

SEQUENCE LISTING

<110> Intrexon Corporation

<120> IMPROVED THERAPEUTIC CONTROL OF HETERODIMER AND SINGLE CHAIN FORMS OF INTERLEUKIN-12

<130> INX00222W0

<140> To Be Assigned

<141> Herewith

<150> 62/053,628

<151> 2014-09-22

<150> 62/074,875

<151> 2014-11-04

<160> 42

<170> PatentIn version 3.5

<210> 1

<211> 987

<212> DNA

<213> Homo sapiens

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gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat	660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac	720
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<210> 2
 <211> 328
 <212> PRT
 <213> Homo sapiens

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			20					25					30		

Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
	35						40					45			

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

Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70				75						80

Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
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Leu	Ser	His	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
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Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
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Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
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Glu Trp Ala Ser Val Pro Cys Ser
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<212> DNA
<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Leu Ser Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val
35 40 45

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

Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg
65 70 75 80

Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr
85 90 95

Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys
100 105 110

Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu
115 120 125

Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys
130 135 140

Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser
145 150 155 160

Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn
165 170 175

Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn
180 185 190

Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser
195 200 205

Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys
210 215 220

Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala
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Val	Thr	Ile	Asp	Arg	Val	Met	Ser	Tyr	Leu	Asn	Ala	Ser
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 <212> DNA
 <213> Mus musculus

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 acctcagacc agagacatgg agtcataggc tctggaaaga ccctgaccat cactgtcaaa 240
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 accgaagtcc aatgcaaagg cgggaatgtc tgcgtgcaag ctcaggatcg ctattacaat 960
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<210> 6
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<212> PRT
<213> Mus musculus

<400> 6

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Val Glu Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr Val Asn Leu
35 40 45

Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr Val Lys
65 70 75 80

Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Thr
85 90 95

Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly Ile Trp
100 105 110

Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu Lys Cys
115 120 125

Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu Val Gln
130 135 140

Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser Ser Pro
145 150 155 160

Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser Ala Glu Lys
165 170 175

Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser Cys Gln
180 185 190

Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu
195 200 205

Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser Thr Ser
210 215 220

Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln
225 230 235 240

Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro
245 250 255

Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe Phe Val
260 265 270

Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu Gly Cys
275 280 285

Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr Glu Val Gln
290 295 300

Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr Tyr Asn
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Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg Ser
325 330 335

<210> 7

<211> 648

<212> DNA

<213> Mus musculus

<400> 7

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ctgaagacca cagatgacat ggtgaagacg gccagagaaa aactgaaaca ttattcctgc	180
actgctgaag acatcgatca tgaagacatc acacgggacc aaaccagcac attgaagacc	240
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gaagcagacc cttacagagt gaaaatgaag ctctgcatcc tgcttcacgc cttcagcacc	600
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<210> 8
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 <212> PRT
 <213> Mus musculus

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Met	Cys	Gln	Ser	Arg	Tyr	Leu	Leu	Phe	Leu	Ala	Thr	Leu	Ala	Leu	Leu
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Asn	His	Leu	Ser	Leu	Ala	Arg	Val	Ile	Pro	Val	Ser	Gly	Pro	Ala	Arg
		20					25					30			

Cys	Leu	Ser	Gln	Ser	Arg	Asn	Leu	Leu	Lys	Thr	Thr	Asp	Asp	Met	Val
	35					40						45			

Lys	Thr	Ala	Arg	Glu	Lys	Leu	Lys	His	Tyr	Ser	Cys	Thr	Ala	Glu	Asp
50					55					60					

Ile	Asp	His	Glu	Asp	Ile	Thr	Arg	Asp	Gln	Thr	Ser	Thr	Leu	Lys	Thr
65				70					75					80	

Cys	Leu	Pro	Leu	Glu	Leu	His	Lys	Asn	Glu	Ser	Cys	Leu	Ala	Thr	Arg
			85					90						95	

Glu Thr Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr
100 105 110

Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys
115 120 125

Met Tyr Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His
130 135 140

Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile Asp
145 150 155 160

Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys
165 170 175

Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys
180 185 190

Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val
195 200 205

Met Gly Tyr Leu Ser Ser Ala
210 215

<210> 9
<211> 1602
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1481273

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gccacggtca tctgccgcaa aaatgccagc attagcgtgc gggcccagga ccgctactat	1560
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<210> 10

<211> 533

<212> PRT
<213> Artificial

<220>
<223> Fusion protein Construct ID 1481273

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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
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Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Pro Ser Arg Asn Leu Pro Val Ala Thr Pro
290 295 300

Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg
305 310 315 320

Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr
325 330 335

Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys
340 345 350

Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu
355 360 365

Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys
370 375 380

Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser
385 390 395 400

Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn
405 410 415

Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn
420 425 430

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

Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys
450 455 460

Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala
465 470 475 480

Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Ser Gly Pro
485 490 495

Ala Pro Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser
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Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala
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Ser Val Pro Cys Ser
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<212> DNA
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<220>

<223> Fusion protein Construct ID 1481272

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gccacgggtca tctgccgcaa aaatgccagc attagcgtgc gggcccagga ccgctactat	1560
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<210> 12
 <211> 533
 <212> PRT
 <213> Artificial

<220>
 <223> Fusion protein Construct ID 1481272

<400> 12

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
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Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
			20					25					30		

Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			

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

Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70				75						80

Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	

Leu	Ser	His	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		

Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Thr	Phe
		115					120					125			

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

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

Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser
275 280 285

Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr
290 295 300

Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr
305 310 315 320

Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu
325 330 335

Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser
340 345 350

Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu
355 360 365

Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu
370 375 380

Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala
385 390 395 400

Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val
405 410 415

Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile
420 425 430

Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile
435 440 445

Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Pro Gln Thr Pro Gly Pro
450 455 460

Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val
465 470 475 480

Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr
485 490 495

Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser
500 505 510

Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala
515 520 525

Ser Val Pro Cys Ser
530

<210> 13
<211> 1623
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480533

<400> 13
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gccccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttgacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatcct gaaggaccag 360
aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga 480
ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactcagcgc cgagagagtc 540
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gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgacct acccaagaac 720
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gaattttacc cttgcacttc tgaagagatt gatcatgaag atatcacaaa agataaaacc	1200
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agagagacct ctttcataac taatgggagt tgcctggcct ccagaaagac ctcttttatg	1320
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accatgaatg caaagctgct gatggacccc aagaggcaga tctttctaga tcaaaacatg	1440
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aaatcctccc ttgaagaacc ggatttttat aaaactaaaa tcaagctctg catacttctt	1560
catgctttca gaatcagagc agtgactatt gatagagtga tgagctatct gaatgcttcc	1620
taa	1623

<210> 14
 <211> 540
 <212> PRT
 <213> Artificial

<220>
 <223> Fusion protein Construct ID 1480533

<400> 14

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
1				5					10					15	

Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
			20					25					30		

Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			

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

Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70					75					80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Arg Ser Pro Val Ser Gly Asp Asn
325 330 335

Ala Phe Pro Ala Pro Thr Gly Arg Asn Leu Pro Val Ala Thr Pro Asp
340 345 350

Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala
355 360 365

Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro
370 375 380

Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
385 390 395 400

Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser
405 410 415

Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu
420 425 430

Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile
435 440 445

Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala
450 455 460

Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met
465 470 475 480

Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu
485 490 495

Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr
500 505 510

Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val
515 520 525

Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 15
<211> 1626
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480534

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gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttggtgacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaaggag gcgagggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatcct gaaggaccag 360
aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga 480
ggctcttctg acccccaagg ggtgacgtgc ggagctgcta cactcagcgc cgagagagtc 540
agagggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcccc 600
gctgctgagg agagtctgcc cattgagggtc atggtggatg ccgttcacaa gctcaagtat 660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac 720
ttgcagctga agcccctgaa gaacagcaga caggtggagg tcagctggga gtaccctgac 780

acctggagta ctccacattc ctactttctcc ctgacattct gcgttcaggt ccagggcaag	840
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cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc	960
gaatgggcat ctgtgccctg ctccagatcc cagcctgtgc ctaccaggga cctggaggtc	1020
cccctcaccg gaagaaacct ccccgtaggc actccagacc caggaatggt cccatgcctt	1080
caccacagcc agaacctgct gagggccgtc agcaacatgc tccagaaggc cagacaaact	1140
ctagaatttt acccttgcac ttctgaagag attgatcatg aagatatcac aaaagataaa	1200
accagcacag tggaggcctg tttaccattg gaattaacca agaatgagag ttgcctaaat	1260
tccagagaga cctctttcat aactaatggg agttgcctgg cctccagaaa gacctctttt	1320
atgatggccc tgtgccttag tagtatttat gaagacttga agatgtacca ggtggagtgc	1380
aagaccatga atgcaaagct gctgatggac cccaagaggc agatctttct agatcaaac	1440
atgctggcag ttattgatga gctgatgcag gccctgaatt tcaacagtga gactgtgcca	1500
caaaaatcct cccttgaaga accggatttt tataaaacta aaatcaagct ctgcatactt	1560
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tcctaa	1626

<210> 16
 <211> 541
 <212> PRT
 <213> Artificial

<220>
 <223> Fusion protein Construct ID 1480534

<400> 16

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
1				5					10					15	

Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
			20					25					30		

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Arg Ser Gln Pro Val Pro Thr Arg
325 330 335

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

Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg
355 360 365

Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr
370 375 380

Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys
385 390 395 400

Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu
405 410 415

Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys
420 425 430

Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser
435 440 445

Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn
450 455 460

Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn
465 470 475 480

Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser
485 490 495

Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys
500 505 510

Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala
515 520 525

Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 17
<211> 1629
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480535

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gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttggaacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatcct gaaggaccag 360
aaagaacca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420

acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga	480
ggctcttctg acccccaagg ggtgacgtgc ggagctgcta cactcagcgc cgagagagtc	540
agagggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca	600
gctgctgagg agagtctgcc cattgaggtc atgggtggatg ccgttcacaa gctcaagtat	660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac	720
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acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggc ccagggcaag	840
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cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc	960
gaatgggcat ctgtgccctg ctccagatcc ggacaccccc ctcagacagg cctggagaag	1020
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cttcaccaca gccagaacct gctgagggcc gtcagcaaca tgctccagaa ggccagacaa	1140
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ccacaaaaat cctcccttga agaaccggat tttataaaaa ctaaaatcaa gctctgcata	1560
cttcttcatg ctttcagaat cagagcagtg actattgata gagtgatgag ctatctgaat	1620
gcttcctaa	1629

<210> 18
 <211> 542
 <212> PRT
 <213> Artificial

<220>

<223> Fusion protein Construct ID 1480535

<400> 18

Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Arg Ser Gly Thr Pro Pro Gln Thr
325 330 335

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

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
355 360 365

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
370 375 380

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
385 390 395 400

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
405 410 415

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
420 425 430

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
435 440 445

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
450 455 460

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
465 470 475 480

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
485 490 495

Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
500 505 510

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
515 520 525

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 19
<211> 1623
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480536

<400> 19
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gccccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg	180
accttggacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa	240
gagtttggag atgctggcca gtacacctgt cacaaaggag gcgaggttct aagccattcg	300
ctcctgctgc ttcacaaaaa ggaagatgga atttggcca ctgatatcct gaaggaccag	360
aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc	420
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gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat	660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgacc acccaagaac	720
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cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc	960
gaatgggcat ctgtgccctg ctccagcgat gtgacaggca ataccggaaa cgctacctat	1020
accattacca gaaacctccc cgtggccact ccagaccag gaatgttccc atgccttcac	1080
cacagccaga acctgctgag ggccgtcagc aacatgctcc agaaggccag acaaactcta	1140
gaattttacc cttgcacttc tgaagagatt gatcatgaag atatcacaaa agataaaacc	1200
agcacagtgg aggcctgttt accattggaa ttaaccaaga atgagagttg cctaaattcc	1260
agagagacct ctttcataac taatgggagt tgcctggcct ccagaaagac ctcttttatg	1320
atggccctgt gccttagtag tatttatgaa gacttgaaga tgtaccaggc ggagttcaag	1380
accatgaatg caaagctgct gatggacccc aagaggcaga tctttctaga tcaaaacatg	1440
ctggcagtta ttgatgagct gatgcaggcc ctgaatttca acagtgagac tgtgccacaa	1500
aaatcctccc ttgaagaacc ggatttttat aaaactaaaa tcaagctctg catacttctt	1560

catgctttca gaatcagagc agtgactatt gatagagtga tgagctatct gaatgcttcc 1620

taa 1623

<210> 20

<211> 540

<212> PRT

<213> Artificial

<220>

<223> Fusion protein Construct ID 1480536

<400> 20

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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Ser Asp Val Thr Gly Asn Thr Gly
325 330 335

Asn Ala Thr Tyr Thr Ile Thr Arg Asn Leu Pro Val Ala Thr Pro Asp
340 345 350

Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala
355 360 365

Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro
370 375 380

Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
385 390 395 400

Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser
405 410 415

Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu
420 425 430

Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile
435 440 445

Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala
450 455 460

Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met
465 470 475 480

Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu
485 490 495

Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr
500 505 510

Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val
515 520 525

Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 21
<211> 1623
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480537

<400> 21
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gccccctggag aaatgggtgt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttggtgacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaaggag gcgagggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatcct gaaggaccag 360
aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
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gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac 720
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agcacagtgg aggcctgttt accattggaa ttaaccaaga atgagagttg cctaaattcc 1260
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 aaatcctccc ttgaagaacc ggatTTTTAT aaaactaaaa tcaagctctg catacttctt 1560
 catgctttca gaatcagagc agtgactatt gatagagtga tgagctatct gaatgcttcc 1620
 taa 1623

<210> 22
 <211> 540
 <212> PRT
 <213> Artificial

<220>
 <223> Fusion protein Construct ID 1480537

<400> 22

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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
 20 25 30

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Gly Ser Pro Lys Asp Gly Pro Glu
325 330 335

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

Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala
355 360 365

Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro
370 375 380

Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
385 390 395 400

Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser
405 410 415

Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu
420 425 430

Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile
435 440 445

Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala
450 455 460

Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met
465 470 475 480

Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu
485 490 495

Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr
500 505 510

Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val
515 520 525

Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 23
<211> 1629
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480538

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gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttgacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgtggcca gtacacctgt cacaaaggag gcgagggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatcct gaaggaccag 360
aaagaacca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
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gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat 660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac 720
ttgcagctga agccccctgaa gaacagcaga caggtggagg tcagctggga gtaccctgac 780
acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggt ccagggaag 840

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gaatgggcat ctgtgccctg ctccggcagg aacgctcccg gaagccctcc cacaggcaat     1020
tacaaactgg aaccagaaaa cctccccgtg gccactccag acccaggaat gttcccatgc     1080
cttcaccaca gccagaacct gctgagggcc gtcagcaaca tgctccagaa ggccagacaa     1140
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aaaaccagca cagtggaggc ctgtttacca ttggaattaa ccaagaatga gagttgccta     1260
aattccagag agacctcttt cataactaat gggagttgcc tggcctccag aaagacctct     1320
tttatgatgg ccctgtgcct tagtagtatt tatgaagact tgaagatgta ccaggtggag     1380
ttcaagacca tgaatgcaaa gctgctgatg gacccaaga ggcagatctt tctagatcaa     1440
aacatgctgg cagttattga tgagctgatg caggccctga atttcaacag tgagactgtg     1500
ccacaaaaat cctcccttga agaaccggat tttataaaaa ctaaaatcaa gctctgcata     1560
cttcttcatg ctttcagaat cagagcagtg actattgata gagtgatgag ctatctgaat     1620
gcttcctaa                                     1629

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<210> 24
<211> 542
<212> PRT
<213> Artificial

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<220>
<223> Fusion protein Construct ID 1480538

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<400> 24

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Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
1           5           10          15

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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20          25          30

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Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35          40          45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Gly Arg Asn Ala Pro Gly Ser Pro
325 330 335

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

Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu
355 360 365

Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
370 375 380

Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
385 390 395 400

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn
405 410 415

Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser
420 425 430

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser
435 440 445

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met
450 455 460

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
465 470 475 480

Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn
485 490 495

Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
500 505 510

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
515 520 525

Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 25
<211> 1632
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480539

<400> 25
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gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttgacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttgggtcca ctgatatcct gaaggaccag 360
aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga 480

ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactcagcgc cgagagagtc	540
agagggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca	600
gctgctgagg agagtctgcc cattgaggtc atggtgatg ccgttcacaa gctcaagtat	660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac	720
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cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttgagc	960
gaatgggcat ctgtgccctg ctcccagaaa ggctccgtgg gattcacaga ccctgaggtc	1020
caccaaagca caaacctcag aaacctcccc gtggccactc cagaccagc aatgttcca	1080
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caaaactctag aattttacc ttgcacttct gaagagattg atcatgaaga tatcacaaaa	1200
gataaaacca gcacagtgga ggcctgttta ccattggaat taaccaagaa tgagagttgc	1260
ctaaattcca gagagacctc tttcataact aatgggagtt gcctggcctc cagaaagacc	1320
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caaaacatgc tggcagttat tgatgagctg atgcaggccc tgaatttcaa cagtgagact	1500
gtgccacaaa aatcctccct tgaagaaccg gatttttata aaactaaaat caagctctgc	1560
atacttcttc atgctttcag aatcagagca gtgactattg atagagtgat gagctatctg	1620
aatgcttcct aa	1632

<210> 26
 <211> 543
 <212> PRT
 <213> Artificial

 <220>
 <223> Fusion protein Construct ID 1480539

<400> 26

Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Gln Lys Gly Ser Val Gly Phe Thr
325 330 335

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

Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu
355 360 365

Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu
370 375 380

Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
385 390 395 400

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys
405 410 415

Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly
420 425 430

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu
435 440 445

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr
450 455 460

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
465 470 475 480

Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe
485 490 495

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

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
515 520 525

Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 27
<211> 1623
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480540

<400> 27
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gccccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg	180
accttggacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa	240
gagtttggag atgctggcca gtacacctgt cacaaaggag gcgaggttct aagccattcg	300
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aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc	420
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agagggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca	600
gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat	660
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aaatcctccc ttgaagaacc ggatttttat aaaactaaaa tcaagctctg catacttctt	1560
catgctttca gaatcagagc agtgactatt gatagagtga tgagctatct gaatgcttcc	1620

taa

1623

<210> 28
<211> 540
<212> PRT
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480540

<400> 28

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Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Gly Asn Val Pro Glu Leu Pro Asp
325 330 335

Thr Thr Glu His Ser Arg Thr Arg Asn Leu Pro Val Ala Thr Pro Asp
340 345 350

Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala
355 360 365

Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro
370 375 380

Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
385 390 395 400

Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser
405 410 415

Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu
420 425 430

Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile
435 440 445

Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala
450 455 460

Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met
465 470 475 480

Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu
485 490 495

Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr
500 505 510

Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val
515 520 525

Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 29
<211> 1635
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480541

<400> 29
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gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
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aaagaacca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
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agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcccc 600
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gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac 720
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ccatgccttc accacagcca gaacctgctg agggccgtca gcaacatgct ccagaaggcc 1140
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tgccataaatt ccagagagac ctctttcata actaatggga gttgcctggc ctccagaaag	1320
acctcttttta tgatggccct gtgccttagt agtatattatg aagacttgaa gatgtaccag	1380
gtggagttca agaccatgaa tgcaaagctg ctgatggacc ccaagaggca gatctttcta	1440
gatcaaaaaca tgctggcagt tattgatgag ctgatgcagg ccctgaattt caacagtgag	1500
actgtgccac aaaaatcctc ccttgaagaa ccggatTTTT ataaaactaa aatcaagctc	1560
tgcatacttc ttcatgcttt cagaatcaga gcagtgacta ttgatagagt gatgagctat	1620
ctgaatgctt cctaa	1635

<210> 30
 <211> 544
 <212> PRT
 <213> Artificial

<220>
 <223> Fusion protein Construct ID 1480541

<400> 30

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
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Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
			20					25					30		

Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			

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

Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70					75				80	

Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Gly Arg Ser His Pro Val Gln Pro
325 330 335

Tyr Pro Gly Ala Phe Val Lys Glu Pro Ile Pro Arg Asn Leu Pro Val
340 345 350

Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn
355 360 365

Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu
370 375 380

Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr
385 390 395 400

Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr
405 410 415

Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn
420 425 430

Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys
435 440 445

Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys
450 455 460

Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu
465 470 475 480

Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn
485 490 495

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

Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg
515 520 525

Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 31
<211> 1623
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480542

<400> 31
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gcccctggag aaatgggtggt cctcacctgt gacaccccctg aagaagatgg tatcacctgg 180
accttgacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttgggtcca ctgatattc gaaggaccag 360
aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga 480
ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactcagcgc cgagagagtc 540
agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca 600
gctgctgagg agagtctgcc cattgaggtc atgggtggatg ccgttcacaa gctcaagtat 660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac 720
ttgcagctga agccccctgaa gaacagcaga caggtggagg tcagctggga gtaccctgac 780
acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggt ccagggaag 840
agcaagagag aaaagaaaga tagagtcttc acggacaaga cctcagccac ggatcatctgc 900

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cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc      960
gaatgggcat ctgtgccctg ctccccgaa agaaaagaga ggatctccga gcaaacctat      1020
cagctgtcca gaaacctccc cgtggccact ccagaccagc gaatgttccc atgccttcac      1080
cacagccaga acctgctgag ggccgtcagc aacatgctcc agaaggccag acaaactcta      1140
gaatthttacc cttgcacttc tgaagagatt gatcatgaag atatcacaaa agataaaacc      1200
agcacagtgg aggcctgttt accattggaa ttaaccaaga atgagagttg cctaaattcc      1260
agagagacct ctttcataac taatgggagt tgcctggcct ccagaaagac ctcttttatg      1320
atggccctgt gccttagtag tatthtatgaa gacttgaaga tgtaccaggt ggagttcaag      1380
accatgaatg caaagctgct gatggacccc aagaggcaga tctthtctaga tcaaaacatg      1440
ctggcagtta ttgatgagct gatgcaggcc ctgaatttca acagtgagac tgtgccacaa      1500
aaatcctccc ttgaagaacc ggatthttat aaactaaaa tcaagctctg catacttctt      1560
catgctthtca gaatcagagc agtgactatt gatagagtga tgagctatct gaatgcttcc      1620
taa                                                                    1623

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<210> 32
<211> 540
<212> PRT
<213> Artificial

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<220>
<223> Fusion protein Construct ID 1480542

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<400> 32

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Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
1              5              10              15

```

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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20              25              30

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```

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35              40              45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Pro Glu Arg Lys Glu Arg Ile Ser
325 330 335

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

Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala
355 360 365

Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro
370 375 380

Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
385 390 395 400

Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser
405 410 415

Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu
420 425 430

Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile
435 440 445

Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala
450 455 460

Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met
465 470 475 480

Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu
485 490 495

Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr
500 505 510

Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val
515 520 525

Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 33
<211> 1623
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480543

<400> 33
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gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg 180
accttggaacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt caciaaggag gcgaggttct aagccattcg 300
ctcctgctgc ttcacaaaaa ggaagatgga atttggcca ctgatatcct gaaggaccag 360
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ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactcagcgc cgagagagtc 540

agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcca	600
gctgctgagg agagtctgcc cattgaggtc atgggtggatg ccgttcacaa gctcaagtat	660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac	720
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cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttgagc	960
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cacagccaga acctgtctgag ggccgtcagc aacatgctcc agaaggccag acaaactcta	1140
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aaatcctccc ttgaagaacc ggatttttat aaaactaaaa tcaagctctg catacttctt	1560
catgctttca gaatcagagc agtgactatt gatagagtga tgagctatct gaatgcttcc	1620
taa	1623

<210> 34
 <211> 540
 <212> PRT
 <213> Artificial

 <220>
 <223> Fusion protein Construct ID 1480543

 <400> 34

Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
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Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly
325 330 335

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

Pro Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala
355 360 365

Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro
370 375 380

Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
385 390 395 400

Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser
405 410 415

Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu
420 425 430

Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile
435 440 445

Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala
450 455 460

Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met
465 470 475 480

Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu
485 490 495

Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr
500 505 510

Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val
515 520 525

Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser
530 535 540

<210> 35
<211> 1599
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480544

<400> 35
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gcccctggag aaatggtggt cctcacctgt gacaccctg aagaagatgg tatcacctgg 180

accttggacc agagcagtga ggtcttaggc tctggcaaga ccctgaccat ccaagtcaaa	240
gagtttggag atgctggcca gtacacctgt cacaaaggag gcgaggttct aagccattcg	300
ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatcct gaaggaccag	360
aaagaaccca agaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc	420
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agaggggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgcccc	600
gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat	660
gaaaactaca ccagcagctt cttcatcagg gacatcatca aacctgaccc acccaagaac	720
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acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggt ccagggcaag	840
agcaagagag aaaagaaaaga tagagtcttc acggacaaga cctcagccac ggtcatctgc	900
cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc	960
gaatgggcat ctgtgccctg ctccggtggc ggtggcggcg gatctagaaa cctccccgtg	1020
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gtcagcaaca tgctccagaa ggccagacaa actctagaat tttacccttg cacttctgaa	1140
gagattgatc atgaagatat cacaaaagat aaaaccagca cagtggaggc ctgtttacca	1200
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gggagttgcc tggcctccag aaagacctct tttatgatgg ccctgtgcct tagtagtatt	1320
tatgaagact tgaagatgta ccaggtggag ttcaagacca tgaatgcaaa gctgctgatg	1380
gacccaaga ggcagatctt tctagatcaa aacatgctgg cagttattga tgagctgatg	1440
caggccctga atttcaacag tgagactgtg ccacaaaaat cctcccttga agaaccggat	1500
ttttataaaa ctaaaatcaa gctctgcata cttcttcatg ctttcagaat cagagcagtg	1560
actattgata gagtgatgag ctatctgaat gcttcctaa	1599

<210> 36
<211> 532
<212> PRT
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480544

<400> 36

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20 25 30

Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

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

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
115 120 125

Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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

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

Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
180 185 190

Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
195 200 205

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
305 310 315 320

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

Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His
340 345 350

His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala
355 360 365

Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His
370 375 380

Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro
385 390 395 400

Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser
405 410 415

Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met
420 425 430

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

Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg
450 455 460

Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met
465 470 475 480

Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser Leu
485 490 495

Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu
500 505 510

His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr
515 520 525

Leu Asn Ala Ser
530

<210> 37
<211> 1653
<212> DNA
<213> Artificial

<220>

<223> Fusion protein Construct ID 1480545

<400> 37

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agccagaacc tgctgagggc cgtcagcaac atgctccaga aggccagaca aactctagaa	180
ttttaccctt gcacttctga agagattgat catgaagata tcacaaaaga taaaaccagc	240
acagtggagg cctgtttacc attggaatta accaagaatg agagttgcct aaattccaga	300
gagacctctt tcataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgatg	360
gccctgtgcc ttagtagtat ttatgaagac ttgaagatgt accaggtgga gttcaagacc	420
atgaatgcaa agctgctgat ggacccaag aggcagatct ttctagatca aaacatgctg	480
gcagttattg atgagctgat gcaggccctg aatttcaaca gtgagactgt gccacaaaaa	540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat	600
gctttcagaa tcagagcagt gactattgat agagtgatga gctatctgaa tgcttcagaa	660
tccgacgtga actccagaac aggccctagc ggagccacac cccctagcgg caaccctac	720
acaatcacag gcatatggga actgaagaaa gatgtttatg tcgtagaatt ggattggtat	780
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gtcaaagagt ttggagatgc tggccagtac acctgtcaca aaggaggcga ggttctaagc	960
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tgcccagctg ctgaggagag tctgcccatt gaggtcatgg tggatgccgt tcacaagctc	1320
aagtatgaaa actacaccag cagcttcttc atcagggaca tcatcaaacc tgaccacccc	1380

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ggcaagagca agagagaaaa gaaagataga gtcttcacgg acaagacctc agccacggtc 1560
atctgccgca aaaatgccag cattagcgtg cgggcccagg accgctacta tagctcatct 1620
tggagcgaat gggcatctgt gccctgctcc taa 1653

<210> 38
<211> 550
<212> PRT
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480545

<400> 38

Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
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Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
20 25 30

Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
35 40 45

Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
50 55 60

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
65 70 75 80

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
85 90 95

Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
100 105 110

Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr
115 120 125

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
130 135 140

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
145 150 155 160

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

Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
180 185 190

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
195 200 205

Ile Asp Arg Val Met Ser Tyr Leu Asn Ala Ser Arg Ser Asp Val Asn
210 215 220

Ser Arg Thr Gly Pro Ser Gly Ala Thr Pro Pro Ser Gly Asn Pro Tyr
225 230 235 240

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

Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys
260 265 270

Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser
275 280 285

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

Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser
305 310 315 320

His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr
325 330 335

Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg
340 345 350

Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr
355 360 365

Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser
370 375 380

Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu
385 390 395 400

Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln
405 410 415

Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val
420 425 430

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

Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln
450 455 460

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

Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys
485 490 495

Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe
500 505 510

Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile
515 520 525

Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp
530 535 540

Ala Ser Val Pro Cys Ser
545 550

<210> 39
<211> 1641
<212> DNA
<213> Artificial

<220>
<223> Fusion protein Construct ID 1480546

<400> 39
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agccagaacc tgctgagggc cgtcagcaac atgctccaga aggccagaca aactctagaa 180
ttttaccctt gcacttctga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgtttacc attggaatta accaagaatg agagttgcct aaattccaga 300
gagacctctt tcataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgatg 360
gccctgtgcc ttagtagtat ttatgaagac ttgaagatgt accagggtgga gttcaagacc 420
atgaatgcaa agctgctgat ggacccaag aggcagatct ttctagatca aaacatgctg 480
gcagttattg atgagctgat gcaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa tcagagcagt gactattgat agagtgatga gctatctgaa tgcttcccc 660
gctccacac cctccaacgg aagccctaag gatggccctg agattcccc taccggaggc 720
atatgggaac tgaagaaaaga tgtttatgtc gtagaattgg attggtatcc cgacgccct 780
ggagaaatgg tggctctcac ctgtgacacc cctgaagaag atggtatcac ctggaccttg 840
gaccagagca gtgaggtctt aggctctggc aagaccctga ccatccaagt caaagagttt 900

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ggagatgctg gccagtacac ctgtcacaaa ggaggcgagg ttctaagcca ttcgctcctg      960
ctgcttcaca aaaaggaaga tggaatttgg tccactgata tcctgaagga ccagaaagaa      1020
cccaagaata agacctttct aagatgcgag gccaagaatt attctggacg tttcacctgc      1080
tgggtggctga cgacaatcag tactgatttg acattcagtg tcaaaagcag cagaggctct      1140
tctgaccccc aaggggtgac gtgcggagct gctacactca gcgccgagag agtcagaggg      1200
gacaacaagg agtatgagta ctcagtggag tgccaggagg acagtgcctg cccagctgct      1260
gaggagagtc tgcccattga ggtcatggtg gatgccgttc acaagctcaa gtatgaaaac      1320
tacaccagca gcttcttcat cagggacatc atcaaacctg acccacccaa gaacttgacg      1380
ctgaagcccc tgaagaacag cagacagggtg gaggtcagct gggagtaccc tgacacctgg      1440
agtactccac attcctactt ctccctgaca ttctgcgttc aggtccaggg caagagcaag      1500
agagaaaaga aagatagagt cttcacggac aagacctcag ccacgggtcat ctgccgcaaa      1560
aatgccagca ttagcgtgcg ggcccaggac cgctactata gctcatcttg gagcgaatgg      1620
gcatctgtgc cctgctccta a                                              1641

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<210> 40
<211> 546
<212> PRT
<213> Artificial

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<220>
<223> Fusion protein Construct ID 1480546

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<400> 40

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Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
1           5           10           15

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Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
20           25           30

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Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
35           40           45

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Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
50 55 60

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
65 70 75 80

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
85 90 95

Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
100 105 110

Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr
115 120 125

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
130 135 140

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
145 150 155 160

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

Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
180 185 190

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
195 200 205

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

Ser Asn Gly Ser Pro Lys Asp Gly Pro Glu Ile Pro Pro Thr Gly Gly
225 230 235 240

Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
245 250 255

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
260 265 270

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
275 280 285

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

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
305 310 315 320

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
325 330 335

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
340 345 350

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
355 360 365

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
370 375 380

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
385 390 395 400

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
405 410 415

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
420 425 430

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
435 440 445

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
450 455 460

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
465 470 475 480

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
485 490 495

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
500 505 510

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
515 520 525

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
530 535 540

Cys Ser
545

<210> 41
<211> 3
<212> PRT
<213> Artificial

<220>
<223> Synthetic linker

<400> 41

Thr Pro Ser
1

<210> 42
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Synthetic linker

<400> 42

Ser Gly Pro Ala Pro
1 5