

SEQUENCE LISTING

<110> Excepgen Inc.

<120> SYSTEMS AND METHODS FOR PROTEIN EXPRESSION

<130> EXCI-001/02W0 336721-2006

<150> US 62/970,628

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<151> 2019-09-16

<160> 96

<170> PatentIn version 3.5

<210> 1

<211> 71

<212> PRT

<213> Cardiovirus Theiler's-like cardiovirus

<400> 1

Met	Ala	Cys	Lys	His	Gly	Tyr	Pro	Leu	Met	Cys	Pro	Leu	Cys	Thr	Ala
1				5					10					15	

Leu	Asp	Lys	Thr	Ser	Asp	Gly	Leu	Phe	Thr	Leu	Leu	Phe	Asp	Asn	Glu
			20					25					30		

Trp	Tyr	Pro	Thr	Asp	Leu	Leu	Thr	Val	Asp	Leu	Glu	Asp	Glu	Val	Phe
		35					40					45			

Tyr	Pro	Asp	Asp	Pro	His	Met	Glu	Trp	Thr	Asp	Leu	Pro	Leu	Ile	Gln
	50					55					60				

Asp	Ile	Glu	Met	Glu	Pro	Gln
65					70	

<210> 2

<211> 67

<212> PRT

<213> Cardiovirus Encephalomyocarditis virus

<400> 2

Met Ala Thr Thr Met Glu Gln Glu Thr Cys Ala His Ser Leu Thr Phe
1 5 10 15

Glu Glu Cys Pro Lys Cys Ser Ala Leu Gln Tyr Arg Asn Gly Phe Tyr
20 25 30

Leu Leu Lys Tyr Asp Glu Glu Trp Tyr Pro Glu Glu Leu Leu Thr Asp
35 40 45

Gly Glu Asp Asp Val Phe Asp Pro Glu Leu Asp Met Glu Val Val Phe
50 55 60

Glu Leu Gln
65

<210> 3

<211> 127

<212> PRT

<213> Enterovirus Enterovirus C

<400> 3

Asn Tyr His Leu Ala Thr Gln Asp Asp Leu Gln Asn Ala Val Asn Val
1 5 10 15

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

Asp Ser Ile Ala Arg Cys Asn Cys Asn Ala Gly Val Tyr Tyr Cys Glu
35 40 45

Ser Arg Arg Lys Tyr Tyr Pro Val Ser Phe Val Gly Pro Thr Phe Gln
50 55 60

Tyr Met Glu Ala Asn Asn Tyr Tyr Pro Ala Arg Tyr Gln Ser His Met
65 70 75 80

Leu Ile Gly His Gly Phe Ala Ser Pro Gly Asp Cys Gly Gly Ile Leu

85

90

95

Arg Cys His His Gly Val Ile Gly Ile Ile Thr Ala Gly Gly Glu Gly
 100 105 110

Leu Val Ala Phe Ser Asp Ile Arg Asp Leu Tyr Ala Tyr Glu Glu
 115 120 125

<210> 4

<211> 219

<212> PRT

<213> Erbovirus Equine rhinitis B virus 1

<400> 4

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

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

Leu Pro Leu Pro Leu Glu Leu Ala Glu Phe Pro Asn Lys Asp Asn Asn
 35 40 45

Cys Trp Val Ala Ala Leu Ser His Tyr Tyr Thr Leu Cys Asp Val Thr
 50 55 60

Asn His Val Thr Lys Val Thr Pro Thr Thr Ser Gly Ile Arg Tyr Tyr
 65 70 75 80

Leu Thr Ala Trp Gln Ser Ile Leu Gln Thr Asp Leu Phe Asn Gly Tyr
 85 90 95

Tyr Pro Ala Ala Phe Ala Val Glu Thr Gly Leu Cys His Gly Pro Phe
 100 105 110

Pro Met Gln Gln His Gly Tyr Val Arg Asn Ala Thr Ser His Pro Tyr
 115 120 125

Asn Phe Cys Leu Cys Ser Glu Pro Val Pro Gly Glu Asp Tyr Trp His
130 135 140

Ala Val Val Lys Val Asp Leu Ser Arg Thr Glu Ala Arg Val Asp Lys
145 150 155 160

Trp Leu Cys Ile Asp Asp Asp Arg Met Tyr Leu Ser Gly Pro Pro Thr
165 170 175

Arg Val Lys Leu Ala Ser Ser Tyr Lys Ile Pro Thr Trp Ile Glu Ser
180 185 190

Leu Ala Gln Phe Cys Leu Gln Leu His Pro Val Gln His Arg Arg Thr
195 200 205

Leu Ala Asn Ser Leu Arg Asn Glu Gln Cys Arg
210 215

<210> 5
<211> 67
<212> PRT
<213> Cardiovirus Encephalomyocarditis virus

<400> 5

Met Ala Thr Thr Met Glu Gln Glu Ile Cys Ala His Ser Met Thr Phe
1 5 10 15

Glu Glu Cys Pro Lys Cys Ser Ala Leu Gln Tyr Arg Asn Gly Phe Tyr
20 25 30

Leu Leu Lys Tyr Asp Glu Glu Trp Tyr Pro Glu Glu Ser Leu Thr Asp
35 40 45

Gly Glu Asp Asp Val Phe Asp Pro Asp Leu Asp Met Glu Val Val Phe
50 55 60

Glu Thr Gln
65

<210> 6
<211> 71
<212> PRT
<213> Cardiovirus Cardiovirus B

<400> 6

Met Ala Cys Lys His Gly Tyr Pro Phe Leu Cys Pro Leu Cys Thr Ala
1 5 10 15

Ile Asp Thr Thr His Asp Gly Ser Phe Thr Leu Leu Ile Asp Asn Glu
20 25 30

Trp Tyr Pro Thr Asp Leu Leu Thr Val Asp Leu Asp Asp Asp Val Phe
35 40 45

His Pro Asp Asp Ser Val Met Glu Trp Thr Asp Leu Pro Leu Ile Gln
50 55 60

Asp Val Val Met Glu Pro Gln
65 70

<210> 7
<211> 149
<212> PRT
<213> Enterovirus Enterovirus C

<400> 7

Gly Phe Gly His Gln Asn Lys Ala Val Tyr Thr Ala Gly Tyr Lys Ile
1 5 10 15

Cys Asn Tyr His Leu Ala Thr Gln Asp Asp Leu Gln Asn Ala Val Asn
20 25 30

Val Met Trp Ser Arg Asp Leu Leu Val Thr Glu Ser Arg Ala Gln Gly
35 40 45

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

Glu Ser Arg Arg Lys Tyr Tyr Pro Val Ser Phe Val Gly Pro Thr Phe
65 70 75 80

Gln Tyr Met Glu Ala Asn Asn Tyr Tyr Pro Ala Arg Tyr Gln Ser His
85 90 95

Met Leu Ile Gly His Gly Phe Ala Ser Pro Gly Asp Cys Gly Gly Ile
100 105 110

Leu Arg Cys His His Gly Val Ile Gly Ile Ile Thr Ala Gly Gly Glu
115 120 125

Gly Leu Val Ala Phe Ser Asp Ile Arg Asp Leu Tyr Ala Tyr Glu Glu
130 135 140

Glu Ala Met Glu Gln
145

<210> 8
<211> 182
<212> PRT
<213> Enterovirus Human rhinovirus 16

<400> 8

Gly Pro Glu Glu Glu Phe Gly Met Ser Ile Ile Lys Asn Asn Thr Cys
1 5 10 15

Val Val Thr Thr Thr Asn Gly Lys Phe Thr Gly Leu Gly Ile Tyr Asp
20 25 30

Arg Ile Leu Ile Leu Pro Thr His Ala Asp Pro Gly Ser Glu Ile Gln
35 40 45

Val Asn Gly Ile His Thr Lys Val Leu Asp Ser Tyr Asp Leu Phe Asn
50 55 60

Lys Glu Gly Val Lys Leu Glu Ile Thr Val Leu Lys Leu Asp Arg Asn
65 70 75 80

Glu Lys Phe Arg Asp Ile Arg Lys Tyr Ile Pro Glu Ser Glu Asp Asp
85 90 95

Tyr Pro Glu Cys Asn Leu Ala Leu Val Ala Asn Gln Thr Glu Pro Thr
100 105 110

Ile Ile Lys Val Gly Asp Val Val Ser Tyr Gly Asn Ile Leu Leu Ser
115 120 125

Gly Thr Gln Thr Ala Arg Met Leu Lys Tyr Asn Tyr Pro Thr Lys Ser
130 135 140

Gly Tyr Cys Gly Gly Val Leu Tyr Lys Ile Gly Gln Ile Leu Gly Ile
145 150 155 160

His Val Gly Gly Asn Gly Arg Asp Gly Phe Ser Ser Met Leu Leu Arg
165 170 175

Ser Tyr Phe Thr Glu Gln
180

<210> 9
<211> 229
<212> PRT
<213> Vesiculovirus Indiana vesiculovirus

<400> 9

Met Ser Ser Leu Lys Lys Ile Leu Gly Leu Lys Gly Lys Gly Lys Lys
1 5 10 15

Ser Lys Lys Leu Gly Ile Ala Pro Pro Pro Tyr Glu Glu Asp Thr Ser
20 25 30

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

Asp Glu Met Asp Thr Tyr Asp Pro Asn Gln Leu Arg Tyr Glu Lys Phe

50

55

60

Phe Phe Thr Val Lys Met Thr Val Arg Ser Asn Arg Pro Phe Arg Thr
65 70 75 80

Tyr Ser Asp Val Ala Ala Val Ser His Trp Asp His Met Tyr Ile
85 90 95

Gly Met Ala Gly Lys Arg Pro Phe Tyr Lys Ile Leu Ala Phe Leu Gly
100 105 110

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

Pro Glu Tyr His Thr His Cys Glu Gly Arg Ala Tyr Leu Pro His Arg
130 135 140

Met Gly Lys Thr Pro Pro Met Leu Asn Val Pro Glu His Phe Arg Arg
145 150 155 160

Pro Phe Asn Ile Gly Leu Tyr Lys Gly Thr Ile Glu Leu Thr Met Thr
165 170 175

Ile Tyr Asp Asp Glu Ser Leu Glu Ala Ala Pro Met Ile Trp Asp His
180 185 190

Phe Asn Ser Ser Lys Phe Ser Asp Phe Arg Glu Lys Ala Leu Met Phe
195 200 205

Gly Leu Ile Val Glu Lys Lys Ala Ser Gly Ala Trp Val Leu Asp Ser
210 215 220

Ile Ser His Phe Lys
225

<210> 10

<211> 230

<212> PRT

<213> Alphainfluenzavirus Influenza A virus

<400> 10

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu Trp
1 5 10 15

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

Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly Arg Gly Ser
35 40 45

Thr Leu Gly Leu Asp Ile Glu Thr Ala Thr Arg Ala Gly Lys Gln Ile
50 55 60

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

Met Ala Ser Val Pro Ala Ser Arg Tyr Leu Thr Asp Met Thr Leu Glu
85 90 95

Glu Met Ser Arg Asp Trp Ser Met Leu Ile Pro Lys Gln Lys Val Ala
100 105 110

Gly Pro Leu Cys Ile Arg Met Asp Gln Ala Ile Met Asp Lys Asn Ile
115 120 125

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

Ile Leu Leu Arg Ala Phe Thr Glu Glu Gly Ala Ile Val Gly Glu Ile
145 150 155 160

Ser Pro Leu Pro Ser Leu Pro Gly His Thr Ala Glu Asp Val Lys Asn
165 170 175

Ala Val Gly Val Leu Ile Gly Gly Leu Glu Trp Asn Asp Asn Thr Val
180 185 190

Arg Val Ser Glu Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser Asn Glu
195 200 205

Asn Gly Arg Pro Pro Leu Thr Pro Lys Gln Lys Arg Glu Met Ala Gly
210 215 220

Thr Ile Arg Ser Glu Val
225 230

<210> 11
<211> 512
<212> PRT
<213> Unknown

<220>
<223> Simplexvirus sp.

<400> 11

Met Ala Thr Asp Ile Asp Met Leu Ile Asp Leu Gly Leu Asp Leu Ser
1 5 10 15

Asp Ser Asp Leu Asp Glu Asp Pro Pro Glu Pro Ala Glu Ser Arg Arg
20 25 30

Asp Asp Leu Glu Ser Asp Ser Ser Gly Glu Cys Ser Ser Ser Asp Glu
35 40 45

Asp Met Glu Asp Pro His Gly Glu Asp Gly Pro Glu Pro Ile Leu Asp
50 55 60

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

Pro Ser Thr Gln Thr Pro Arg Pro Thr Glu Arg Gln Gly Pro Asn Asp
85 90 95

Pro Gln Pro Ala Pro His Ser Val Trp Ser Arg Leu Gly Ala Arg Arg
100 105 110

Pro Ser Cys Ser Pro Glu Gln His Gly Gly Lys Val Ala Arg Leu Gln
115 120 125

Pro Pro Pro Thr Lys Ala Gln Pro Ala Arg Gly Gly Arg Arg Gly Arg
130 135 140

Arg Arg Gly Arg Gly Arg Gly Gly Pro Gly Ala Ala Asp Gly Leu Ser
145 150 155 160

Asp Pro Arg Arg Arg Ala Pro Arg Thr Asn Arg Asn Pro Gly Gly Pro
165 170 175

Arg Pro Gly Ala Gly Trp Thr Asp Gly Pro Gly Ala Pro His Gly Glu
180 185 190

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

Arg Gly Val Arg Gln Ala Pro Pro Pro Leu Met Thr Leu Ala Ile Ala
210 215 220

Pro Pro Pro Ala Asp Pro Arg Ala Pro Ala Pro Glu Arg Lys Ala Pro
225 230 235 240

Ala Ala Asp Thr Ile Asp Ala Thr Thr Arg Leu Val Leu Arg Ser Ile
245 250 255

Ser Glu Arg Ala Ala Val Asp Arg Ile Ser Glu Ser Phe Gly Arg Ser
260 265 270

Ala Gln Val Met His Asp Pro Phe Gly Gly Gln Pro Phe Pro Ala Ala
275 280 285

Asn Ser Pro Trp Ala Pro Val Leu Ala Gly Gln Gly Gly Pro Phe Asp
290 295 300

Ala Glu Thr Arg Arg Val Ser Trp Glu Thr Leu Val Ala His Gly Pro
305 310 315 320

Ser Leu Tyr Arg Thr Phe Ala Gly Asn Pro Arg Ala Ala Ser Thr Ala
325 330 335

Lys Ala Met Arg Asp Cys Val Leu Arg Gln Glu Asn Phe Ile Glu Ala
340 345 350

Leu Ala Ser Ala Asp Glu Thr Leu Ala Trp Cys Lys Met Cys Ile His
355 360 365

His Asn Leu Pro Leu Arg Pro Gln Asp Pro Ile Ile Gly Thr Thr Ala
370 375 380

Ala Val Leu Asp Asn Leu Ala Thr Arg Leu Arg Pro Phe Leu Gln Cys
385 390 395 400

Tyr Leu Lys Ala Arg Gly Leu Cys Gly Leu Asp Glu Leu Cys Ser Arg
405 410 415

Arg Arg Leu Ala Asp Ile Lys Asp Ile Ala Ser Phe Val Phe Val Ile
420 425 430

Leu Ala Arg Leu Ala Asn Arg Val Glu Arg Gly Val Ala Glu Ile Asp
435 440 445

Tyr Ala Thr Leu Gly Val Gly Val Gly Glu Lys Met His Phe Tyr Leu
450 455 460

Pro Gly Ala Cys Met Ala Gly Leu Ile Glu Ile Leu Asp Thr His Arg
465 470 475 480

Gln Glu Cys Ser Ser Arg Val Cys Glu Leu Thr Ala Ser His Ile Val
485 490 495

Ala Pro Pro Tyr Val His Gly Lys Tyr Phe Tyr Cys Asn Ser Leu Phe
500 505 510

<210> 12
<211> 700
<212> PRT
<213> Artificial Sequence

<220>
<223> target protein sequence

<400> 12

Met Arg Thr Leu Asn Thr Ser Ala Met Asp Gly Thr Gly Leu Val Val
1 5 10 15

Glu Arg Asp Phe Ser Val Arg Ile Leu Thr Ala Cys Phe Leu Ser Leu
20 25 30

Leu Ile Leu Ser Thr Leu Leu Gly Asn Thr Leu Val Cys Ala Ala Val
35 40 45

Ile Arg Phe Arg His Leu Arg Ser Lys Val Thr Asn Phe Phe Val Ile
50 55 60

Ser Leu Ala Val Ser Asp Leu Leu Val Ala Val Leu Val Met Pro Trp
65 70 75 80

Lys Ala Val Ala Glu Ile Ala Gly Phe Trp Pro Phe Gly Ser Phe Cys
85 90 95

Asn Ile Trp Val Ala Phe Asp Ile Met Cys Ser Thr Ala Ser Ile Leu
100 105 110

Asn Leu Cys Val Ile Ser Val Asp Arg Tyr Trp Ala Ile Ser Ser Pro
115 120 125

Phe Arg Tyr Glu Arg Lys Met Thr Pro Lys Ala Ala Phe Ile Leu Ile
130 135 140

Ser Val Ala Trp Thr Leu Ser Val Leu Ile Ser Phe Ile Pro Val Gln
145 150 155 160

Leu Ser Trp His Lys Ala Lys Pro Thr Ser Pro Ser Asp Gly Asn Ala
165 170 175

Thr Ser Leu Ala Glu Thr Ile Asp Asn Cys Asp Ser Ser Leu Ser Arg
180 185 190

Thr Tyr Ala Ile Ser Ser Ser Val Ile Ser Phe Tyr Ile Pro Val Ala
195 200 205

Ile Met Ile Val Thr Tyr Thr Arg Ile Tyr Arg Ile Ala Gln Lys Gln
210 215 220

Ile Arg Arg Ile Ala Ala Leu Glu Arg Ala Ala Val His Ala Lys Asn
225 230 235 240

Cys Gln Thr Thr Thr Gly Asn Gly Lys Pro Val Glu Cys Ser Gln Pro
245 250 255

Glu Ser Ser Phe Lys Met Ser Phe Lys Arg Glu Thr Lys Val Leu Lys
260 265 270

Thr Leu Ser Val Ile Met Gly Val Phe Val Cys Cys Trp Leu Pro Phe
275 280 285

Phe Ile Leu Asn Cys Ile Leu Pro Phe Cys Gly Ser Gly Glu Thr Gln
290 295 300

Pro Phe Cys Ile Asp Ser Asn Thr Phe Asp Val Phe Val Trp Phe Gly
305 310 315 320

Trp Ala Asn Ser Ser Leu Asn Pro Ile Ile Tyr Ala Phe Asn Ala Asp
325 330 335

Phe Arg Lys Ala Phe Ser Thr Leu Leu Gly Cys Tyr Arg Leu Cys Pro
340 345 350

Ala Thr Asn Asn Ala Ile Glu Thr Val Ser Ile Asn Asn Asn Gly Ala
355 360 365

Ala Met Phe Ser Ser His His Glu Pro Arg Gly Ser Ile Ser Lys Glu
370 375 380

Cys Asn Leu Val Tyr Leu Ile Pro His Ala Val Gly Ser Ser Glu Asp
385 390 395 400

Leu Lys Lys Glu Glu Ala Ala Gly Ile Ala Arg Pro Leu Glu Lys Leu
405 410 415

Ser Pro Ala Leu Ser Val Ile Leu Asp Tyr Asp Thr Asp Val Ser Leu
420 425 430

Glu Lys Ile Gln Pro Ile Thr Gln Asn Gly Gln His Pro Thr Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Met Val Ser
450 455 460

Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
465 470 475 480

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
485 490 495

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
500 505 510

Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr
515 520 525

Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp
530 535 540

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
545 550 555 560

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
565 570 575

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
580 585 590

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
595 600 605

Ser His Lys Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys
610 615 620

Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
625 630 635 640

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

Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Lys Leu Ser Lys Asp
660 665 670

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
675 680 685

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
690 695 700

<210> 13
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> target protein sequence

<400> 13

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

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

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Lys Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Lys Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 14
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> target protein sequence

<400> 14

Met Arg Thr Leu Asn Thr Ser Ala Met Asp Gly Thr Gly Leu Val Val
1 5 10 15

Glu Arg Asp Phe Ser Val Arg Ile Leu Thr Ala Cys Phe Leu Ser Leu
20 25 30

Leu Ile Leu Ser Thr Leu Leu Gly Asn Thr Leu Val Cys Ala Ala Val
35 40 45

Ile Arg Phe Arg His Leu Arg Ser Lys Val Thr Asn Phe Phe Val Ile
50 55 60

Ser Leu Ala Val Ser Asp Leu Leu Val Ala Val Leu Val Met Pro Trp
65 70 75 80

Lys Ala Val Ala Glu Ile Ala Gly Phe Trp Pro Phe Gly Ser Phe Cys
85 90 95

Asn Ile Trp Val Ala Phe Asp Ile Met Cys Ser Thr Ala Ser Ile Leu
100 105 110

Asn Leu Cys Val Ile Ser Val Asp Arg Tyr Trp Ala Ile Ser Ser Pro
115 120 125

Phe Arg Tyr Glu Arg Lys Met Thr Pro Lys Ala Ala Phe Ile Leu Ile
130 135 140

Ser Val Ala Trp Thr Leu Ser Val Leu Ile Ser Phe Ile Pro Val Gln
145 150 155 160

Leu Ser Trp His Lys Ala Lys Pro Thr Ser Pro Ser Asp Gly Asn Ala
165 170 175

Thr Ser Leu Ala Glu Thr Ile Asp Asn Cys Asp Ser Ser Leu Ser Arg
180 185 190

Thr Tyr Ala Ile Ser Ser Ser Val Ile Ser Phe Tyr Ile Pro Val Ala
195 200 205

Ile Met Ile Val Thr Tyr Thr Arg Ile Tyr Arg Ile Ala Gln Lys Gln
210 215 220

Ile Arg Arg Ile Ala Ala Leu Glu Arg Ala Ala Val His Ala Lys Asn
225 230 235 240

Cys Gln Thr Thr Thr Gly Asn Gly Lys Pro Val Glu Cys Ser Gln Pro
245 250 255

Glu Ser Ser Phe Lys Met Ser Phe Lys Arg Glu Thr Lys Val Leu Lys
260 265 270

Thr Leu Ser Val Ile Met Gly Val Phe Val Cys Cys Trp Leu Pro Phe
275 280 285

Phe Ile Leu Asn Cys Ile Leu Pro Phe Cys Gly Ser Gly Glu Thr Gln
290 295 300

Pro Phe Cys Ile Asp Ser Asn Thr Phe Asp Val Phe Val Trp Phe Gly
305 310 315 320

Trp Ala Asn Ser Ser Leu Asn Pro Ile Ile Tyr Ala Phe Asn Ala Asp
325 330 335

Phe Arg Lys Ala Phe Ser Thr Leu Leu Gly Cys Tyr Arg Leu Cys Pro
340 345 350

Ala Thr Asn Asn Ala Ile Glu Thr Val Ser Ile Asn Asn Asn Gly Ala
355 360 365

Ala Met Phe Ser Ser His His Glu Pro Arg Gly Ser Ile Ser Lys Glu
370 375 380

Cys Asn Leu Val Tyr Leu Ile Pro His Ala Val Gly Ser Ser Glu Asp
385 390 395 400

Leu Lys Lys Glu Glu Ala Ala Gly Ile Ala Arg Pro Leu Glu Lys Leu
405 410 415

Ser Pro Ala Leu Ser Val Ile Leu Asp Tyr Asp Thr Asp Val Ser Leu
420 425 430

Glu Lys Ile Gln Pro Ile Thr Gln Asn Gly Gln His Pro Thr Thr Gly
435 440 445

Thr Arg Pro Leu Trp Ser His Pro Gln Phe Glu Lys
450 455 460

<210> 15
<211> 635
<212> PRT
<213> Artificial Sequence

<220>
<223> target protein sequence

<400> 15

Met Asn Asn Phe Ile Leu Leu Glu Glu Gln Leu Ile Lys Lys Ser Gln
1 5 10 15

Gln Lys Arg Arg Thr Ser Pro Ser Asn Phe Lys Val Arg Phe Phe Val
20 25 30

Leu Thr Lys Ala Ser Leu Ala Tyr Phe Glu Asp Arg His Gly Lys Lys
35 40 45

Arg Thr Leu Lys Gly Ser Ile Glu Leu Ser Arg Ile Lys Cys Val Glu
50 55 60

Ile Val Lys Ser Asp Ile Ser Ile Pro Cys His Tyr Lys Tyr Pro Phe
65 70 75 80

Gln Val Val His Asp Asn Tyr Leu Leu Tyr Val Phe Ala Pro Asp Arg
85 90 95

Glu Ser Arg Gln Arg Trp Val Leu Ala Leu Lys Glu Glu Thr Arg Asn
100 105 110

Asn Asn Ser Leu Val Pro Lys Tyr His Pro Asn Phe Trp Met Asp Gly
115 120 125

Lys Trp Arg Cys Cys Ser Gln Leu Glu Lys Leu Ala Thr Gly Cys Ala
130 135 140

Gln Tyr Asp Pro Thr Lys Asn Ala Ser Lys Lys Pro Leu Pro Pro Thr
145 150 155 160

Pro Glu Asp Asn Arg Arg Pro Leu Trp Glu Pro Glu Glu Thr Val Val
165 170 175

Ile Ala Leu Tyr Asp Tyr Gln Thr Asn Asp Pro Gln Glu Leu Ala Leu
180 185 190

Arg Arg Asn Glu Glu Tyr Cys Leu Leu Asp Ser Ser Glu Ile His Trp
195 200 205

Trp Arg Val Gln Asp Arg Asn Gly His Glu Gly Tyr Val Pro Ser Ser
210 215 220

Tyr Leu Val Glu Lys Ser Pro Asn Asn Leu Glu Thr Tyr Glu Trp Tyr
225 230 235 240

Asn Lys Ser Ile Ser Arg Asp Lys Ala Glu Lys Leu Leu Leu Asp Thr
245 250 255

Gly Lys Glu Gly Ala Phe Met Val Arg Asp Ser Arg Thr Ala Gly Thr
260 265 270

Tyr Thr Val Ser Val Phe Thr Lys Ala Val Val Ser Glu Asn Asn Pro
275 280 285

Cys Ile Lys His Tyr His Ile Lys Glu Thr Asn Asp Asn Pro Lys Arg
290 295 300

Tyr Tyr Val Ala Glu Lys Tyr Val Phe Asp Ser Ile Pro Leu Leu Ile
305 310 315 320

Asn Tyr His Gln His Asn Gly Gly Gly Leu Val Thr Arg Leu Arg Tyr
325 330 335

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

Tyr Gly Lys Trp Val Ile Asp Pro Ser Glu Leu Thr Phe Val Gln Glu
355 360 365

Ile Gly Ser Gly Gln Phe Gly Leu Val His Leu Gly Tyr Trp Leu Asn
370 375 380

Lys Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly Ala Met Ser Glu
385 390 395 400

Glu Asp Phe Ile Glu Glu Ala Glu Val Met Met Lys Leu Ser His Pro
405 410 415

Lys Leu Val Gln Leu Tyr Gly Val Cys Leu Glu Gln Ala Pro Ile Cys
420 425 430

Leu Val Phe Glu Phe Met Glu His Gly Cys Leu Ser Asp Tyr Leu Arg
435 440 445

Thr Gln Arg Gly Leu Phe Ala Ala Glu Thr Leu Leu Gly Met Cys Leu
450 455 460

Asp Val Cys Glu Gly Met Ala Tyr Leu Glu Glu Ala Cys Val Ile His
465 470 475 480

Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn Gln Val Ile
485 490 495

Lys Val Ser Asp Phe Gly Met Thr Arg Phe Val Leu Asp Asp Gln Tyr
500 505 510

Thr Ser Ser Thr Gly Thr Lys Phe Pro Val Lys Trp Ala Ser Pro Glu
515 520 525

Val Phe Ser Phe Ser Arg Tyr Ser Ser Lys Ser Asp Val Trp Ser Phe
530 535 540

Gly Val Leu Met Trp Glu Val Phe Ser Glu Gly Lys Ile Pro Tyr Glu
545 550 555 560

Asn Arg Ser Asn Ser Glu Val Val Glu Asp Ile Ser Thr Gly Phe Arg
565 570 575

Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
580 585 590

His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
595 600 605

Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu Gly Gly Gly Gly
610 615 620

Gly Gly Gly Gly His His His His His His Val
625 630 635

<210> 16
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> target protein sequence

<400> 16

Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala
1 5 10 15

Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln
20 25 30

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

Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
85 90 95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
100 105 110

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
115 120 125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Glu Asn Thr Lys Thr Asn
180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
385 390 395 400

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

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
420 425 430

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

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
485 490 495

Asp Pro Arg Ala
500

<210> 17

<211> 883

<212> PRT

<213> Artificial Sequence

<220>

<223> target protein sequence

<400> 17

Met Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu
1 5 10 15

Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu
20 25 30

Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
50 55 60

Ala Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys
65 70 75 80

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
85 90 95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
165 170 175

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Gly Tyr Trp Ala
275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile
305 310 315 320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

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

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

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

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
725 730 735

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

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
865 870 875 880

Ala Phe Ala

<210> 18
<211> 1480
<212> PRT
<213> Artificial Sequence

<220>
<223> target protein sequence

<400> 18

Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe
1 5 10 15

Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg Gln Arg Leu
20 25 30

Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser Ala Asp Asn
35 40 45

Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu Ala Ser Lys
50 55 60

Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg
65 70 75 80

Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala
85 90 95

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

Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys
115 120 125

Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly
130 135 140

Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile
145 150 155 160

Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser
165 170 175

Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp
180 185 190

Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val
195 200 205

Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe
210 215 220

Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu
225 230 235 240

Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser
245 250 255

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

Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu
275 280 285

Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr
290 295 300

Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val Val Phe Leu
305 310 315 320

Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile
325 330 335

Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg
340 345 350

Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu Gly Ala Ile
355 360 365

Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys Thr Leu Glu
370 375 380

Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val Thr Ala Phe
385 390 395 400

Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys Gln Asn Asn
405 410 415

Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe Phe Ser Asn
420 425 430

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

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

Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro Ser Glu Gly
465 470 475 480

Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln Phe Ser Trp
485 490 495

Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly Val Ser Tyr
500 505 510

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

Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly
530 535 540

Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg
545 550 555 560

Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly
565 570 575

Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys
580 585 590

Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu
595 600 605

His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu His Glu Gly Ser Ser
610 615 620

Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe
625 630 635 640

Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu
645 650 655

Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu
660 665 670

Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys
675 680 685

Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro
690 695 700

Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln
705 710 715 720

Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg Arg Leu
725 730 735

Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro Arg Ile
740 745 750

Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg Gln Ser
755 760 765

Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn Ile His
770 775 780

Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro Gln Ala
785 790 795 800

Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln Glu Thr
805 810 815

Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys Glu Cys
820 825 830

Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr Trp Asn Thr
835 840 845

Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val Leu Ile
850 855 860

Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu Val Val
865 870 875 880

Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn Ser Thr
885 890 895

His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser Thr Ser Ser
900 905 910

Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr Leu Leu Ala
915 920 925

Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile Thr Val
930 935 940

Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln Ala Pro
945 950 955 960

Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe
965 970 975

Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe
980 985 990

Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val
995 1000 1005

Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro Val Ile
1010 1015 1020

Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser Gln
1025 1030 1035

Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr
1040 1045 1050

His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe
1055 1060 1065

Gly Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn
1070 1075 1080

Leu His Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp
1085 1090 1095

Phe Gln Met Arg Ile Glu Met Ile Phe Val Ile Phe Phe Ile Ala
1100 1105 1110

Val Thr Phe Ile Ser Ile Leu Thr Thr Gly Glu Gly Glu Gly Arg
1115 1120 1125

Val Gly Ile Ile Leu Thr Leu Ala Met Asn Ile Met Ser Thr Leu
1130 1135 1140

Gln Trp Ala Val Asn Ser Ser Ile Asp Val Asp Ser Leu Met Arg
1145 1150 1155

Ser Val Ser Arg Val Phe Lys Phe Ile Asp Met Pro Thr Glu Gly
1160 1165 1170

Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn Gly Gln Leu Ser
1175 1180 1185

Lys Val Met Ile Ile Glu Asn Ser His Val Lys Lys Asp Asp Ile
1190 1195 1200

Trp Pro Ser Gly Gly Gln Met Thr Val Lys Asp Leu Thr Ala Lys
1205 1210 1215

Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn Ile Ser Phe Ser
1220 1225 1230

Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg Thr Gly Ser
1235 1240 1245

Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu Asn Thr
1250 1255 1260

Glu Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile Thr
1265 1270 1275

Leu Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val
1280 1285 1290

Phe Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu
1295 1300 1305

Gln Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly
1310 1315 1320

Leu Arg Ser Val Ile Glu Gln Phe Pro Gly Lys Leu Asp Phe Val
1325 1330 1335

Leu Val Asp Gly Gly Cys Val Leu Ser His Gly His Lys Gln Leu
1340 1345 1350

Met Cys Leu Ala Arg Ser Val Leu Ser Lys Ala Lys Ile Leu Leu
1355 1360 1365

Leu Asp Glu Pro Ser Ala His Leu Asp Pro Val Thr Tyr Gln Ile
1370 1375 1380

Ile Arg Arg Thr Leu Lys Gln Ala Phe Ala Asp Cys Thr Val Ile
1385 1390 1395

Leu Cys Glu His Arg Ile Glu Ala Met Leu Glu Cys Gln Gln Phe
1400 1405 1410

Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr Asp Ser Ile Gln
1415 1420 1425

Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala Ile Ser Pro
1430 1435 1440

Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser Lys Cys
1445 1450 1455

Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr Glu Glu
1460 1465 1470

Glu Val Gln Asp Thr Arg Leu
1475 1480

<210> 19
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> target protein sequence

<400> 19

Met Arg Thr Leu Asn Thr Ser Ala Met Asp Gly Thr Gly Leu Val Val
1 5 10 15

Glu Arg Asp Phe Ser Val Arg Ile Leu Thr Ala Cys Phe Leu Ser Leu
20 25 30

Leu Ile Leu Ser Thr Leu Leu Gly Asn Thr Leu Val Cys Ala Ala Val
35 40 45

Ile Arg Phe Arg His Leu Arg Ser Lys Val Thr Asn Phe Phe Val Ile
50 55 60

Ser Leu Ala Val Ser Asp Leu Leu Val Ala Val Leu Val Met Pro Trp
65 70 75 80

Lys Ala Val Ala Glu Ile Ala Gly Phe Trp Pro Phe Gly Ser Phe Cys
85 90 95

Asn Ile Trp Val Ala Phe Asp Ile Met Cys Ser Thr Ala Ser Ile Leu
100 105 110

Asn Leu Cys Val Ile Ser Val Asp Arg Tyr Trp Ala Ile Ser Ser Pro
115 120 125

Phe Arg Tyr Glu Arg Lys Met Thr Pro Lys Ala Ala Phe Ile Leu Ile
130 135 140

Ser Val Ala Trp Thr Leu Ser Val Leu Ile Ser Phe Ile Pro Val Gln
145 150 155 160

Leu Ser Trp His Lys Ala Lys Pro Thr Ser Pro Ser Asp Gly Asn Ala
165 170 175

Thr Ser Leu Ala Glu Thr Ile Asp Asn Cys Asp Ser Ser Leu Ser Arg
180 185 190

Thr Tyr Ala Ile Ser Ser Ser Val Ile Ser Phe Tyr Ile Pro Val Ala
195 200 205

Ile Met Ile Val Thr Tyr Thr Arg Ile Tyr Arg Ile Ala Gln Lys Gln
210 215 220

Ile Arg Arg Ile Ala Ala Leu Glu Arg Ala Ala Val His Ala Lys Asn
225 230 235 240

Cys Gln Thr Thr Thr Gly Asn Gly Lys Pro Val Glu Cys Ser Gln Pro
245 250 255

Glu Ser Ser Phe Lys Met Ser Phe Lys Arg Glu Thr Lys Val Leu Lys
260 265 270

Thr Leu Ser Val Ile Met Gly Val Phe Val Cys Cys Trp Leu Pro Phe
275 280 285

Phe Ile Leu Asn Cys Ile Leu Pro Phe Cys Gly Ser Gly Glu Thr Gln
290 295 300

Pro Phe Cys Ile Asp Ser Asn Thr Phe Asp Val Phe Val Trp Phe Gly
305 310 315 320

Trp Ala Asn Ser Ser Leu Asn Pro Ile Ile Tyr Ala Phe Asn Ala Asp
325 330 335

Phe Arg Lys Ala Phe Ser Thr Leu Leu Gly Cys Tyr Arg Leu Cys Pro
340 345 350

Ala Thr Asn Asn Ala Ile Glu Thr Val Ser Ile Asn Asn Asn Gly Ala
355 360 365

Ala Met Phe Ser Ser His His Glu Pro Arg Gly Ser Ile Ser Lys Glu
370 375 380

Cys Asn Leu Val Tyr Leu Ile Pro His Ala Val Gly Ser Ser Glu Asp
385 390 395 400

Leu Lys Lys Glu Glu Ala Ala Gly Ile Ala Arg Pro Leu Glu Lys Leu
405 410 415

Ser Pro Ala Leu Ser Val Ile Leu Asp Tyr Asp Thr Asp Val Ser Leu
420 425 430

Glu Lys Ile Gln Pro Ile Thr Gln Asn Gly Gln His Pro Thr
435 440 445

<210> 20

<211> 702

<212> PRT

<213> Artificial Sequence

<220>

<223> target protein sequence

<400> 20

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

Thr Gly Pro Trp Trp Ala Ala Gly Gly Arg Gly Pro Arg Glu Val Ser
20 25 30

Pro Gly Ala Gly Thr Glu Val Gln Asp Ala Leu Glu Arg Ala Leu Pro
35 40 45

Glu Leu Gln Gln Ala Leu Ser Ala Leu Lys Gln Ala Gly Gly Ala Arg
50 55 60

Ala Val Gly Ala Gly Leu Ala Glu Val Phe Gln Leu Val Glu Glu Ala
65 70 75 80

Trp Leu Leu Pro Ala Val Gly Arg Glu Val Ala Gln Gly Leu Cys Asp
85 90 95

Ala Ile Arg Leu Asp Gly Gly Leu Asp Leu Leu Leu Arg Leu Leu Gln
100 105 110

Ala Pro Glu Leu Glu Thr Arg Val Gln Ala Ala Arg Leu Leu Glu Gln
115 120 125

Ile Leu Val Ala Glu Asn Arg Asp Arg Val Ala Arg Ile Gly Leu Gly
130 135 140

Val Ile Leu Asn Leu Ala Lys Glu Arg Glu Pro Val Glu Leu Ala Arg
145 150 155 160

Ser Val Ala Gly Ile Leu Glu His Met Phe Lys His Ser Glu Glu Thr
165 170 175

Cys Gln Arg Leu Val Ala Ala Gly Gly Leu Asp Ala Val Leu Tyr Trp
180 185 190

Cys Arg Arg Thr Asp Pro Ala Leu Leu Arg His Cys Ala Leu Ala Leu
195 200 205

Gly Asn Cys Ala Leu His Gly Gly Gln Ala Val Gln Arg Arg Met Val
210 215 220

Glu Lys Arg Ala Ala Glu Trp Leu Phe Pro Leu Ala Phe Ser Lys Glu
225 230 235 240

Asp Glu Leu Leu Arg Leu His Ala Cys Leu Ala Val Ala Val Leu Ala
245 250 255

Thr Asn Lys Glu Val Glu Arg Glu Val Glu Arg Ser Gly Thr Leu Ala
260 265 270

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

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

Leu Gln Arg Leu Val Pro Leu Leu Asp Ser Asn Arg Leu Glu Ala Gln
305 310 315 320

Cys Ile Gly Ala Phe Tyr Leu Cys Ala Glu Ala Ala Ile Lys Ser Leu
325 330 335

Gln Gly Lys Thr Lys Val Phe Ser Asp Ile Gly Ala Ile Gln Ser Leu
340 345 350

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

Lys Arg Ala Leu Arg Leu Leu Gly Glu Glu Val Pro Arg Pro Ile Leu
370 375 380

Pro Ser Val Pro Ser Trp Lys Glu Ala Glu Val Gln Thr Trp Leu Gln
385 390 395 400

Gln Ile Gly Phe Ser Lys Tyr Cys Glu Ser Phe Arg Glu Gln Gln Val
405 410 415

Asp Gly Asp Leu Leu Leu Arg Leu Thr Glu Glu Glu Leu Gln Thr Asp
420 425 430

Leu Gly Met Lys Ser Gly Ile Thr Arg Lys Arg Phe Phe Arg Glu Leu
435 440 445

Thr Glu Leu Lys Thr Phe Ala Asn Tyr Ser Thr Cys Asp Arg Ser Asn
450 455 460

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

Tyr Gly Leu Val Ser Cys Gly Leu Asp Arg Ser Leu Leu His Arg Val
485 490 495

Ser Glu Gln Gln Leu Leu Glu Asp Cys Gly Ile His Leu Gly Val His
500 505 510

Arg Ala Arg Ile Leu Thr Ala Ala Arg Glu Met Leu His Ser Pro Leu
515 520 525

Pro Cys Thr Gly Gly Lys Pro Ser Gly Asp Thr Pro Asp Val Phe Ile
530 535 540

Ser Tyr Arg Arg Asn Ser Gly Ser Gln Leu Ala Ser Leu Leu Lys Val
545 550 555 560

His Leu Gln Leu His Gly Phe Ser Val Phe Ile Asp Val Glu Lys Leu
565 570 575

Glu Ala Gly Lys Phe Glu Asp Lys Leu Ile Gln Ser Val Met Gly Ala
580 585 590

Arg Asn Phe Val Leu Val Leu Ser Pro Gly Ala Leu Asp Lys Cys Met
595 600 605

Gln Asp His Asp Cys Lys Asp Trp Val His Lys Glu Ile Val Thr Ala
610 615 620

Leu Ser Cys Gly Lys Asn Ile Val Pro Ile Ile Asp Gly Phe Glu Trp
625 630 635 640

Pro Glu Pro Gln Val Leu Pro Glu Asp Met Gln Ala Val Leu Thr Phe
645 650 655

Asn Gly Ile Lys Trp Ser His Glu Tyr Gln Glu Ala Thr Ile Glu Lys
660 665 670

Ile Ile Arg Phe Leu Gln Gly Arg Ser Ser Arg Asp Ser Ser Ala Gly
675 680 685

Ser Asp Thr Ser Leu Glu Gly Ala Ala Pro Met Gly Pro Thr
690 695 700

<210> 21
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG tag

<400> 21

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 22
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 22
gcccgggatc caccggctgc caccatgggtg agcaagggcg aggagc

<210> 23
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 23
agatggctgg caactagaag gcacagttac ttgtacagct cgtccatgcc gag 53

<210> 24
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 24
cactctcggc atggacgagc tgtacaagta actgtgcctt ctagttgcca gccatctgt 59

<210> 25
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 25
cagctcctcg cccttgctca ccatggtggc gaccggtgga tccc 44

<210> 26
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 26
cggccagtaa cgtaggggg gggggattac ttgtacagct cgtccatgcc gag 53

<210> 27
<211> 57

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 27
 cggtagccgcg ggcccgggat ccaccggtcg ccaccatggt gagcaagggc gaggagc 57

 <210> 28
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 28
 ctcggcatgg acgagctgta caagtaatcc ccccccccta acgttactgg 50

 <210> 29
 <211> 81
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 29
 acggggggagg ggcaaacaac agatggctgg caactagaag gcacagctgt aactcgaaaa 60
 cgacttccat gtctaattcg g 81

 <210> 30
 <211> 72
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 30
 cgcgggccccg ggatccaccg gtcgccacca tgaacaccat caatattgcc aagaacgact 60
 tttctgacat cg 72

<210> 31
 <211> 59
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 31
 agatggctgg caactagaag gcacagttag ggtcaggcaa atgcgaaatc ggactccag 59

<210> 32
 <211> 62
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 32
 cctggagtcc gatttcgcat ttgcctgacc ctaactgtgc cttctagttg ccagccatct 60
 gt 62

<210> 33
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 33
 cgttcttggc aatattgatg gtgttcatgg tggcgaccgg tggatcccgg gcc 53

<210> 34
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <400> 34
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<400> 51

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29

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36

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<400> 84
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<400> 87

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 <400> 93
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