacaaggccg cctttaccga atgttgctca gccgccgata aggcagcgtg cctgctgccg	540
aagttggacg agctcaggg aagaggaaag gcctcgtccg ccaagcagag gctgaagtgc	600
gcgtcgctcc agaagtttgg agagcgggct ttttaaggcct gggcagtggt taggttgagc	660
cagaggttcc ccaaggcgga gtttgccgaa gtgtccaagc tcgtgactga cctgactaaa	720
gtccataaccg aatgctgcca cggcgatctg ctcgaatgcg cagatgaccg ggcggatttg	780
gccaagtaca tttgcgaaaa ccaagactcc ataagctcca agctgaagga gtgctgtgaa	840
aagcctctgc tcgagaagtc ccactgtatc gccgaggtgg agaacgacga aatgccggca	900
gacctcccta gcctggcagc cgacttcgtc gaatccaagg acgtgtgcaa gaactacgcc	960
gaagcgaagg acgtgttcct gggaatgttc ctgtacgagt acgccagacg gcatccagac	1020
tactccgtgg tgcttctctt gcggctggcc aagacttatg aaacgaccct ggagaaatgt	1080
tgcgtgctg ctgaccaca cgagtgtac gccaaagtgt tcgacgagtt taagcctctc	1140
gtggaggaac ccagaaacct catcaagcag aactgcgaac ttttcgagca gctcggggag	1200
tacaagttcc aaaacgcgct gcttgtccgc tacaccaaga aagtgccgca agtgtccaca	1260
ccgaccctcg tggaagtgtc caggaacctg ggcaaagtcg gaagcaaagt ttgcaagcac	1320
cccgaagcca agcgcgtgcc gtgcgcagag gactaccttt cgggtggtgtt gaaccagctc	1380
tgcgtcctgc acgaaaagac cccggtgtca gaccgcgtga ccaagtgtg taccgaaagc	1440

ctcgtgaatc ggcgcccctg cttctcggcc ctggaggtgg acgaaactta cgtgccgaaa 1500
gagttcaacg cggaaacctt cacctttcat gccgatatct gcaccctgtc cgagaaggag 1560
cggcagatca agaagcagac cgccctgggtg gagcttgtga aacacaagcc gaaggccact 1620
aaggaacagc tgaaggccgt catggacgat ttcgctgcct tcgtcgagaa gtgctgcaag 1680
gccgacgaca aggagacttg cttcgtgaa gaagggaaga agcttgtggc cgctagccag 1740
gctgcactgg gactgggtag cgggtggaggg ggatcagggg gtggtggatc gggaggagga 1800
ggatcaggag gtggcggctc aggaggaggc ggatcaggcg gtggaggatc cggaggcgga 1860
ggatcgggtg gaggaggctc agatcattgt ccccttggac cgggtagatg ctgtcgcctg 1920
cacactgtgc gggcttcact ggaggacctc ggctgggctg actgggtgct gtccccacgg 1980
gaggtgcaag tgaccatgtg catcggcgcc tgtccttcgc aattccgggc cgcgaatatg 2040
cacgcccaga tcaagacctc cctgcatcgc ctcaagcccg acactgtgcc tgctccatgc 2100
tgtgtgccgg cctcctataa ccccatggtg ctgatccaga aaaccgatac cggcgtcagc 2160
ctgcagacgt atgatgatct gctggccaag gactgccatt gcatc 2205

<210> 111
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 111

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

485

490

495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Ser
 580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His
 625 630 635 640

Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu
 645 650 655

Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser
 660 665 670

Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His
 675 680 685

Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser
 690 695 700

Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu
705 710 715 720

Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
725 730

<210> 112
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 112

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

130

135

140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
595 600 605

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu
625 630 635 640

Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met
645 650 655

Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala
660 665 670

Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala
675 680 685

Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys
690 695 700

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

Asp Cys His Cys Ile
725

<210> 113
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 113

His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn
1 5 10 15

Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Ser
20 25 30

Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala
35 40 45

Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu
50 55 60

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

Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg
85 90 95

Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg
100 105 110

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

Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His
130 135 140

Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys
145 150 155 160

Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu
165 170 175

Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala
180 185 190

Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala
195 200 205

Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala
210 215 220

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

Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala
245 250 255

Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys
260 265 270

Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile
275 280 285

Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala
290 295 300

Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala
305 310 315 320

Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His
325 330 335

Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu
340 345 350

Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr
355 360 365

Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn
370 375 380

Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys
385 390 395 400

Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val
405 410 415

Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly
420 425 430

Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu
435 440 445

Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys
450 455 460

Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val
465 470 475 480

Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val
485 490 495

Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys
500 505 510

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

Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala
530 535 540

Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp
545 550 555 560

Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala
565 570 575

Ser Gln Ala Ala Leu Gly Leu Gly Ser Gly Gly Gly Gly Ser Gly Gly
580 585 590

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
595 600 605

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
610 615 620

Ser Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr

625		630		635		640
Val Arg Ala Ser	Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser					
	645		650		655	
Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln						
	660		665		670	
Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg						
	675		680		685	
Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr						
	690		695		700	
Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln						
705		710		715		720
Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile						
	725		730			

<210> 114
 <211> 2199
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion protein coding sequence

<400> 114	
cacaagagtg aggttgctca tcggtttaaa gatttgggag aagaaaattt caaagccttg	60
gtgttgattg cctttgctca gtatcttcag cagtcccat ttgaagatca tgtaaaatta	120
gtgaatgaag taactgaatt tgcaaaaaca tgtgttgctg atgagtcagc tgaaaattgt	180
gacaaatcac ttcataacct ttttgagagac aaattatgca cagttgcaac tcttcgtgaa	240
acctatggtg aaatggctga ctgctgtgca aaacaagaac ctgagagaaa tgaatgcttc	300
ttgcaacaca aagatgacaa cccaaacctc ccccgattgg tgagaccaga ggttgatgtg	360
atgtgcactg cttttcatga caatgaagag acatttttga aaaaatactt atatgaaatt	420
gccagaagac atccttactt ttatgccccg gaactccttt tctttgctaa aaggtataaa	480
gctgctttta cagaatgttg ccaagctgct gataaagctg cctgcctgtt gccaaagctc	540

gatgaacttc gggatgaagg gaaggcttcg tctgccaaac agagactcaa gtgtgccagt	600
ctccaaaaat ttggagaaag agctttcaaa gcatgggcag tagctcgctt gagccagaga	660
tttcccaaag ctgagtttgc agaagtttcc aagttagtga cagatcttac caaagtccac	720
acggaatgct gccatggaga tctgcttgaa tgtgctgatg acagggcgga ccttgccaag	780
tatatctgtg aaaatcaaga ttcgatctcc agtaaactga aggaatgctg tgaaaaacct	840
ctgttgghaaa aatcccactg cattgccgaa gtggaaaatg atgagatgcc tgctgacttg	900
ccttcattag ctgctgattt tgttgaaagt aaggatgttt gcaaaaacta tgctgaggca	960
aaggatgtct tcctgggcat gtttttgtat gaatatgcaa gaaggcatcc tgattactct	1020
gtcgtgctgc tgctgagact tgccaagaca tatgaaacca ctctagagaa gtgctgtgcc	1080
gctgcagatc ctcatgaatg ctatgccaaa gtgttcgatg aatttaaacc tcttgtggaa	1140
gagcctcaga atttaataca acaaaattgt gagctttttg agcagcttgg agagtacaaa	1200
ttccagaatg cgctattagt tcgttacacc aagaaagtac cccaagtgtc aactccaact	1260
cttgtagagg tctcaagaaa cctaggaaaa gtgggcagca aatgttgtaa acatcctgaa	1320
gcaaaaagaa tgccctgtgc agaagactat ctatccgtgg tcctgaacca gttatgtgtg	1380
ttgcatgaga aaacgccagt aagtacaga gtcaccaa atgctgcacaga atccttggtg	1440
aacaggcgac catgcttttc agctctggaa gtcgatgaaa catacgttcc caaagagttt	1500
aatgctgaaa cattcacctt ccatgcagat atatgcacac tttctgagaa ggagagacaa	1560
atcaagaaac aaactgcact tgttgagctc gtgaaacaca agcccaaggc aacaaaagag	1620
caactgaaag ctgttatgga tgatttcgca gctttttagt agaagtgtg caaggctgac	1680
gataaggaga cctgctttgc cgaggagggt aaaaaacttg ttgctgcaag tcaagctgcc	1740
ttagggcttg gaagcggcgg aggggggagt ggcggcggtg gctccggggg gggcggatcc	1800
ggcggagggg gcagcggggg tggaggaggat ggcgggggag gatcaggggg aggaggatca	1860
ggagggggcg gaagtgatca ttgccctctc gggcccggac ggtgttgccg cctccacact	1920
gtgagggctt cacttgaaga ccttggaagg gccgactggg tgctgtcccc aagagaggta	1980
caagtcacaa tgtgtatttg cgcctgcccc agccagtttc gcgccgctaa catgcacgcc	2040
cagataaaaa ccagcctgca ccgcctgaag cccgacacgg tgccagcgcc ctgctgcgtg	2100

cccgccagct acaatcccat ggtgctcatt caaaagaccg acaccggggt gtcgctccag 2160

acctatgatg acttgtagc caaagactgc cactgcata 2199

<210> 115

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein

<400> 115

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ala Gly Gly Gly Gly Ala
580 585 590

Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Gly
595 600 605

Gly Gly Gly Ala Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Gly Gly
610 615 620

Gly Gly Ala Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
625 630 635 640

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
645 650 655

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
660 665 670

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
675 680 685

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
690 695 700

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
705 710 715 720

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
725 730 735

<210> 116
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 116
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60
gccttgggtgt tgattgcctt tgctcagtat cttcagcagt cccatttga agatcatgta 120

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atgggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattgggtgag accagagggt	360
gatgtgatgt gcaactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat	420
gaaattgccca gaagacatcc ttactttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgccca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcacccctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctgagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaagtg ttgtaaakat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc	1440
ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttggtgc tgcaagtcaa	1740

gctgccttag ggcttggtgc tggaggaggc ggggcgggcg gcgggggtgc cgggtgggggt 1800
ggcgcagggg gaggtggtgc ggggtggtggt ggggctggtg ggggaggtgc aggcggtggc 1860
ggtgccgggg ggggtggcgc ggatcattgc cctctcgggc ccggacggtg ttgccgcctc 1920
cacactgtga gggcttcact tgaagacctt ggatgggccg actgggtgct gtccccaaga 1980
gaggtacaag tcacaatgtg tattggcgcc tgccccagcc agtttcgcgc cgctaacatg 2040
cacgcccaga taaaaaccag cctgcaccgc ctgaagcccg acacggtgcc agcgccctgc 2100
tgcgtgcccc ccagctacaa tcccatggtg ctcatcctaaa agaccgacac cggggtgtcg 2160
ctccagacct atgatgactt gttagccaaa gactgccact gcata 2205

<210> 117
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 117

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100

105

110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Ala Pro Ala Pro Ala
580 585 590

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Asp His Cys
595 600 605

Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser
610 615 620

Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val
625 630 635 640

Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala
645 650 655

Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp
660 665 670

Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val
675 680 685

Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp
690 695 700

Leu Leu Ala Lys Asp Cys His Cys Ile
705 710

<210> 118
<211> 2139
<212> DNA
<213> Artificial Sequence

<220>

<223> fusion protein coding sequence

<400> 118

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa	60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt cccatttga agatcatgta	120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt	360
gatgtgatgt gactgcttt tcatgacaat gaagagacat ttttgaaaaa ataccttat	420
gaaattgcc aagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaa	720
gtccacacgg aatgctgcc tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcacctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcaagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gcagcaaatg ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc	1440

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa	1500
gagtттаatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca	1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag	1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa	1740
gctgccttag ggcttgccacc agcccctgcc cctgcacctg cacctgctcc cgcaccggct	1800
ccagccccag ctccggatca ttgccctctc gggcccggac ggtggtgccg cctccacact	1860
gtgagggctt cacttgaaga ccttgatgg gccgactggg tgctgtcccc aagagaggta	1920
caagtcacaa tgtgtattgg cgcctgcccc agccagtttc gcgccgctaa catgcacgcc	1980
cagataaaaa ccagcctgca ccgcctgaag cccgacacgg tgccagcgcc ctgctgcgtg	2040
cccgccagct acaatcccat ggtgctcatt caaaagaccg acaccggggt gtcgctccag	2100
acctatgatg acttgtttagc caaagactgc cactgcata	2139

<210> 119
 <211> 717
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein

<400> 119

Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu
1				5					10					15	

Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln
			20					25					30		

Gln	Ser	Pro	Phe	Glu	Asp	His	Val	Lys	Leu	Val	Asn	Glu	Val	Thr	Glu
		35					40					45			

Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys
	50					55					60				

Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu
65					70					75				80	

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Ala Pro Ala Pro Ala
580 585 590

Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
595 600 605

Pro Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu His Thr
610 615 620

Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val Leu Ser
625 630 635 640

Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro Ser Gln
645 650 655

Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu His Arg
660 665 670

Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr
675 680 685

Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser Leu Gln
690 695 700

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

705

710

715

<210> 120
<211> 2151
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 120
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt cccatttga agatcatgta 120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt 360
gatgtgatgt gactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420
gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa 720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900
gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140
gtggaagagc ctcaagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag 1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact 1260

ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gcagcaaata ttgtaaacaat 1320
 cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta 1380
 tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatactg cacagaatcc 1440
 ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa 1500
 gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560
 agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca 1620
 aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680
 gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttggtgc tgcaagtcaa 1740
 gctgccttag ggcttgacc agcccctgcc cctgcacctg cacctgctcc cgcaccggct 1800
 ccagccccag ctccgggtcc agctcctgat cattgccctc tcgggcccgg acggtgttgc 1860
 cgctccaca ctgtgagggc ttcacttgaa gaccttgat gggccgactg ggtgctgtcc 1920
 ccaagagagg tacaagtcac aatgtgtatt ggcgcctgcc ccagccagtt tcgcgccgct 1980
 aacatgcacg cccagataaa aaccagcctg caccgcctga agcccgacac ggtgccagcg 2040
 ccctgctgcg tgcccgcag ctacaatccc atggtgctca ttcaaaagac cgacaccggg 2100
 gtgtcgctcc agacctatga tgacttgta gccaaagact gccactgcat a 2151

<210> 121
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein

<400> 121

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser

465		470		475		480
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr						
		485		490		495
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp						
		500		505		510
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala						
		515		520		525
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu						
		530		535		540
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys						
545			550		555	560
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val						
		565		570		575
Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Gly Ser Glu Gly Lys Ser						
		580		585		590
Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly						
		595		600		605
Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly Ser Gly						
		610		615		620
Ser Glu Ser Lys Ser Thr Gly Gly Ser Asp His Cys Pro Leu Gly Pro						
625			630		635	640
Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu						
		645		650		655
Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met						
		660		665		670
Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala						
		675		680		685

Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val Pro Ala
690 695 700

Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys
705 710 715 720

Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys
725 730 735

Asp Cys His Cys Ile
740

<210> 122
<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 122
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt cccatttga agatcatgta 120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt 360
gatgtgatgt gactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420
gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa 720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcctcctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcagaattt aatcaaacia aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaacctt ggaaaagtgg gcagcaaagt ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca caaatgctg tactgagagc	1440
ttggtcaaca ggcggccgtg cttcagcgcc ctcgaggtgg atgagactta tgtcccaaag	1500
gagtttaatg cggaaacttt tactttccac gcagacattt gcaccttgct tgaaaaggaa	1560
agacagatta agaaacagac tgctcttgct gaactggtaa aacataaacc aaaagctacg	1620
aaggagcagc ttaaggctgt tatggatgat ttcgccgctg ttgtcgagaa gtgctgcaaa	1680
gcggacgata aggaaacttg ctttgcagag gaaggtaaga aactcgtagc ggcaagtcag	1740
gctgcgcttg gccttggagg cagtgaaggc aaatcctctg ggagtggctc tgaaagtaaa	1800
tccaccgagg gcaaatccag tggatctggg tctgaatcta agtctaccga ggggaagtct	1860
tctggcagtg ggtcagaatc taaatctaca ggcggctctg accattgccc gttgggacca	1920
ggacgctgct gtcgccttca tacagtgcga gcgagtttgg aagacctggg ctgggctgac	1980
tgggtgctta gccctcggga ggtccaggtc acaatgtgca ttggcgctg tcccagtcaa	2040
tttagagcag caaatatgca cgcccaaata aaaacctccc tgcataggct taagccagat	2100
actgtccccg caccatgctg tgtgcctgct tcttacaatc ctatggtact catccagaag	2160
accgacacgg gagttagcct ccagacttat gacgacctt tggctaaaga ttgccattgt	2220
att	2223

<210> 123

<211> 735

<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 123

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser

180

185

190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Pro Gly Gly Gly Ser
580 585 590

Pro Gly Gly Gly Ser Pro Gly Gly Gly Ser Pro Gly Gly Gly Ser Pro
595 600 605

Gly Gly Gly Ser Pro Gly Gly Gly Ser Pro Gly Gly Gly Ser Pro Gly
610 615 620

Gly Gly Ser Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
625 630 635 640

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
645 650 655

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
660 665 670

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
675 680 685

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
690 695 700

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
705 710 715 720

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
725 730 735

<210> 124
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 124
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt cccatttga agatcatgta 120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt 360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat	420
gaaattgccca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgccca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcacctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcagaattt aatcaaaca aattgtgagc tttttgagca gcttggagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaagtg ttgtaaacad	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca cgaaatgttg cacagagtca	1440
ctggtcaaca ggagaccttg cttctccgct cttgaggttg acgaaacgta tgtcccaaaa	1500
gagttcaacg ccgaaacgtt tacgtttcat gcggacatat gcactctcag tgagaaggag	1560
cgacaaatca aaaaacagac tgctcttgta gagttggtaa aacacaaacc taaagcaaca	1620
aaagagcaat tgaaagctgt gatggacgat tttgcagctt tcgtagaaaa gtgctgcaag	1680
gccgacgata aagaaacctg tttcgtgaa gaaggcaaaa aacttgttgc ggcactctcag	1740
gccgctcttg gacttgggag cccgggtggc gggctctccag gcggaggctc tccgggcgga	1800
ggtagtcccg gagggggtag tccgggcggc ggttctccag gtggagggtt tcctgggtgt	1860
ggcagtcctg gcggaggatc tgatcactgt ccccttgggc ccgggaggtg ctgccgactt	1920

catacagttc gcgccagcct tgaagatttg ggggtgggccg actgggtggtt gagcccgaga 1980
gaggtccaag tcacgatgtg tattggagcc tgtccctctc aattccgagc cgcaaatatg 2040
catgcgcaaa taaagacgag tctccatcgg ttgaagcctg atactgtccc agctccgtgc 2100
tgcgtccccg cgagttataa tcccatggtc cttatacaga aaacagacac tgggtgtcagc 2160
cttcagacgt atgacgattt gcttgctaaa gactgtcatt gtatt 2205

<210> 125
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 125

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr

340

345

350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Ser Ala Gly Gly Gly Ser
580 585 590

Ala Gly Gly Gly Ser Ala Gly Gly Gly Ser Ala Gly Gly Gly Ser Ala
595 600 605

Gly Gly Gly Ser Ala Gly Gly Gly Ser Ala Gly Gly Gly Ser Ala Gly
610 615 620

Gly Gly Ser Asp His Cys Pro Leu Gly Pro Gly Arg Cys Cys Arg Leu
625 630 635 640

His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly Trp Ala Asp Trp Val
645 650 655

Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys Ile Gly Ala Cys Pro
660 665 670

Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln Ile Lys Thr Ser Leu
675 680 685

His Arg Leu Lys Pro Asp Thr Val Pro Ala Pro Cys Cys Val Pro Ala
690 695 700

Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr Asp Thr Gly Val Ser
705 710 715 720

Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp Cys His Cys Ile
725 730 735

<210> 126
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 126

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa	60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt ccccatTTga agatcatgta	120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa	180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt	240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa	300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt	360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat	420
gaaattgcca gaagacatcc ttactttttat gccccggaac tccttttctt tgctaaaagg	480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca	540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgagaa gtttccaagt tagtgacaga tcttaccaaa	720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt	780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct	900
gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct	960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcacctgat	1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt	1140
gtggaagagc ctcagaattt aatcaaaca aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaag ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtgggtcct gaaccagtta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ctaaagtgtg taccgagtct	1440
cttgtaata ggcgccatg cttcagtgc ttggaagtcg acgaaaccta tgtaccaaag	1500
gagttcaacg cagaaacatt tacattccat gctgatatct gcacattgag cgagaaagag	1560

agacagatta agaaacagac agcgcttggt gaactggtta aacacaaacc aaaagctacc 1620
 aaggagcagc ttaaggcagt aatggatgac ttgcgggcct ttgtcgagaa atgttgtaaa 1680
 gcggatgata aagagacatg cttcgccgaa gagggcaaaa aacttgtagc ggcaagccag 1740
 gccgcactgg gtctcggttag tgcgggcggt gggtcagcgg ggggaggatc tgcaggtggt 1800
 ggctcagcgg gtggcggttag cgctgggggg ggctccgcag gtgggggatc agcaggcggc 1860
 ggatcagccg gcggtggatc cgaccactgt cctctcgggc ctggtcggtg ttgccgcctc 1920
 catactgtgc gcgcgtctct tgaggatctg ggggtgggctg attgggttct ctctccccgc 1980
 gaagtgcagg tgaccatgtg tattggtgct tgcccaagtc aattccgagc agctaacatg 2040
 cacgcccaga tcaagactag cctgcatcgg cttaagcccg acactgttcc tgccccttgc 2100
 tgtgttcctg catcttataa tccaatggtc ctgatccaga aaaccgatac ggggtgtatca 2160
 ttgcaaacat acgacgactt gcttgccaaa gattgccatt gcatt 2205

<210> 127
 <211> 727
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein

<400> 127

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Ser Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

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

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

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

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp

500

505

510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Gly Gly Ser Glu Gly Lys Ser
 580 585 590

Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Glu Gly Lys Ser Ser Gly
 595 600 605

Ser Gly Ser Glu Ser Lys Ser Thr Gly Gly Ser Asp His Cys Pro Leu
 610 615 620

Gly Pro Gly Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu
 625 630 635 640

Asp Leu Gly Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val
 645 650 655

Thr Met Cys Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met
 660 665 670

His Ala Gln Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Val
 675 680 685

Pro Ala Pro Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile
 690 695 700

Gln Lys Thr Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu
 705 710 715 720

Ala Lys Asp Cys His Cys Ile
725

<210> 128
<211> 2181
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion protein coding sequence

<400> 128
gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60
gccttggtgt tgattgcctt tgctcagtat cttcagcagt ccccatTTga agatcatgta 120
aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
tgcttcttgc aacacaaaga tgacaacca aacctcccc gattggtgag accagaggtt 360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420
gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg 480
tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca 540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa 720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840
aaacctctgt tggaaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct 900
gacttgccctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960
gaggcaaagg atgtcttcct gggcatgttt ttgtatgaat atgcaagaag gcacctgat 1020
tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080
tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140

gtggaagagc ctcagaattht aatcaaacia aattgtgagc tttttgagca gcttgagag	1200
tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact	1260
ccaactcttg tagaggcttc aagaaaccta ggaaaagtgg gcagcaaattg ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggctct gaaccagtta	1380
tgtgtgttg atgagaaaac gccagtaagt gacagagtca cgaaatgctg tacagaatcc	1440
ctcgtgaata gaaggccctg cttctctgcc cttgaggtgg acgagactta cgtccctaag	1500
gagtttaacg ccgagacctt tacttttcat gctgatattt gcaccctttc cgaaaaggag	1560
cggcagatca agaaaciaac agccttggtg gaactcgtaa aacataaacc caaagccacc	1620
aaggaacaac ttaaagctgt tatggatgac ttcgcagcct tcgtcgagaa atgttgcaag	1680
gcggatgata aggaaactg ttttgctgag gaagggaaga agttggttg tgcctctcaa	1740
gcggctctgg ggcttggcgg atcagagggg aagtcctccg ggtccggtag cgagtccaaa	1800
tctacggaag ggaagtcatc cggttctggg tcagagtcca aatccacagg aggatcagac	1860
cattgccccat tgggaccagg acgatgttgt cgcctgcata cggtaagagc gtctctggag	1920
gatctcggct gggccgattg ggttctctca ccacgagaag tacaggtcac aatgtgcata	1980
ggagcttgct cgagccaatt ccgggcggct aatatgcacg cacagatcaa gacctcttg	2040
caccgcttga agcccgatac cgtgccagca ccgtgttgcg tcccagcatc ttacaacct	2100
atggttttga tacagaaaac tgacacaggt gtgagcctcc agacatatga tgatttgctg	2160
gctaaggatt gccactgtat a	2181