

SEQUENCE LISTING

<110> GILEAD SCIENCES, INC.

<120> HBV VACCINES AND METHODS TREATING HBV

<130> 1324.PF

<140>

<141>

<150> 62/908,494

<151> 2019-09-30

<160> 102

<170> PatentIn version 3.5

<210> 1

<211> 226

<212> PRT

<213> Hepatitis B virus

<400> 1

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

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

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

Leu	Gly	Gln	Asn	Ser	Gln	Ser	Pro	Thr	Ser	Asn	His	Ser	Pro	Thr	Ser
	50					55					60				

Cys	Pro	Pro	Ile	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe
65					70					75					80

Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val
			85						90					95	

Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly
			100					105					110		

Ser	Thr	Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	Thr	Thr	Pro	Ala
			115				120					125			

Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp
130 135 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys
145 150 155 160

Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
165 170 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
180 185 190

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
195 200 205

Leu Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 2
<211> 226
<212> PRT
<213> Hepatitis B virus

<400> 2
Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
1 5 10 15

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

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

Pro Gly Gln Asn Leu Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
50 55 60

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65 70 75 80

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
85 90 95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
100 105 110

Ser Ser Thr Thr Ser Thr Gly Pro Cys Arg Thr Cys Thr Thr Pro Ala
115 120 125

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp
130 135 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys
145 150 155 160

Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
165 170 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
180 185 190

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
195 200 205

Leu Ser Pro Phe Met Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 3
<211> 226
<212> PRT
<213> Hepatitis B virus

<400> 3
Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
1 5 10 15

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

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

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
50 55 60

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65 70 75 80

Ile Ile Phe Leu Cys Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
85 90 95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
100 105 110

Ser Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala
115 120 125

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp
130 135 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
145 150 155 160

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
165 170 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
180 185 190

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
195 200 205

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 4
<211> 226
<212> PRT
<213> Hepatitis B virus

<400> 4

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

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

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys
35 40 45

Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
50 55 60

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65 70 75 80

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
85 90 95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
100 105 110

Ser Ser Thr Thr Ser Thr Gly Pro Cys Arg Thr Cys Thr Thr Pro Ala
115 120 125

Gln Gly Thr Ser Met Tyr Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
130 135 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys
145 150 155 160

Phe Leu Trp Glu Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu
165 170 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
180 185 190

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile
195 200 205

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 5
<211> 755
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 5
Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

Glu Thr Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp
20 25 30

Glu Asp Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu
35 40 45

Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu
50 55 60

Tyr Ser Ser Thr Val Pro Ile Phe Asn Pro Glu Trp Gln Thr Pro Ser
65 70 75 80

Phe Pro Lys Ile His Leu His Glu Asp Ile Ala Asn Arg Cys Gln Gln
85 90 95

Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Arg Leu Ile
100 105 110

Met Pro Ala Arg Phe Tyr Pro Asn Ser Thr Lys Tyr Leu Pro Leu Asp
115 120 125

Lys Gly Ile Lys Pro Tyr Tyr Pro Asp His Val Val Asn His Tyr Phe
130 135 140

Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr
145 150 155 160

Lys Arg Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser
165 170 175

Trp Glu Gln Glu Leu His His Gly Arg Leu Val Ile Lys Thr Ser Gln
180 185 190

Arg His Gly Asp Glu Pro Phe Cys Ser Gln Pro Ser Gly Ile Leu Ser
195 200 205

Arg Ser Ser Val Gly Pro Glu Phe His Ser Phe Pro Pro Ser Ser Ala
210 215 220

Arg Ser Gln Ser Gln Gly Pro Val Phe Ser Cys Trp Trp Leu Gln Phe
225 230 235 240

Arg Asn Thr Gln Pro Cys Ser Lys Tyr Cys Leu Ser His Leu Val Asn
245 250 255

Leu Leu Glu Asp Trp Gly Pro Cys Asp Glu His Gly Glu His His Ile
260 265 270

Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val
275 280 285

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

Ser Gln Phe Ser Arg Gly Ile Thr Arg Val Ser Trp Pro Lys Phe Ala
305 310 315 320

Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser
325 330 335

Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Ile Pro Leu His

340

345

350

Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg
 355 360 365

Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile His Asn Asn Gln His
 370 375 380

Gly Thr Leu Gln Asn Leu His Asp Ser Cys Ser Arg Gln Leu Tyr Val
 385 390 395 400

Ser Leu Met Leu Leu Tyr Lys Thr Tyr Gly Arg Lys Leu His Leu Tyr
 405 410 415

Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly
 420 425 430

Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val
 435 440 445

Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp
 450 455 460

Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Tyr Thr
 465 470 475 480

Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn
 485 490 495

Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile
 500 505 510

Gly Ser Trp Gly Thr Leu Pro Gln Asp His Ile Val Gln Lys Ile Lys
 515 520 525

His Cys Phe Arg Lys Leu Pro Ile Asn Arg Pro Ile Asp Trp Lys Val
 530 535 540

Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln
 545 550 555 560

Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys
565 570 575

Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Ser Lys Gln
580 585 590

Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln
595 600 605

Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala Ile Gly His
610 615 620

Gln Arg Met Arg Gly Thr Phe Val Ala Pro Leu Pro Ile His Thr Ala
625 630 635 640

His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu
645 650 655

Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe
660 665 670

Pro Trp Leu Leu Gly Cys Thr Ala Asn Trp Ile Leu Arg Gly Thr Ser
675 680 685

Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg
690 695 700

Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro Tyr Arg Pro
705 710 715 720

Thr Thr Gly Arg Thr Ser Leu Tyr Ala Val Ser Pro Ser Val Pro Ser
725 730 735

His Leu Pro Val Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp
740 745 750

Arg Pro Pro
755

<211> 749
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 6
Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro
65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Val Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Ser Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Asp Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Lys Arg His
180 185 190

Gly Asp Lys Ser Phe Cys Pro Gln Ser Pro Gly Ile Leu Pro Arg Ser
195 200 205

Glu Leu His His Phe Pro Pro Ser Ser Ser Arg Ser Gln Ser Gln Gly
210 215 220

Pro Val Leu Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Glu Pro Cys
225 230 235 240

Ser Glu Tyr Cys Leu Cys His Ile Val Asn Leu Ile Glu Asp Trp Gly
245 250 255

Pro Cys Thr Glu His Gly Glu His Arg Ile Arg Thr Pro Arg Thr Pro
260 265 270

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

Thr Thr Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly
290 295 300

Asn Thr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser
305 310 315 320

Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val
325 330 335

Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His
340 345 350

Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser
355 360 365

Ser Asn Ser Arg Ile Ile Asn Asn Gln His Arg Thr Met Gln Asn Leu
370 375 380

His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu Leu Tyr
385 390 395 400

Lys Thr Tyr Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu
405 410 415

Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu
420 425 430

Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro
435 440 445

His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly Ala Lys
450 455 460

Ser Val Gln His Leu Glu Ser Leu Tyr Ala Ala Val Thr Asn Phe Leu
465 470 475 480

Leu Ser Leu Gly Ile His Leu Asn Pro His Lys Thr Lys Arg Trp Gly
485 490 495

Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu
500 505 510

Pro Gln Glu His Ile Val Gln Lys Ile Lys Met Cys Phe Arg Lys Leu
515 520 525

Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly
530 535 540

Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu
545 550 555 560

Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser
565 570 575

Pro Thr Tyr Lys Ala Phe Leu Ser Lys Gln Tyr Leu His Leu Tyr Pro
580 585 590

Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp Ala Thr
595 600 605

Pro Thr Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Ala
610 615 620

Phe Val Ser Pro Leu Pro Ile His Thr Ala His Leu Leu Ala Ala Cys
625 630 635 640

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

Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys
660 665 670

Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser
675 680 685

Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr
690 695 700

Arg Pro Leu Leu Arg Leu Leu Tyr Arg Pro Thr Thr Gly Arg Thr Ser
705 710 715 720

Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val
725 730 735

His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
740 745

<210> 7

<211> 753

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 7

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro
65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Thr Val Asn His Tyr Phe Lys Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Glu Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Thr Arg His
180 185 190

Gly Asp Glu Ser Phe Cys Ser Gln Ser Ser Gly Ile Leu Ser Arg Ser
195 200 205

Pro Val Gly Pro Glu Leu His Asn Phe Pro Pro Ser Ser Ala Arg Ser
210 215 220

Gln Ser Glu Gly Pro Leu Leu Ser Cys Trp Trp Leu Gln Phe Arg Asn
225 230 235 240

Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu

245

250

255

Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu His Asn Ile Arg Ile
 260 265 270

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

Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val Val Asp Phe Ser Gln
 290 295 300

Phe Ser Arg Gly Ser Thr His Val Ser Trp Pro Lys Phe Ala Val Pro
 305 310 315 320

Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu
 325 330 335

Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala
 340 345 350

Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val
 355 360 365

Ala Arg Leu Ser Ser Thr Ser Arg Asn Ile Asn Tyr Gln His Gly Ala
 370 375 380

Met Gln Asp Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu
 385 390 395 400

Leu Leu Leu Tyr Lys Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His
 405 410 415

Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser
 420 425 430

Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg
 435 440 445

Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val
 450 455 460

Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val
465 470 475 480

Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr
485 490 495

Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser
500 505 510

Trp Gly Thr Leu Pro Gln Glu His Ile Val Leu Lys Ile Lys Gln Cys
515 520 525

Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln
530 535 540

Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly
545 550 555 560

Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala
565 570 575

Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu
580 585 590

Asn Leu Tyr Pro Val Ala Arg Gln Arg Ser Gly Leu Cys Gln Val Phe
595 600 605

Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala Val Gly His Gln Arg
610 615 620

Met Arg Gly Thr Phe Val Ser Pro Leu Pro Ile His Thr Ala His Leu
625 630 635 640

Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly
645 650 655

Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp
660 665 670

Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val

675

680

685

Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg
 690 695 700

Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr
 705 710 715 720

Gly Arg Thr Ser Leu Tyr Ala Val Ser Pro Ser Val Pro Ser His Leu
 725 730 735

Pro Val Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro
 740 745 750

Pro

<210> 8

<211> 742

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 8

Met Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp
 1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
 35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro
 65 70 75 80

Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Glu Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser Ser Gly
180 185 190

Ile Leu Ser Arg Pro Pro Val Gly Ser Glu Leu His Asn Leu Pro Pro
195 200 205

Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp Trp
210 215 220

Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His
225 230 235 240

Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu
245 250 255

His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
260 265 270

Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val
275 280 285

Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro
290 295 300

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
305 310 315 320

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
325 330 335

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
340 345 350

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn
355 360 365

Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn
370 375 380

Leu Tyr Val Ser Leu Met Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu
385 390 395 400

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
405 410 415

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

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr
435 440 445

Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser
450 455 460

Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu
465 470 475 480

Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met Gly
485 490 495

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

Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp
515 520 525

Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro
530 535 540

Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile
545 550 555 560

Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu
565 570 575

Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly
580 585 590

Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Val
595 600 605

Met Gly His Gln Arg Met Arg Gly Thr Phe Lys Ala Pro Leu Pro Ile
610 615 620

His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly
625 630 635 640

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

Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg
660 665 670

Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp
675 680 685

Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro
690 695 700

Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser
705 710 715 720

Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His
725 730 735

Val Ala Trp Arg Pro Pro
740

<210> 9
<211> 705
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 9
Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

Glu Thr Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp
20 25 30

Glu Asp Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu
35 40 45

Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu
50 55 60

Tyr Ser Ser Thr Val Pro Ile Phe Asn Pro Glu Trp Gln Thr Pro Ser
65 70 75 80

Phe Pro Lys Ile His Leu His Glu Asp Ile Ala Asn Arg Cys Gln Gln
85 90 95

Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Arg Leu Ile
100 105 110

Met Pro Ala Arg Phe Tyr Pro Asn Ser Thr Lys Tyr Leu Pro Leu Asp
115 120 125

Lys Gly Ile Lys Pro Tyr Tyr Pro Asp His Val Val Asn His Tyr Phe
130 135 140

Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr

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

Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser
370 375 380

Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg
385 390 395 400

Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val
405 410 415

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

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

Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser
450 455 460

Trp Gly Thr Leu Pro Gln Asp His Ile Val Gln Lys Ile Lys His Cys
465 470 475 480

Phe Arg Lys Leu Pro Ile Asn Arg Pro Ile Asp Trp Lys Val Cys Gln
485 490 495

Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly
500 505 510

Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala
515 520 525

Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Ser Lys Gln Tyr Leu
530 535 540

Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe
545 550 555 560

Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala Ile Gly His Gln Arg
565 570 575

Met Arg Gly Thr Phe Val Ala Pro Leu Pro Ile His Thr Ala His Leu

580

585

590

Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly
 595 600 605

Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp
 610 615 620

Leu Leu Gly Cys Thr Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val
 625 630 635 640

Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg
 645 650 655

Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro Tyr Arg Pro Thr Thr
 660 665 670

Gly Arg Thr Ser Leu Tyr Ala Val Ser Pro Ser Val Pro Ser His Leu
 675 680 685

Pro Val Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro
 690 695 700

Pro
 705

<210> 10

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 10

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
 1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro
65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Val Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Ser Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Asp Leu Gln His Gly Cys Trp Trp Leu Gln Phe Arg Asn Ser Glu
180 185 190

Pro Cys Ser Glu Tyr Cys Leu Cys His Ile Val Asn Leu Ile Glu Asp
195 200 205

Trp Gly Pro Cys Thr Glu His Gly Glu His Arg Ile Arg Thr Pro Arg
210 215 220

Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro
225 230 235 240

His Asn Thr Thr Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser
245 250 255

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

Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu
275 280 285

Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met
290 295 300

Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg
305 310 315 320

Leu Ser Ser Asn Ser Arg Ile Ile Asn Asn Gln His Arg Thr Met Gln
325 330 335

Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu
340 345 350

Leu Tyr Lys Thr Tyr Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile
355 360 365

Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe
370 375 380

Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala
385 390 395 400

Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly
405 410 415

Ala Lys Ser Val Gln His Leu Glu Ser Leu Tyr Ala Ala Val Thr Asn
420 425 430

Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro His Lys Thr Lys Arg
435 440 445

Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly
450 455 460

Thr Leu Pro Gln Glu His Ile Val Gln Lys Ile Lys Met Cys Phe Arg
465 470 475 480

Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile
485 490 495

Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro
500 505 510

Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr
515 520 525

Phe Ser Pro Thr Tyr Lys Ala Phe Leu Ser Lys Gln Tyr Leu His Leu
530 535 540

Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp
545 550 555 560

Ala Thr Pro Thr Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg
565 570 575

Gly Ala Phe Val Ser Pro Leu Pro Ile His Thr Ala His Leu Leu Ala
580 585 590

Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp
595 600 605

Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu
610 615 620

Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val
625 630 635 640

Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly
645 650 655

Leu Tyr Arg Pro Leu Leu Arg Leu Leu Tyr Arg Pro Thr Thr Gly Arg
660 665 670

Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp
675 680 685

Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
690 695 700

<210> 11
<211> 703
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 11
Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro
65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Thr Val Asn His Tyr Phe Lys Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg

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

Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe
370 375 380

Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala
385 390 395 400

Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly
405 410 415

Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn
420 425 430

Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg
435 440 445

Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly
450 455 460

Thr Leu Pro Gln Glu His Ile Val Leu Lys Ile Lys Gln Cys Phe Arg
465 470 475 480

Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile
485 490 495

Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro
500 505 510

Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr
515 520 525

Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu
530 535 540

Tyr Pro Val Ala Arg Gln Arg Ser Gly Leu Cys Gln Val Phe Ala Asp
545 550 555 560

Ala Thr Pro Thr Gly Trp Gly Leu Ala Val Gly His Gln Arg Met Arg
565 570 575

Gly Thr Phe Val Ser Pro Leu Pro Ile His Thr Ala His Leu Leu Ala

580

585

590

Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp
 595 600 605

Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu
 610 615 620

Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val
 625 630 635 640

Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly
 645 650 655

Leu Tyr Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg
 660 665 670

Thr Ser Leu Tyr Ala Val Ser Pro Ser Val Pro Ser His Leu Pro Val
 675 680 685

Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
 690 695 700

<210> 12

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 12

Met Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp
 1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
 35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro
65 70 75 80

Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Glu Leu Gln His Gly Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys
180 185 190

Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp
195 200 205

Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile Pro Arg
210 215 220

Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro
225 230 235 240

His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser
245 250 255

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

Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu
275 280 285

Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met
290 295 300

Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg
305 310 315 320

Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His Gly Thr Met Gln
325 330 335

Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu
340 345 350

Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile
355 360 365

Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe
370 375 380

Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala
385 390 395 400

Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly
405 410 415

Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn
420 425 430

Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg
435 440 445

Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr Gly
450 455 460

Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe Arg
465 470 475 480

Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile
485 490 495

Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro
500 505 510

Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr
515 520 525

Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu
530 535 540

Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp
545 550 555 560

Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met Arg
565 570 575

Gly Thr Phe Lys Ala Pro Leu Pro Ile His Thr Ala His Leu Leu Ala
580 585 590

Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Asn Ile Leu Gly Thr Asp
595 600 605

Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu
610 615 620

Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val
625 630 635 640

Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly
645 650 655

Leu Tyr Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg
660 665 670

Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp
675 680 685

Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
690 695 700

<210> 13
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 13
Met Ser Ser Arg Ser Gln Ser Gln Gly Pro Val Leu Ser Cys Trp Trp
1 5 10 15

Leu Gln Phe Arg Asn Ser Glu Pro Cys Ser Glu Tyr Cys Leu Cys His
20 25 30

Ile Val Asn Leu Ile Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu
35 40 45

His Arg Ile Arg Thr Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
50 55 60

Phe Leu Val Asp Lys Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val
65 70 75 80

Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Thr Arg Val Ser Trp Pro
85 90 95

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
100 105 110

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
115 120 125

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
130 135 140

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Ile Asn
145 150 155 160

Asn Gln His Arg Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn

165

170

175

Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr Tyr Gly Arg Lys Leu
 180 185 190

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
 195 200 205

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

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr
 225 230 235 240

Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser
 245 250 255

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

Asn Pro His Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly
 275 280 285

Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln Glu His Ile Val Gln
 290 295 300

Lys Ile Lys Met Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp
 305 310 315 320

Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro
 325 330 335

Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile
 340 345 350

Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu
 355 360 365

Ser Lys Gln Tyr Leu His Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly
 370 375 380

Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala
385 390 395 400

Ile Gly His Gln Arg Met Arg Gly Ala Phe Val Ser Pro Leu Pro Ile
405 410 415

His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly
420 425 430

Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr
435 440 445

Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg
450 455 460

Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp
465 470 475 480

Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Leu
485 490 495

Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser
500 505 510

Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His
515 520 525

Val Ala Trp Arg Pro Pro
530

<210> 14

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 14

Met Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp Trp
1 5 10 15

Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His
20 25 30

Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly Glu
35 40 45

His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
50 55 60

Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val
65 70 75 80

Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro
85 90 95

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
100 105 110

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
115 120 125

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
130 135 140

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn
145 150 155 160

Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn
165 170 175

Leu Tyr Val Ser Leu Met Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu
180 185 190

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
195 200 205

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

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr
225 230 235 240

Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser
245 250 255

Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu
260 265 270

Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met Gly
275 280 285

Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp His Ile Ile Gln
290 295 300

Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp
305 310 315 320

Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro
325 330 335

Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile
340 345 350

Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu
355 360 365

Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly
370 375 380

Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Val
385 390 395 400

Met Gly His Gln Arg Met Arg Gly Thr Phe Lys Ala Pro Leu Pro Ile
405 410 415

His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly
420 425 430

Ala Asn Ile Leu Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr
435 440 445

Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg
450 455 460

Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp
465 470 475 480

Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro
485 490 495

Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser
500 505 510

Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His
515 520 525

Val Ala Trp Arg Pro Pro
530

<210> 15
<211> 1030
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 15
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala

65

70

75

80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
 145 150 155 160

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
 165 170 175

Arg Ser Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His
 180 185 190

Phe Arg Lys Leu Leu Leu Leu Asp Asp Glu Thr Glu Ala Gly Pro Leu
 195 200 205

Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Asp Leu Asn Arg Arg Val
 210 215 220

Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr
 225 230 235 240

His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Ile
 245 250 255

Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro Lys Ile His Leu His
 260 265 270

Glu Asp Ile Ala Asn Arg Cys Gln Gln Phe Val Gly Pro Leu Thr Val
 275 280 285

Asn Glu Lys Arg Arg Leu Arg Leu Ile Met Pro Ala Arg Phe Tyr Pro
290 295 300

Asn Ser Thr Lys Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr
305 310 315 320

Pro Asp His Val Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His
325 330 335

Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr Arg Ser
340 345 350

Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu His His
355 360 365

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

Cys Ser Gln Pro Ser Gly Ile Leu Ser Arg Ser Ser Val Gly Pro Cys
385 390 395 400

Ile Arg Ser Gln Phe Lys Gln Ser Arg Leu Gly Leu Gln Pro His Gln
405 410 415

Gly Pro Leu Ala Thr Ser Gln Ser Gly Arg Ser Gly Ser Ile Arg Ala
420 425 430

Arg Val His Ser Pro Thr Arg Arg Cys Phe Gly Val Glu Pro Ser Gly
435 440 445

Ser Gly His Ile Gly His Ser Ala Ser Ser Ser Ser Ser Cys Leu His
450 455 460

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

Arg Gln Ser Ser Ser Gly His Ala Val Glu Phe His Ser Phe Pro Pro
485 490 495

Ser Ser Ala Arg Ser Gln Ser Gln Gly Pro Val Phe Ser Cys Trp Trp

500

505

510

Leu Gln Phe Arg Asn Thr Gln Pro Cys Ser Lys Tyr Cys Leu Ser His
 515 520 525

Leu Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Asp Glu His Gly Glu
 530 535 540

His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
 545 550 555 560

Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val
 565 570 575

Val Asp Phe Ser Gln Phe Ser Arg Gly Ile Thr Arg Val Ser Trp Pro
 580 585 590

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
 595 600 605

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Ile
 610 615 620

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
 625 630 635 640

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile His Asn
 645 650 655

Asn Gln His Gly Thr Leu Gln Asn Leu His Asp Ser Cys Ser Arg Gln
 660 665 670

Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr Tyr Gly Arg Lys Leu
 675 680 685

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
 690 695 700

Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile
 705 710 715 720

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr
725 730 735

Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser
740 745 750

Leu Tyr Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu
755 760 765

Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly
770 775 780

Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln Asp His Ile Val Gln
785 790 795 800

Lys Ile Lys His Cys Phe Arg Lys Leu Pro Ile Asn Arg Pro Ile Asp
805 810 815

Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro
820 825 830

Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile
835 840 845

Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu
850 855 860

Ser Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly
865 870 875 880

Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala
885 890 895

Ile Gly His Gln Arg Met Arg Gly Thr Phe Val Ala Pro Leu Pro Ile
900 905 910

His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly
915 920 925

Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr

930

935

940

Thr Ser Phe Pro Trp Leu Leu Gly Cys Thr Ala Asn Trp Ile Leu Arg
 945 950 955 960

Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp
 965 970 975

Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro
 980 985 990

Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Val Ser Pro Ser
 995 1000 1005

Val Pro Ser His Leu Pro Val Arg Val His Phe Ala Ser Pro Leu
 1010 1015 1020

His Val Ala Trp Arg Pro Pro
 1025 1030

<210> 16

<211> 1026

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 16

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
 1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
180 185 190

Lys Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
195 200 205

Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu
210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro Glu
245 250 255

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

Asn Arg Cys Gln Gln Tyr Val Gly Pro Leu Thr Val Asn Glu Lys Arg
275 280 285

Arg Leu Lys Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Leu Thr Lys
290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Val
305 310 315 320

Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

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

Gly Ser Pro Tyr Ser Trp Glu Gln Asp Leu Gln His Gly Arg Leu Val
355 360 365

Phe Gln Thr Ser Lys Arg His Gly Asp Lys Ser Phe Cys Pro Gln Ser
370 375 380

Pro Gly Ile Leu Pro Arg Ser Ser Val Gly Pro Cys Ile Gln Asn Gln
385 390 395 400

Leu Arg Lys Ser Arg Leu Gly Pro Gln Pro Ala Gln Gly Gln Leu Ala
405 410 415

Gly Arg Gln Gln Gly Gly Ser Gly Ser Ile Arg Ala Arg Val His Pro
420 425 430

Ser Pro Trp Gly Thr Val Gly Val Glu Pro Ser Gly Ser Gly His Ile
435 440 445

His Asn Cys Ala Ser Asn Ser Ser Ser Cys Leu His Gln Ser Ala Val
450 455 460

Arg Lys Ala Ala Tyr Ser His Ile Ser Thr Ser Lys Gly His Ser Ser
465 470 475 480

Ser Gly His Ala Val Glu Leu His His Phe Pro Pro Ser Ser Ser Arg
485 490 495

Ser Gln Ser Gln Gly Pro Val Leu Ser Cys Trp Trp Leu Gln Phe Arg
500 505 510

Asn Ser Glu Pro Cys Ser Glu Tyr Cys Leu Cys His Ile Val Asn Leu
515 520 525

Ile Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu His Arg Ile Arg
530 535 540

Thr Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp
545 550 555 560

Lys Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val Val Asp Phe Ser
565 570 575

Gln Phe Ser Arg Gly Asn Thr Arg Val Ser Trp Pro Lys Phe Ala Val
580 585 590

Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp
595 600 605

Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro
610 615 620

Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr
625 630 635 640

Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Ile Asn Asn Gln His Arg
645 650 655

Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser
660 665 670

Leu Met Leu Leu Tyr Lys Thr Tyr Gly Arg Lys Leu His Leu Tyr Ser
675 680 685

His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu
690 695 700

Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val
705 710 715 720

Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val
725 730 735

Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Tyr Ala Ala
740 745 750

Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro His Lys
755 760 765

Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly
770 775 780

Ser Trp Gly Thr Leu Pro Gln Glu His Ile Val Gln Lys Ile Lys Met
785 790 795 800

Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys
805 810 815

Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys
820 825 830

Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln
835 840 845

Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Ser Lys Gln Tyr
850 855 860

Leu His Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val
865 870 875 880

Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala Ile Gly His Gln
885 890 895

Arg Met Arg Gly Ala Phe Val Ser Pro Leu Pro Ile His Thr Ala His
900 905 910

Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile
915 920 925

Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro
930 935 940

Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe
945 950 955 960

Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly
965 970 975

Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Leu Tyr Arg Pro Thr
980 985 990

Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His
995 1000 1005

Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp
1010 1015 1020

Arg Pro Pro
1025

<210> 17
<211> 1026
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 17
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
180 185 190

Lys Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
195 200 205

Pro Arg Leu Ala Asp Glu Asp Leu Asn Arg Arg Val Ala Glu Asp Leu
210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro Glu
245 250 255

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

Asn Arg Cys Gln Gln Tyr Val Gly Pro Leu Thr Val Asn Glu Lys Arg

275

280

285

Arg Leu Lys Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Leu Thr Lys
 290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Thr
 305 310 315 320

Val Asn His Tyr Phe Lys Thr Arg His Tyr Leu His Thr Leu Trp Lys
 325 330 335

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

Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Arg Leu Val
 355 360 365

Phe Gln Thr Ser Thr Arg His Gly Asp Glu Ser Phe Cys Ser Gln Ser
 370 375 380

Ser Gly Ile Leu Ser Arg Ser Pro Val Gly Pro Cys Ile Arg Ser Gln
 385 390 395 400

Leu Lys Gln Ser Arg Leu Gly Leu Gln Pro Gln Gln Gly Ser Leu Ala
 405 410 415

Arg Ser Lys Ser Gly Arg Ser Gly Ser Ile Arg Ala Arg Val His Pro
 420 425 430

Thr Thr Arg Gln Ser Phe Gly Val Glu Pro Ser Gly Ser Gly His Ile
 435 440 445

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

Arg Lys Thr Ala Tyr Ser His Leu Ser Thr Ser Lys Arg Gln Ser Ser
 465 470 475 480

Ser Gly His Ala Val Glu Leu His Asn Phe Pro Pro Ser Ser Ala Arg
 485 490 495

Ser Gln Ser Glu Gly Pro Leu Leu Ser Cys Trp Trp Leu Gln Phe Arg
500 505 510

Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu
515 520 525

Leu Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu His Asn Ile Arg
530 535 540

Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp
545 550 555 560

Lys Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val Val Asp Phe Ser
565 570 575

Gln Phe Ser Arg Gly Ser Thr His Val Ser Trp Pro Lys Phe Ala Val
580 585 590

Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp
595 600 605

Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro
610 615 620

Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr
625 630 635 640

Val Ala Arg Leu Ser Ser Thr Ser Arg Asn Ile Asn Tyr Gln His Gly
645 650 655

Ala Met Gln Asp Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser
660 665 670

Leu Leu Leu Leu Tyr Lys Thr Phe Gly Arg Lys Leu His Leu Tyr Ser
675 680 685

His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu
690 695 700

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

705		710		715		720									
Arg	Arg	Ala	Phe	Pro	His	Cys	Leu	Ala	Phe	Ser	Tyr	Met	His	Asp	Val
				725					730					735	
Val	Leu	Gly	Ala	Lys	Ser	Val	Gln	His	Leu	Glu	Ser	Leu	Phe	Thr	Ala
			740					745					750		
Val	Thr	Asn	Phe	Leu	Leu	Ser	Leu	Gly	Ile	His	Leu	Asn	Pro	Asn	Lys
		755					760					765			
Thr	Lys	Arg	Trp	Gly	Tyr	Ser	Leu	Asn	Phe	Met	Gly	Tyr	Val	Ile	Gly
	770					775					780				
Ser	Trp	Gly	Thr	Leu	Pro	Gln	Glu	His	Ile	Val	Leu	Lys	Ile	Lys	Gln
785					790					795					800
Cys	Phe	Arg	Lys	Leu	Pro	Val	Asn	Arg	Pro	Ile	Asp	Trp	Lys	Val	Cys
				805					810					815	
Gln	Arg	Ile	Val	Gly	Leu	Leu	Gly	Phe	Ala	Ala	Pro	Phe	Thr	Gln	Cys
			820					825					830		
Gly	Tyr	Pro	Ala	Leu	Met	Pro	Leu	Tyr	Ala	Cys	Ile	Gln	Ala	Lys	Gln
		835					840					845			
Ala	Phe	Thr	Phe	Ser	Pro	Thr	Tyr	Lys	Ala	Phe	Leu	Cys	Lys	Gln	Tyr
	850					855					860				
Leu	Asn	Leu	Tyr	Pro	Val	Ala	Arg	Gln	Arg	Ser	Gly	Leu	Cys	Gln	Val
865					870					875					880
Phe	Ala	Asp	Ala	Thr	Pro	Thr	Gly	Trp	Gly	Leu	Ala	Val	Gly	His	Gln
				885					890					895	
Arg	Met	Arg	Gly	Thr	Phe	Val	Ser	Pro	Leu	Pro	Ile	His	Thr	Ala	His
			900					905					910		
Leu	Leu	Ala	Ala	Cys	Phe	Ala	Arg	Ser	Arg	Ser	Gly	Ala	Lys	Leu	Ile
		915					920				925				

Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro
930 935 940

Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe
945 950 955 960

Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly
965 970 975

Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr
980 985 990

Thr Gly Arg Thr Ser Leu Tyr Ala Val Ser Pro Ser Val Pro Ser His
995 1000 1005

Leu Pro Val Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp
1010 1015 1020

Arg Pro Pro
1025

<210> 18
<211> 1015
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 18
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
180 185 190

Arg Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
195 200 205

Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu
210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His
245 250 255

Trp Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp Ile Ile
260 265 270

Lys Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg
275 280 285

Arg Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys
290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu
305 310 315 320

Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys
340 345 350

Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Ala Glu Ser
355 360 365

Phe His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro Val Gly Ser
370 375 380

Ser Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu Gln Ser Gln
385 390 395 400

Gln Gly His Leu Ala Arg Arg Gln Gln Gly Arg Gly Trp Ser Ile Arg
405 410 415

Ala Gly Ile His Pro Thr Ala Arg Arg Pro Phe Gly Val Glu Pro Ser
420 425 430

Gly Ser Gly His Thr Ala Asn Leu Ala Ser Lys Ser Ala Ser Cys Leu
435 440 445

Tyr Gln Ser Ala Val Arg Lys Ala Ala Tyr Pro Val Val Ser Thr Phe
450 455 460

Lys Lys His Ser Ser Ser Gly His Ala Val Glu Leu His Asn Leu Pro
465 470 475 480

Pro Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe Pro Cys Trp
485 490 495

Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser
500 505 510

His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Ala Glu His Gly
515 520 525

Glu His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly
530 535 540

Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu
545 550 555 560

Val Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp
565 570 575

Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser
580 585 590

Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His
595 600 605

Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser
610 615 620

Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe
625 630 635 640

Asn Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg
645 650 655

Asn Leu Tyr Val Ser Leu Met Leu Leu Tyr Gln Thr Phe Gly Arg Lys
660 665 670

Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro
675 680 685

Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala
690 695 700

Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser
705 710 715 720

Tyr Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu
725 730 735

Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His
740 745 750

Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met
755 760 765

Gly Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp His Ile Ile
770 775 780

Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile
785 790 795 800

Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala
805 810 815

Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys
820 825 830

Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe
835 840 845

Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro
850 855 860

Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu
865 870 875 880

Val Met Gly His Gln Arg Met Arg Gly Thr Phe Lys Ala Pro Leu Pro
885 890 895

Ile His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser
900 905 910

Gly Ala Asn Ile Leu Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys
915 920 925

Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu
930 935 940

Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp
945 950 955 960

Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu
965 970 975

Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro
980 985 990

Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu
995 1000 1005

His Val Ala Trp Arg Pro Pro
1010 1015

<210> 19
<211> 940
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 19
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala

65

70

75

80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
 145 150 155 160

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
 165 170 175

Arg Ser Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His
 180 185 190

Phe Arg Lys Leu Leu Leu Leu Asp Asp Glu Thr Glu Ala Gly Pro Leu
 195 200 205

Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Asp Leu Asn Arg Arg Val
 210 215 220

Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr
 225 230 235 240

His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Ile
 245 250 255

Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro Lys Ile His Leu His
 260 265 270

Glu Asp Ile Ala Asn Arg Cys Gln Gln Phe Val Gly Pro Leu Thr Val
 275 280 285

Asn Glu Lys Arg Arg Leu Arg Leu Ile Met Pro Ala Arg Phe Tyr Pro
290 295 300

Asn Ser Thr Lys Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr
305 310 315 320

Pro Asp His Val Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His
325 330 335

Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr Arg Ser
340 345 350

Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu His His
355 360 365

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

Cys Ser Gln Pro Ser Gly Ile Leu Ser Arg Ser Ser Val Gly Pro Glu
385 390 395 400

Phe His Ser Phe Pro Pro Ser Ser Ala Arg Ser Gln Ser Gln Gly Pro
405 410 415

Val Phe Ser Cys Trp Trp Leu Gln Phe Arg Asn Thr Gln Pro Cys Ser
420 425 430

Lys Tyr Cys Leu Ser His Leu Val Asn Leu Leu Glu Asp Trp Gly Pro
435 440 445

Cys Asp Glu His Gly Glu His His Ile Arg Ile Pro Arg Thr Pro Ala
450 455 460

Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr
465 470 475 480

Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Ile
485 490 495

Thr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu

500

505

510

Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser
 515 520 525

Ala Ala Phe Tyr His Ile Pro Leu His Pro Ala Ala Met Pro His Leu
 530 535 540

Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser
 545 550 555 560

Asn Ser Arg Ile His Asn Asn Gln His Gly Thr Leu Gln Asn Leu His
 565 570 575

Asp Ser Cys Ser Arg Gln Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys
 580 585 590

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

Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala
 610 615 620

Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His
 625 630 635 640

Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly Ala Lys Ser
 645 650 655

Val Gln His Leu Glu Ser Leu Tyr Thr Ala Val Thr Asn Phe Leu Leu
 660 665 670

Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr
 675 680 685

Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro
 690 695 700

Gln Asp His Ile Val Gln Lys Ile Lys His Cys Phe Arg Lys Leu Pro
 705 710 715 720

Ile Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu
725 730 735

Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met
740 745 750

Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro
755 760 765

Thr Tyr Lys Ala Phe Leu Ser Lys Gln Tyr Leu Asn Leu Tyr Pro Val
770 775 780

Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro
785 790 795 800

Thr Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Thr Phe
805 810 815

Val Ala Pro Leu Pro Ile His Thr Ala His Leu Leu Ala Ala Cys Phe
820 825 830

Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val
835 840 845

Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Thr
850 855 860

Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala
865 870 875 880

Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg
885 890 895

Pro Leu Leu Arg Leu Pro Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu
900 905 910

Tyr Ala Val Ser Pro Ser Val Pro Ser His Leu Pro Val Arg Val His
915 920 925

Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro

930

935

940

<210> 20

<211> 932

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 20

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
 1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
 65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
 85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
180 185 190

Lys Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
195 200 205

Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu
210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro Glu
245 250 255

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

Asn Arg Cys Gln Gln Tyr Val Gly Pro Leu Thr Val Asn Glu Lys Arg
275 280 285

Arg Leu Lys Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Leu Thr Lys
290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Val
305 310 315 320

Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

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

Gly Ser Pro Tyr Ser Trp Glu Gln Asp Leu Gln His Gly Arg Leu Val
355 360 365

Phe Gln Thr Ser Lys Arg His Gly Asp Lys Ser Phe Cys Pro Gln Ser
370 375 380

Pro Gly Ile Leu Pro Arg Ser Glu Leu His His Phe Pro Pro Ser Ser
385 390 395 400

Ser Arg Ser Gln Ser Gln Gly Pro Val Leu Ser Cys Trp Trp Leu Gln
405 410 415

Phe Arg Asn Ser Glu Pro Cys Ser Glu Tyr Cys Leu Cys His Ile Val
420 425 430

Asn Leu Ile Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu His Arg
435 440 445

Ile Arg Thr Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu
450 455 460

Val Asp Lys Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val Val Asp
465 470 475 480

Phe Ser Gln Phe Ser Arg Gly Asn Thr Arg Val Ser Trp Pro Lys Phe
485 490 495

Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu
500 505 510

Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu
515 520 525

His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser
530 535 540

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

His Arg Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr
565 570 575

Val Ser Leu Met Leu Leu Tyr Lys Thr Tyr Gly Arg Lys Leu His Leu
580 585 590

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

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

Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met His
625 630 635 640

Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Tyr
645 650 655

Ala Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro
660 665 670

His Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val
675 680 685

Ile Gly Ser Trp Gly Thr Leu Pro Gln Glu His Ile Val Gln Lys Ile
690 695 700

Lys Met Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys
705 710 715 720

Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr
725 730 735

Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ala
740 745 750

Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Ser Lys
755 760 765

Gln Tyr Leu His Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys
770 775 780

Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala Ile Gly
785 790 795 800

His Gln Arg Met Arg Gly Ala Phe Val Ser Pro Leu Pro Ile His Thr
805 810 815

Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Lys
820 825 830

Leu Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser
835 840 845

Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr
850 855 860

Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser
865 870 875 880

Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Leu Tyr Arg
885 890 895

Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro
900 905 910

Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala
915 920 925

Trp Arg Pro Pro
930

<210> 21

<211> 936

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 21

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys

35

40

45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
 65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
 85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
 180 185 190

Lys Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
 195 200 205

Pro Arg Leu Ala Asp Glu Asp Leu Asn Arg Arg Val Ala Glu Asp Leu
 210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
 225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro Glu
 245 250 255

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

Asn Arg Cys Gln Gln Tyr Val Gly Pro Leu Thr Val Asn Glu Lys Arg
275 280 285

Arg Leu Lys Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Leu Thr Lys
290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Thr
305 310 315 320

Val Asn His Tyr Phe Lys Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

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

Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Arg Leu Val
355 360 365

Phe Gln Thr Ser Thr Arg His Gly Asp Glu Ser Phe Cys Ser Gln Ser
370 375 380

Ser Gly Ile Leu Ser Arg Ser Pro Val Gly Pro Glu Leu His Asn Phe
385 390 395 400

Pro Pro Ser Ser Ala Arg Ser Gln Ser Glu Gly Pro Leu Leu Ser Cys
405 410 415

Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu
420 425 430

Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Thr Glu His
435 440 445

Gly Glu His Asn Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly
450 455 460

Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Thr Glu Ser Arg

465		470		475		480
Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Ser Thr His Val Ser						
		485		490		495
Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu						
		500		505		510
Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr						
		515		520		525
His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser						
		530		535		540
Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Thr Ser Arg Asn						
545				550		555
Ile Asn Tyr Gln His Gly Ala Met Gln Asp Leu His Asp Ser Cys Ser						
		565		570		575
Arg Asn Leu Tyr Val Ser Leu Leu Leu Leu Tyr Lys Thr Phe Gly Arg						
		580		585		590
Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile						
		595		600		605
Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser						
		610		615		620
Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe						
625				630		635
Ser Tyr Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu						
		645		650		655
Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile						
		660		665		670
His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe						
		675		680		685

Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln Glu His Ile
690 695 700

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

Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala
725 730 735

Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala
740 745 750

Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala
755 760 765

Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg
770 775 780

Ser Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly
785 790 795 800

Leu Ala Val Gly His Gln Arg Met Arg Gly Thr Phe Val Ser Pro Leu
805 810 815

Pro Ile His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg
820 825 830

Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg
835 840 845

Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile
850 855 860

Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala
865 870 875 880

Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg
885 890 895

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

900

905

910

Pro Ser Val Pro Ser His Leu Pro Val Arg Val His Phe Ala Ser Pro
915 920 925

Leu His Val Ala Trp Arg Pro Pro
930 935

<210> 22

<211> 925

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 22

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
180 185 190

Arg Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
195 200 205

Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu
210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His
245 250 255

Trp Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp Ile Ile
260 265 270

Lys Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg
275 280 285

Arg Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys
290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu
305 310 315 320

Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys
340 345 350

Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Ala Glu Ser
355 360 365

Phe His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro Val Gly Ser
370 375 380

Glu Leu His Asn Leu Pro Pro Asn Ser Ala Arg Ser Gln Ser Glu Arg
385 390 395 400

Pro Val Phe Pro Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys
405 410 415

Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly
420 425 430

Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile Pro Arg Thr Pro
435 440 445

Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn
450 455 460

Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly
465 470 475 480

Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser
485 490 495

Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val
500 505 510

Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His
515 520 525

Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser
530 535 540

Ser Asn Ser Arg Ile Phe Asn Tyr Gln His Gly Thr Met Gln Asn Leu
545 550 555 560

His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu Leu Tyr
565 570 575

Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu
580 585 590

Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu
595 600 605

Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro
610 615 620

His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly Ala Lys
625 630 635 640

Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu
645 650 655

Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly
660 665 670

Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr Gly Ser Leu
675 680 685

Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe Arg Lys Leu
690 695 700

Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly
705 710 715 720

Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu
725 730 735

Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser
740 745 750

Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro
755 760 765

Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp Ala Thr
770 775 780

Pro Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met Arg Gly Thr
785 790 795 800

Phe Lys Ala Pro Leu Pro Ile His Thr Ala His Leu Leu Ala Ala Cys
805 810 815

Phe Ala Arg Ser Arg Ser Gly Ala Asn Ile Leu Gly Thr Asp Asn Ser
820 825 830

Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys
835 840 845

Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser
850 855 860

Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr
865 870 875 880

Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser
885 890 895

Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val
900 905 910

His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
915 920 925

<210> 23

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 23

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

20

25

30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
 65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
 145 150 155 160

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
 165 170 175

Arg Ser Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His
 180 185 190

Phe Arg Lys Leu Leu Leu Leu Asp Asp Glu Thr Glu Ala Gly Pro Leu
 195 200 205

Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Asp Leu Asn Arg Arg Val
 210 215 220

Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr
 225 230 235 240

His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Ile
245 250 255

Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro Lys Ile His Leu His
260 265 270

Glu Asp Ile Ala Asn Arg Cys Gln Gln Phe Val Gly Pro Leu Thr Val
275 280 285

Asn Glu Lys Arg Arg Leu Arg Leu Ile Met Pro Ala Arg Phe Tyr Pro
290 295 300

Asn Ser Thr Lys Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr
305 310 315 320

Pro Asp His Val Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His
325 330 335

Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr Arg Ser
340 345 350

Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu His His
355 360 365

Gly Cys Trp Trp Leu Gln Phe Arg Asn Thr Gln Pro Cys Ser Lys Tyr
370 375 380

Cys Leu Ser His Leu Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Asp
385 390 395 400

Glu His Gly Glu His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val
405 410 415

Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu
420 425 430

Ser Arg Leu Val Val Asp Phe Ser Gln Phe Ser Arg Gly Ile Thr Arg
435 440 445

Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn

450

455

460

Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala
 465 470 475 480

Phe Tyr His Ile Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val
 485 490 495

Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser
 500 505 510

Arg Ile His Asn Asn Gln His Gly Thr Leu Gln Asn Leu His Asp Ser
 515 520 525

Cys Ser Arg Gln Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr Tyr
 530 535 540

Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg
 545 550 555 560

Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe
 565 570 575

Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu
 580 585 590

Ala Phe Ser Tyr Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln
 595 600 605

His Leu Glu Ser Leu Tyr Thr Ala Val Thr Asn Phe Leu Leu Ser Leu
 610 615 620

Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu
 625 630 635 640

Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln Asp
 645 650 655

His Ile Val Gln Lys Ile Lys His Cys Phe Arg Lys Leu Pro Ile Asn
 660 665 670

Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly
675 680 685

Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu
690 695 700

Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr
705 710 715 720

Lys Ala Phe Leu Ser Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg
725 730 735

Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly
740 745 750

Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Thr Phe Val Ala
755 760 765

Pro Leu Pro Ile His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg
770 775 780

Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val Leu
785 790 795 800

Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Thr Ala Asn
805 810 815

Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn
820 825 830

Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu
835 840 845

Leu Arg Leu Pro Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala
850 855 860

Val Ser Pro Ser Val Pro Ser His Leu Pro Val Arg Val His Phe Ala
865 870 875 880

Ser Pro Leu His Val Ala Trp Arg Pro Pro

<210> 24

<211> 886

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 24

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
 1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
 65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
 85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
180 185 190

Lys Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
195 200 205

Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu
210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro Glu
245 250 255

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

Asn Arg Cys Gln Gln Tyr Val Gly Pro Leu Thr Val Asn Glu Lys Arg
275 280 285

Arg Leu Lys Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Leu Thr Lys
290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Val
305 310 315 320

Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

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

Gly Ser Pro Tyr Ser Trp Glu Gln Asp Leu Gln His Gly Cys Trp Trp
355 360 365

Leu Gln Phe Arg Asn Ser Glu Pro Cys Ser Glu Tyr Cys Leu Cys His
370 375 380

Ile Val Asn Leu Ile Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu
385 390 395 400

His Arg Ile Arg Thr Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
405 410 415

Phe Leu Val Asp Lys Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val
420 425 430

Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Thr Arg Val Ser Trp Pro
435 440 445

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
450 455 460

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
465 470 475 480

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
485 490 495

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Ile Asn
500 505 510

Asn Gln His Arg Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn
515 520 525

Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr Tyr Gly Arg Lys Leu
530 535 540

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
545 550 555 560

Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile
565 570 575

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr
580 585 590

Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser
595 600 605

Leu Tyr Ala Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu
610 615 620

Asn Pro His Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly
625 630 635 640

Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln Glu His Ile Val Gln
645 650 655

Lys Ile Lys Met Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp
660 665 670

Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro
675 680 685

Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile
690 695 700

Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu
705 710 715 720

Ser Lys Gln Tyr Leu His Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly
725 730 735

Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala
740 745 750

Ile Gly His Gln Arg Met Arg Gly Ala Phe Val Ser Pro Leu Pro Ile
755 760 765

His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly
770 775 780

Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr
785 790 795 800

Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg
805 810 815

Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp
820 825 830

Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Leu
835 840 845

Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser
850 855 860

Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His
865 870 875 880

Val Ala Trp Arg Pro Pro
885

<210> 25
<211> 886
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 25
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys

85

90

95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
 165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
 180 185 190

Lys Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
 195 200 205

Pro Arg Leu Ala Asp Glu Asp Leu Asn Arg Arg Val Ala Glu Asp Leu
 210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
 225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro Glu
 245 250 255

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

Asn Arg Cys Gln Gln Tyr Val Gly Pro Leu Thr Val Asn Glu Lys Arg
 275 280 285

Arg Leu Lys Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Leu Thr Lys
 290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Thr
305 310 315 320

Val Asn His Tyr Phe Lys Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

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

Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Cys Trp Trp
355 360 365

Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His
370 375 380

Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys Thr Glu His Gly Glu
385 390 395 400

His Asn Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
405 410 415

Phe Leu Val Asp Lys Asn Pro His Asn Thr Thr Glu Ser Arg Leu Val
420 425 430

Val Asp Phe Ser Gln Phe Ser Arg Gly Ser Thr His Val Ser Trp Pro
435 440 445

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
450 455 460

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
465 470 475 480

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
485 490 495

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Thr Ser Arg Asn Ile Asn
500 505 510

Tyr Gln His Gly Ala Met Gln Asp Leu His Asp Ser Cys Ser Arg Asn

515

520

525

Leu Tyr Val Ser Leu Leu Leu Tyr Lys Thr Phe Gly Arg Lys Leu
 530 535 540

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
 545 550 555 560

Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile
 565 570 575

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr
 580 585 590

Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser
 595 600 605

Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu
 610 615 620

Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly
 625 630 635 640

Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln Glu His Ile Val Leu
 645 650 655

Lys Ile Lys Gln Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp
 660 665 670

Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro
 675 680 685

Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile
 690 695 700

Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu
 705 710 715 720

Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Ser Gly
 725 730 735

Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Ala
740 745 750

Val Gly His Gln Arg Met Arg Gly Thr Phe Val Ser Pro Leu Pro Ile
755 760 765

His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly
770 775 780

Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr
785 790 795 800

Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg
805 810 815

Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp
820 825 830

Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro
835 840 845

Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Val Ser Pro Ser
850 855 860

Val Pro Ser His Leu Pro Val Arg Val His Phe Ala Ser Pro Leu His
865 870 875 880

Val Ala Trp Arg Pro Pro
885

<210> 26

<211> 886

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 26

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Pro Leu Ser Tyr Gln His Phe Arg
180 185 190

Arg Leu Leu Leu Leu Asp Asp Glu Ala Gly Pro Leu Glu Glu Glu Leu
195 200 205

Pro Arg Leu Ala Asp Glu Gly Leu Asn Arg Arg Val Ala Glu Asp Leu
210 215 220

Asn Leu Gly Asn Leu Asn Val Ser Ile Pro Trp Thr His Lys Val Gly
225 230 235 240

Asn Phe Thr Gly Leu Tyr Ser Ser Thr Val Pro Val Phe Asn Pro His
245 250 255

Trp Lys Thr Pro Ser Phe Pro Asn Ile His Leu His Gln Asp Ile Ile
260 265 270

Lys Lys Cys Glu Gln Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg
275 280 285

Arg Leu Gln Leu Ile Met Pro Ala Arg Phe Tyr Pro Asn Val Thr Lys
290 295 300

Tyr Leu Pro Leu Asp Lys Gly Ile Lys Pro Tyr Tyr Pro Glu His Leu
305 310 315 320

Val Asn His Tyr Phe Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys
325 330 335

Ala Gly Ile Leu Tyr Lys Arg Glu Thr Thr His Ser Ala Ser Phe Cys
340 345 350

Gly Ser Pro Tyr Ser Trp Glu Gln Glu Leu Gln His Gly Cys Trp Trp
355 360 365

Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp Tyr Cys Leu Ser His
370 375 380

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

His His Ile Arg Ile Pro Arg Thr Pro Ala Arg Val Thr Gly Gly Val
405 410 415

Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val
420 425 430

Val Asp Phe Ser Gln Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro
435 440 445

Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser
450 455 460

Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu
465 470 475 480

Pro Leu His Pro Ala Ala Met Pro His Leu Leu Val Gly Ser Ser Gly
485 490 495

Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn
500 505 510

Tyr Gln His Gly Thr Met Gln Asn Leu His Asp Ser Cys Ser Arg Asn
515 520 525

Leu Tyr Val Ser Leu Met Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu
530 535 540

His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met
545 550 555 560

Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile
565 570 575

Cys Ser Val Val Arg Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr
580 585 590

Met His Asp Val Val Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser
595 600 605

Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu
610 615 620

Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser Leu His Phe Met Gly
625 630 635 640

Tyr Val Ile Gly Cys Tyr Gly Ser Leu Pro Gln Asp His Ile Ile Gln
645 650 655

Lys Ile Lys Glu Cys Phe Arg Lys Leu Pro Val Asn Arg Pro Ile Asp
660 665 670

Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu Gly Phe Ala Ala Pro
675 680 685

Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile
690 695 700

Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu
705 710 715 720

Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly
725 730 735

Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr Gly Trp Gly Leu Val
740 745 750

Met Gly His Gln Arg Met Arg Gly Thr Phe Lys Ala Pro Leu Pro Ile
755 760 765

His Thr Ala His Leu Leu Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly
770 775 780

Ala Asn Ile Leu Gly Thr Asp Asn Ser Val Val Leu Ser Arg Lys Tyr
785 790 795 800

Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg
805 810 815

Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu Asn Pro Ala Asp Asp
820 825 830

Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro
835 840 845

Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser
850 855 860

Val Pro Ser His Leu Pro Asp Arg Val His Phe Ala Ser Pro Leu His
865 870 875 880

Val Ala Trp Arg Pro Pro
885

<210> 27
<211> 2247
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 27
atgcccctga gctaccagca cttcaggaag ctgctgctgc tggatgatga ggctggcctt 60
ctggaggagg agctgccag gctggcagat gagggcctca acaggagagt ggcagaggac 120
ctgaacctgg gcaacctgaa tgtgagcatc ccctggaccc acaaagtggg gaacttcact 180
ggcctctaca gcagcacagt gccagtgttc aaccctgagt ggcagacccc ctccttcccc 240
cacatccacc tccaggagga catcatcaac agatgtcagc agtatgtggg ccctctgaca 300
gtcaatgaga agaggaggct gaagctgata atgcctgccg ggttctaccc caacctgacc 360
aagtacctcc cactggacaa gggcatcaag ccatactatc ctgagcatgt ggtgaaccac 420
tactttcaga ccaggcacta cctgcacaca ctgtggaagg ctggcatcct gtacaagagg 480
gagagcacca gatcagcctc tttctgtggc tccccctaca gctgggagca ggatctccag 540
catggcagac tgggtgttca gacctcaag aggcatgggg acaagtcctt ttgccccag 600
agccctggca tcctgcccag gagcgagctc caccatttc cccctcctc cagcagaagc 660
cagtcccagg gacctgtgct gtcctgctgg tggctccagt tcaggaacag tgagccctgc 720
agtgagtact gtctgtgtca cattgtgaac ctgattgagg actgggggcc ctgcactgag 780
catggagagc acaggatcag aacccccagg accccagcca gagtgactgg aggtgtgttc 840
ctggtggaca agaaccccc caacaccaca gagagcagac tgggtggtgga cttctcccag 900
ttttcaaggg gcaacaccag agtgtcctgg cccaagtttg cagtgcccaa cctccagagc 960
ctgaccaacc tgctgtcatc aaacctgagc tggctgtccc tggatgtgtc tgctgccttc 1020
taccacctgc ccctgcaccc tgcagccatg cctcacctcc tgggtgggcag ctcaggcctg 1080
agcaggtatg tggccaggct gtcaagcaac tccagaatca tcaacaacca gcacaggacc 1140

atgcagaacc tgcattgactc ttgcagcagg aacctgtatg tgagcctgat gctgctgtac	1200
aagacctatg gcaggaagct gcacctgtac tcccacccca tcattcctggg ttccaggaag	1260
atcccatgg gagtgggact gtcccccttc ctgctggccc agttcacctc tgccattctgc	1320
tctgtggtga ggagagcctt cccccactgc ctggccttct cctacatgca tgatgtggtg	1380
ctgggggcca agtcagtga gcacctggag tctctgtatg ctgcagtcac caacttcctg	1440
ctcagcctgg gcatccacct gaacccccac aagaccaaga ggtggggcta ctctctgaac	1500
ttcatgggct atgtgatagg cagctggggc accctgccac aggagcacat agtgcagaag	1560
atcaagatgt gcttcaggaa gctgccagtg aacaggccca ttgattggaa ggtgtgccag	1620
aggattgtgg gcctgctggg ctttgcagca cccttcacac agtgtggcta cccagctctg	1680
atgcccctgt atgcctgcat ccaggccaag caggccttca ccttctcccc cacttacaag	1740
gccttcctgt ccaagcagta cctgcacctg taccctgtgg caaggcagag gccaggcctc	1800
tgccagggtg ttgcagatgc cccccaca ggctggggcc tggccattgg ccaccagagg	1860
atgagagggg cttttgtgag cccactgcca atccacacag cccacctgct ggcagcatgc	1920
tttgccaggc ccaggctctg tgcaaagctg attggcactg acaacagtgt ggtgctgtcc	1980
agaaagtaca ccagcttccc ctggctgctg ggatgtgctg ccaactggat tctgaggggc	2040
accagctttg tctatgtgcc ctctgcactg aaccctgcag atgaccctc caggggcaga	2100
ctggggctgt acaggccact gctcagactg ctgtacaggc ccaccactgg cagaacctcc	2160
ctgtatgcag acagcccctc agtgcctctt cacctgccag acagagtga ctttgccagc	2220
cccctgcatg ttgcctggag gcccc	2247

<210> 28

<211> 2109

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 28

atgcccctga gctaccagca cttcaggaag ctgctgctgc tggatgatga ggctggccct	60
---	----

ctggaggagg agctgccag gctggcagat gagggcctca acaggagagt ggcagaggac	120
--	-----

ctgaacctgg gcaacctgaa tgtgagcatc ccctggaccc acaaagtggg gaacttcact	180
ggcctctaca gcagcacagt gccagtgttc aaccctgagt ggagacccc ctccttcccc	240
cacatccacc tccaggagga catcatcaac agatgtcagc agtatgtggg ccctctgaca	300
gtcaatgaga agaggaggct gaagctgata atgcctgcca ggttctaccc caacctgacc	360
aagtacctcc cactggacaa gggcatcaag ccatactatc ctgagcatgt ggtgaaccac	420
tactttcaga ccaggcacta cctgcacaca ctgtggaagg ctggcatcct gtacaagagg	480
gagagcacca gatcagcctc tttctgtggc tccccctaca gctgggagca ggatctccag	540
catggctgct ggtggctcca gttcaggaac agtgagccct gcagttagta ctgtctgtgt	600
cacattgtga acctgattga ggactggggg ccctgcactg agcatggaga gcacaggatc	660
agaaccccc aagacccagc cagagtgact ggaggtgtgt tcctggtgga caagaacccc	720
cacaacacca cagagagcag actggtggtg gacttctccc agttttcaag gggcaacacc	780
agagtgtcct ggcccaagtt tgcagtgcc aacctccaga gcctgaccaa cctgctgtca	840
tcaaacctga gctggctgtc cctggatgtg tctgctgcct tctaccacct gcccctgcac	900
cctgcagcca tgcctcacct cctggtgggc agctcaggcc tgagcaggta tgtggccagg	960
ctgtcaagca actccagaat catcaacaac cagcacagga ccatgcagaa cctgcatgac	1020
tcttgagca ggaacctgta tgtgagcctg atgctgctgt acaagacctg tggcaggaag	1080
ctgcacctgt actccacccc catcatcctg ggtttcagga agatcccat gggagtggga	1140
ctgtccccct tcctgctggc ccagttcacc tctgccatct gctctgtggt gaggagagcc	1200
ttccccact gcctggcctt ctctacatg catgatgtgg tgctgggggc caagtcagtg	1260
cagcacctgg agtctctgta tgctgcagtc accaacttcc tgctcagcct gggcatccac	1320
ctgaaccccc acaagaccaa gaggtggggc tactctctga acttcatggg ctatgtgata	1380
ggcagctggg gcacctgcc acaggagcac atagtgcaga agatcaagat gtgcttcagg	1440
aagctgccag tgaacaggcc cattgattgg aaggtgtgcc agaggattgt gggcctgctg	1500
ggctttgcag cacccttcac acagtgtggc taccagctc tgatgcccct gtatgcctgc	1560
atccaggcca agcaggcctt caccttctcc ccacttaca aggccttcct gtccaagcag	1620
tacctgcacc tgtaccctgt ggcaaggcag aggccaggcc tctgccagggt gtttgcagat	1680
gccaccccc caggctgggg cctggccatt ggccaccaga ggatgagagg ggcctttgtg	1740

agcccactgc caatccacac agcccacctg ctggcagcat gctttgccag gtccaggtct	1800
ggtgcaaagc tgattggcac tgacaacagt gtgggtgctgt ccagaaagta caccagcttc	1860
ccctggctgc tgggatgtgc tgccaactgg attctgaggg gcaccagctt tgtctatgtg	1920
ccctctgcac tgaaccctgc agatgacccc tccaggggca gactggggct gtacaggcca	1980
ctgctcagac tgctgtacag gcccaccact ggcagaacct ccctgtatgc agacagcccc	2040
tcagtgccct ctcacctgcc agacagagtg cactttgccca gccccctgca tgttgccctgg	2100
aggcccccc	2109

<210> 29

<211> 1602

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 29

atgtccagca gaagccagtc ccagggacct gtgctgtcct gctgggtggct ccagttcagg	60
aacagtgagc cctgcagtga gtactgtctg tgtcacattg tgaacctgat tgaggactgg	120
gggccctgca ctgagcatgg agagcacagg atcagaacct ccaggacccc agccagagtg	180
actggaggtg tgttcctggg ggacaagaac cccacaaca ccacagagag cagactgggtg	240
gtggacttct cccagttttc aaggggcaac accagagtgt cctggcccaa gtttgcagtg	300
cccaacctcc agagcctgac caacctgctg tcatcaaacc tgagctggct gtccctggat	360
gtgtctgctg ctttctacca cctgcccctg caccctgcag ccatgcctca cctcctgggtg	420
ggcagctcag gcctgagcag gtatgtggcc aggctgtcaa gcaactccag aatcatcaac	480
aaccagcaca ggacctgca gaacctgcat gactcttgca gcaggaacct gtatgtgagc	540
ctgatgctgc tgtacaagac ctatggcagg aagctgcacc tgtactcca cccatcatc	600
ctggggtttca ggaagatccc catgggagtg ggactgtccc ctttctgct ggcccagttc	660
acctctgcca tctgctctgt ggtgaggaga gccttcccc actgcctggc cttctcttac	720
atgcatgatg tgggtgctggg ggccaagtca gtgcagcacc tggagtctct gtatgctgca	780
gtcaccaact tcctgctcag cctgggcatc cacctgaacc cccacaagac caagaggtgg	840

ggctactctc tgaacttcat gggctatgtg ataggcagct ggggcaccct gccacaggag	900
cacatagtgc agaagatcaa gatgtgcttc aggaagctgc cagtgaacag gccattgat	960
tggaaggtgt gccagaggat tgtgggcctg ctgggctttg cagcaccctt cacacagtgt	1020
ggctaccag ctctgatgcc cctgtatgcc tgcattcagg ccaagcaggc cttcaccttc	1080
tccccactt acaaggcctt cctgtccaag cagtacctgc acctgtacc tgtggcaagg	1140
cagaggccag gcctctgcca ggtgtttgca gatgccaccc ccacaggctg gggcctggcc	1200
attggccacc agaggatgag aggggccttt gtgagccac tgccaatcca cacagccac	1260
ctgctggcag catgctttgc caggtccagg tctggtgcaa agctgattgg cactgacaac	1320
agtgtggtgc tgtccagaaa gtacaccagc ttcccctggc tgctgggatg tgctgccaac	1380
tggattctga ggggcaccag ctttgtctat gtgccctctg cactgaacc tgcagatgac	1440
ccctccaggg gcagactggg gctgtacagg ccactgctca gactgctgta caggcccacc	1500
actggcagaa cctcccctgta tgcagacagc ccctcagtgc cctctcacct gccagacaga	1560
gtgcactttg ccagccccct gcatgttgcc tggaggcccc cc	1602

<210> 30

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 30

atgcccccta gctaccaaca cttcaggaga ctgctgctgc tggatgatga ggcaggccct	60
ctggaggagg agctgcccag gctggcagat gagggcctga acaggagggt ggctgaggac	120
ctgaacctgg gcaacctgaa tgtgagcatc ctttgaccc acaaagtggg caacttcaca	180
ggcctgtaca gcagactgt gcctgtgttc aacccccact ggaagacacc cagcttcccc	240
aacatccacc tgcaccagga catcatcaag aagtgtgagc agtttgtggg cccctgaca	300
gtcaatgaga agaggaggct ccagctgatc atgccagcca ggttctacc caatgtgacc	360
aagtacctcc ccctggacaa gggcatcaag ctttactatc cagagcacct ggtgaaccac	420
tacttccaga ccagacacta cctgcacaca ctgtggaagg caggcatcct gtacaagagg	480

gagaccacac acagtgcctc cttctgtggc agcccctact cctgggagca ggagctgcaa	540
catggagctg agtccttcca ccagcagtcc agtggcatcc tgagcaggcc ccctgtgggc	600
agcgagctgc acaacctgcc ccccaactct gccagatccc agtctgagag gccagtgttc	660
ccttgctggg ggctccagtt caggaacagc aagccctgct cagactactg cctgagccac	720
attgtgaacc tgctggagga ctggggcccc tgtgcagagc atggggagca ccacatcaga	780
atccccagga cccctgccag ggtgacagga ggggtgttcc tgggtggaaa gaacccccac	840
aacactgcag agtccaggct ggtggtggac ttctcccagt tcagcagggg caactacaga	900
gtctcctggc caaagtttgc tgtgccaac ctccagagcc tgacaaacct gctgagcagc	960
aacctgtcct ggctctccct ggatgtgagt gcagccttct atcacctgcc cctgcaccca	1020
gcagccatgc cacacctgct ggtgggctcc agtggcctgt ccaggtatgt ggccaggctc	1080
tcctccaact ccaggatctt caactatcag catggcacca tgcagaacct gcatgacagc	1140
tgctccagga acctgtatgt gtccctgatg ctgctctatc agacctttgg caggaagctg	1200
cacctgtaca gccaccccat catcctgggg ttccaggaaga tcccatggg tgtgggcctg	1260
tcccccttcc tgctggccca gttcaccagt gccatctgct cagtgggtgag gagggccttc	1320
ccacactgcc tggccttctc ttacatgcat gatgtggtcc tgggtgccaa gtctgtgcag	1380
cacctggaga gcctgttcac agctgtgaca aacttttctc tgagcctggg catccacctg	1440
aacccaaca agaccaagag gtgggggttat tctactgcact tcatgggcta tgtgattggc	1500
tgctatggct ctctgccaca ggaccacatc atccagaaga tcaaggagtg cttcagaaag	1560
ctgccagtga acaggccaat tgactggaag gtgtgccaga ggattgtggg cctgctgggc	1620
tttgagccc cttcaccca gtgtggctac cctgccctga tgcccctgta tgcctgcac	1680
cagagcaagc aggccttcac cttttcccc acttacaagg ccttcctgtg caagcagtac	1740
ctgaacctgt accctgtggc caggcagaga cctgggctgt gccagggtgt tgcagatgcc	1800
acccccacag gatggggact ggtcatggga caccagagga tgaggggcac cttcaaggca	1860
cccctgcca tccacacagc ccacctgctg gctgcctgct ttgccaggag caggagtggg	1920
gccaacatcc tgggcacaga caactctgtg gtgctgagca ggaagtacac atccttcccc	1980
tggctgctgg gatgtgcagc caactggatc ctgaggggca ccagctttgt gtatgtgccc	2040
tctgccctca accctgcaga tgatccaagc aggggcaggc tgggactgta caggccactg	2100

ctcagactgc ccttcaggcc caccactggc aggaccagcc tgtatgctga ctccccatct	2160
gtgccctccc acctgcctga cagagtgcac ttgacctccc cactgcatgt ggcctggagg	2220
cccca	2226

<210> 31
 <211> 2109
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 31	
atgcccctga gttaccaaca cttcaggaga ctgctgctgc tggatgatga ggcaggccct	60
ctggaggagg agctgcccag gctggcagat gagggcctga acaggagggt ggctgaggac	120
ctgaacctgg gcaacctgaa tgtgagcatc ctttgacccc aaaaagtggg caacttcaca	180
ggcctgtaca gcagcactgt gcctgtgttc aacccccact ggaagacacc cagcttcccc	240
aacatccacc tgcaccagga catcatcaag aagtgtgagc agtttgtggg cccctgaca	300
gtcaatgaga agaggaggct ccagctgata atgccagcca ggttctaccc caatgtgacc	360
aagtacctcc ccctggacaa gggcatcaag ctttactatc cagagcacct ggtgaaccac	420
tacttccaga ccagacacta cctgcacaca ctgtggaagg caggcatcct gtacaagagg	480
gagaccacac acagtgcctc cttctgtggc agcccctact cctgggagca ggagctgcaa	540
catggatgct ggtggctcca gttcaggaac agcaagccct gctcagacta ctgcctgagc	600
cacattgtga acctgctgga ggactggggc ccctgtgcag agcatgggga gcaccacatc	660
agaatcccca ggacccctgc cagggtgaca ggaggggtgt tcctggtgga caagaacccc	720
cacaacactg cagagtccag gctgggtgtg gacttctccc agttcagcag gggcaactac	780
agagtctcct ggccaaagt tgcctgtgccc aacctccaga gcctgacaaa cctgctgagc	840
agcaacctgt cctggctctc cctggatgtg agtgcagcct tctatcacct gccctgcac	900
ccagcagcca tgccacacct gctgggtggc tccagtggcc tgtccaggta tgtggccagg	960
ctctcctcca actccaggat cttcaactat cagcatggca ccatgcagaa cctgcatgac	1020
agctgctcca ggaacctgta tgtgtccctg atgctgctct atcagacctt tggcaggaag	1080

ctgcacctgt acagccaccc catcatcctg gggttcagga agatcccat ggggtgtgggc	1140
ctgtccccct tcctgctggc ccagttcacc agtgccatct gctcagtggg gaggagggcc	1200
ttccacact gcctggcctt ctcttacatg catgatgtgg tcctgggtgc caagtctgtg	1260
cagcacctgg agagcctggt cacagctgtg acaaactttc tcctgagcct gggcatccac	1320
ctgaaccca acaagaccaa gaggtggggg tatttactgc acttcatggg ctatgtgatt	1380
ggctgctatg gctctctgcc acaggaccac atcatccaga agatcaagga gtgcttcaga	1440
aagctgccag tgaacaggcc aattgactgg aaggtgtgcc agaggattgt gggcctgctg	1500
ggctttgcag ccccttcac ccagtgtggc taccctgccc tgatgccct gtatgcctgc	1560
atccagagca agcaggcctt caccttttcc cccacttaca aggccttcct gtgcaagcag	1620
tacctgaacc tgtaccctgt ggccaggcag agacctgggc tgtgccaggt gtttgcagat	1680
gccaccccca caggatgggg actggtcatg ggacaccaga ggatgagggg caccttcaag	1740
gcacccctgc ccatccacac agcccacctg ctggctgcct gctttgccag gagcaggagt	1800
ggggccaaca tcctgggcac agacaactct gtgggtgctga gcaggaagta cacatccttc	1860
ccctggctgc tgggatgtgc agccaactgg atcctgaggg gcaccagctt tgtgtatgtg	1920
ccctctgccc tcaaccctgc agatgatcca agcaggggca ggctgggact gtacaggcca	1980
ctgctcagac tgcccttcag gccaccact ggcaggacca gcctgtatgc tgactcccca	2040
tctgtgccct cccacctgcc tgacagagtg cactttgcct cccactgca tgtggcctgg	2100
aggcccca	2109

<210> 32

<211> 1602

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 32

atgtctgcca gatccagtc tgagaggcca gtgttcctt gctgggtggct ccagttcagg	60
aacagcaagc cctgctcaga ctactgcctg agccacattg tgaacctgct ggaggactgg	120
ggcccctgtg cagagcatgg ggagcaccac atcagaatcc ccaggacccc tgccagggtg	180

acaggagggg	tgttcctggt	ggacaagaac	ccccacaaca	ctgcagagtc	caggctgggtg	240
gtggacttct	cccagttcag	caggggcaac	tacagagtct	cctggccaaa	gtttgctgtg	300
cccaacctcc	agagcctgac	aaacctgctg	agcagcaacc	tgtcctggct	ctccctggat	360
gtgagtgcag	ccttctatca	cctgcccctg	cacccagcag	ccatgccaca	cctgctgggtg	420
ggctccagtg	gcctgtccag	gtatgtggcc	aggctctcct	ccaactccag	gatcttcaac	480
tatcagcatg	gcacatgca	gaacctgcat	gacagctgct	ccaggaacct	gtatgtgtcc	540
ctgatgctgc	tctatcagac	ctttggcagg	aagctgcacc	tgtacagcca	ccccatcatc	600
ctggggttca	ggaagatccc	catgggtgtg	ggcctgtccc	ccttcctgct	ggcccagttc	660
accagtgcc	tctgctcagt	ggtgaggagg	gccttccac	actgcctggc	cttctcttac	720
atgcatgatg	tggtcctggg	tgccaagtct	gtgcagcacc	tggagagcct	gttcacagct	780
gtgacaaact	ttctcctgag	cctgggcatc	cacctgaacc	ccaacaagac	caagaggtgg	840
ggttattcac	tgcacttcat	gggctatgtg	attggctgct	atggctctct	gccacaggac	900
cacatcatcc	agaagatcaa	ggagtgcctt	agaaagctgc	cagtgaacag	gccaattgac	960
tggaagggtg	gccagaggat	tgtgggcctg	ctgggccttg	cagccccctt	cacccagtgt	1020
ggctaccctg	ccctgatgcc	cctgtatgcc	tgcatccaga	gcaagcaggc	cttcaccttt	1080
tccccactt	acaaggcctt	cctgtgcaag	cagtacctga	acctgtacct	tgtggccagg	1140
cagagacctg	ggctgtgcca	ggtgtttgca	gatgccaccc	ccacaggatg	gggactggtc	1200
atgggacacc	agaggatgag	gggcacctt	aaggcacccc	tgcccatcca	cacagcccac	1260
ctgctggctg	cctgctttgc	caggagcagg	agtggggcca	acatcctggg	cacagacaac	1320
tctgtgggtg	tgagcaggaa	gtacacatcc	ttcccctggc	tgctgggatg	tgagccaac	1380
tggtacctga	ggggcaccag	ctttgtgtat	gtgccctctg	ccctcaacct	tgagatgat	1440
ccaagcaggg	gcaggctggg	actgtacagg	ccactgctca	gactgccctt	caggcccacc	1500
actggcagga	ccagcctgta	tgctgactcc	ccatctgtgc	cctccacct	gcctgacaga	1560
gtgcactttg	cctccccact	gcatgtggcc	tggaggcccc	ca		1602

<210> 33

<211> 1227

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 33

atggacattg acccctacaa ggagtttggg gccagtgtgg agctgctgtc ttttctgcca	60
tctgacttct tccccagtgt gagggacctg ctggacactg cctcagcact gtacagagag	120
gccctggaga gccagagca ctgctcccc caccacacag ccctgaggca ggccatcctc	180
tgctgggggg agctgatgaa cctggccacc tgggtgggct ccaacctgga ggaccctgcc	240
tcaaggagc tgggtggtcag ctatgtcaat gtgaacatgg gcctcaagat caggcagctg	300
ctgtggttcc acatctcctg cctgacctt ggaggggaga cagtcctgga gtacctggtg	360
agctttgggg tgtggatcag gacccccct gcctacaggc ccccaatgc tccatcctg	420
tccacctgc cagagaccac tgtggtcagg agaaggggca ggtccccag gaggagaacc	480
ccctctcca ggaggaggag aagccagtcc ccagggagga ggaggagcca gagcagagag	540
tctcagtgc tggagagcac cacatcaggc ttctggggc ccctgctggt gctccaggca	600
ggcttctttc tgctgaccag gattctgacc atccccagt ccctggacag ctggtggacc	660
tccctgaatt ttctgggggg gggccctacc tgtcctggcc agaactctca gtctcccacc	720
tcgaatcact caccaaccag ctgtcccccc atctgtcctg gctacagggt gatgtgcctg	780
aggagattca tcatcttcct gtgcatcctg ctgctgtgcc tgatctttct gctggtgctg	840
ctggactacc agggcatgct gccagtgtgc cctctcatcc caggcagctc caccacatcc	900
acaggacctt gcaagacatg caccacacca gccaggggca ccagcatgtt cccctcctgc	960
tgttgacca agccaacaga tggcaactgc acatgcattc ccacccctc cagctgggcc	1020
tttgccaggt ttctgtggga gtgggccaagt gtgagatttt cctggctgtc tcttctggtg	1080
ccctttgtgc agtggtttgt gggcctgtcc cctacagtgt ggctgagtgt catctggatg	1140
atgtggtact gggggccctc cctgtacaac atcctctctc ctttctgcc tctgctgcca	1200
atcttctttt gcctgtgggt gtacatc	1227

<210> 34

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 34

atggacattg acccctacaa ggagtttggg gccagtgtgg agctgctgtc ttttctgcca	60
tctgacttct tccccagtgt gagggacctg ctggacactg cctcagcact gtacagagag	120
gccctggaga gccagagca ctgctcccc caccacacag ccctgaggca ggccatcctc	180
tgctgggggg agctgatgaa cctggccacc tgggtgggct ccaacctgga ggaccctgcc	240
tcaaggagc tgggtggtcag ctatgtcaat gtgaacatgg gcctcaagat caggcagctg	300
ctgtggttcc acatctcctg cctgacctt ggaggggaga cagtcctgga gtacctggtg	360
agctttgggg tgtggatcag gacccccct gcctacaggc ccccaatgc tccatcctg	420
tccacctgc cagagaccac tgtggtcagg agaaggggca ggtccccag gaggagaacc	480
ccctctcca ggaggaggag aagccagtcc ccagggagga ggaggagcca gagcagagag	540
tctcagtgcg gcagtggggc aaccaacttc agcctcctga aacaggcagg ggatgtggag	600
gaaaaccag gccccgagag caccacatca ggcttcctgg gccccctgct ggtgctccag	660
gcaggcttct ttctgctgac caggattctg accatcccc agtccttgga cagctggtgg	720
acctccctga attttctggg gggggcccct acctgtcctg gccagaactc tcagtctccc	780
acctgaatc actcaccaac cagctgtccc cccatctgtc ctggctacag gtggatgtgc	840
ctgaggagat tcatcatctt cctgtgcac ctgctgctgt gcctgatctt tctgctggtg	900
ctgctggact accagggcat gctgccagtg tgccctctca tcccaggcag ctccaccaca	960
tccacaggac cttgcaagac atgcaccaca ccagcccagg gcaccagcat gttcccctcc	1020
tgctgttgca ccaagccaac agatggcaac tgcacatgca ttcccatccc ctccagctgg	1080
gcctttgcca ggtttctgtg ggagtgggcc agtgtgagat tttcctggct gtctcttctg	1140
gtgccctttg tgcagtgggt tgtgggcctg tcccctacag tgtggctgag tgtcatctgg	1200
atgatgtggt actggggccc ctccctgtac aacatcctct ctccctttct gcctctgctg	1260
ccaatcttct ttgcctgtg ggtgtacatc	1290

<210> 35

<211> 1227

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 35

atggacattg acccctacaa ggagtttggg gccagtgtgg agctgctctc cttcctgccc	60
tcagacttct ttcccagtgt gagggacctg cttgacacag cctctgccct ctacagagag	120
gccctggaga gcccagagca ttgctcccc caccacacag cactgaggca ggccatcctg	180
tgctgggggg agctcatgaa cctggccacc tgggtgggtg tcaacctgga ggaccagct	240
tccagggatc tgggtggtcag ctatgtgaac acaaacatgg gcctcaagtt caggcagctg	300
ctctggttcc acatctcctg cctgaccttt ggcagggaga ctgtgctgga gtacctggtg	360
agctttggag tgtggatcag gacccacct gcctacaggc cccccaatgc ccccatcctg	420
tccaccctgc ctgagaccac agtggtaggg aggaggggga ggtccccag aaggaggacc	480
ccttctcca ggaggaggag gagtcatgtc cccaggagga ggaggagcca gagcagagag	540
tcccagtgta tggagaacat cacctctggc tttctgggac ccctgctggt gctccaggca	600
ggctttttcc tgctgaccag gacacctgacc atccctcaga gcctggactc ctggtggaca	660
tctctgaatt ttcttggggg caccactgtg tgcctgggac agaactcca gtctcccacc	720
tccaaccaca gccaacatc ctgtcccccc atctgcccag gctacaggtg gatgtgcctg	780
aggaggttca tcatcttctt gttcatcctg ctgctgtgcc tgatctttct gctggtgctc	840
ctggactatc agggcatgct gccagtgtgc cactgatcc caggcagctc caccacaagc	900
acaggacctt gcaggacatg caccacacct gccaggggca cttccatgta cccatcttgc	960
tgttgacca agccatctga tggcaattgc acctgcatcc ccatcccctc aagctgggcc	1020
tttggcaagt tcctgtggga gtgggcaagt gccagattct cttggctgag cctgctggtc	1080
ccttttgtgc agtggtttgt gggcctgagc cccactgtgt ggctgtctgt gatctggatg	1140
atgtggtact ggggcccctc cctgtattca atcctgagcc cttttctgcc actgctgccc	1200
atcttctttt gtctgtgggt gtacatc	1227

<210> 36

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 36

atggacattg acccctacaa ggagtttggg gccagtgtgg agctgctctc cttcctgccc	60
tcagacttct ttcccagtgt gagggacctg cttgacacag cctctgccct ctacagagag	120
gccctggaga gcccagagca ttgctcccc caccacacag cactgaggca ggccatcctg	180
tgctgggggg agctcatgaa cctggccacc tgggtgggtg tcaacctgga ggaccagct	240
tccagggatc tgggtggtcag ctatgtgaac acaaacatgg gcctcaagtt caggcagctg	300
ctctggttcc acatctcctg cctgacctt ggacaggaga ctgtgctgga gtacctggtg	360
agctttggag tgtggatcag gacccacct gcctacaggc cccccaatgc ccccatcctg	420
tccaccctgc ctgagaccac agtggtaggg aggaggggga ggtccccag aaggaggacc	480
ccttctcca ggaggaggag gagtcatgtc cccaggagga ggaggagcca gagcagagag	540
tcccagtggt gcagtggggc aaccaacttc agcctcctga aacaggcagg ggatgtggag	600
gaaaaccag gccccgagaa catcacctct ggctttctgg gaccctgct ggtgctccag	660
gcaggctttt tcctgctgac caggatcctg accatccctc agagcctgga ctctggtg	720
acatctctga attttcttgg gggcaccact gtgtgcctgg gacagaactc ccagtctccc	780
acctccaacc acagcccaac atcctgtccc cccatctgcc caggctacag gtggatgtgc	840
ctgaggaggt tcatcatctt cctgttcac ctgctgctgt gcctgatctt tctgctggtg	900
ctcctggact atcagggcag gctgccagtg tgcccactga tcccaggcag ctccaccaca	960
agcacaggac cttgcaggac atgcaccaca cctgcccagg gcacttccat gtacccatct	1020
tgctgttgca ccaagccatc tgatggcaat tgcacctgca tccccatccc ctcaagctgg	1080
gcctttggca agttcctgtg ggagtgggca agtgccagat tctcttggct gagcctgctg	1140
gtcccttttg tgagtgggtt tgtgggcctg agccccactg tgtggctgtc tgtgatctgg	1200
atgatgtggt actggggccc ctccctgtat tcaatcctga gcccttttct gccactgctg	1260
cccatcttct tttgtctgtg ggtgtacatc	1290

<210> 37
<211> 1290
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 37
atggacattg acccctacaa ggagtttggg gccagtgtgg agctgctgtc ttttctgcca 60
tctgacttct tccccagtgt gagggacctg ctggacactg cctcagcact gtacagagag 120
gccctggaga gcccagagca ctgctcccc caccacacag ccctgaggca ggccatcctc 180
tgctgggggg agctgatgaa cctggccacc tgggtgggcg tcaacctgga ggaccctgcc 240
tcaagggacc tgggtggtcag ctatgtcaat acgaacatgg gcctcaagtt caggcagctg 300
ctgtggttcc acatctcctg cctgaccttt ggcagggaga cagtcctgga gtacctggtg 360
agctttgggg tgtggatcag gacccccct gcctacaggc cccccaatgc tcccatcctg 420
tccaccctgc cagagaccac tgtggtcagg agaaggggca ggtccccag gaggagaacc 480
ccctctcca ggaggaggag aagccagtcc cccaggagga ggaggagcca gagcagagag 540
tctcagtgcg gcagtggggc aaccaacttc agcctcctga aacaggcagg ggatgtggag 600
gaaaaccag gccccgagaa catcacatca ggcttcctgg gccccctgct ggtgctccag 660
gcaggcttct ttctgctgac caggattctg accatcccc agtccctgga cagctggtgg 720
acctccctga attttctggg ggggaccact gtctgtcttg gccagaactc tcagtctccc 780
acctcgaatc actcaccaac cagctgtccc cccatctgtc ctggctacag gtggatgtgc 840
ctgaggagat tcatcatctt cctgttcac ctgctgctgt gcctgatctt tctgctggtg 900
ctgctggact accagggcat gctgccagtg tgccctctca tcccaggcag ctccaccaca 960
tccacaggac cttgcaggac atgcaccaca ccagcccagg gcaccagcat gtaccctcc 1020
tgctgttgca ccaagccatc agatggcaac tgcacatgca ttcccatccc ctccagctgg 1080
gcctttggca agtttctgtg ggagtgggcc agtgcgagat tttcctggct gtctcttctg 1140
tgccctttg tgagtggtt tgtgggcctg tcccctacag tgtggctgag tgtcatctgg 1200
atgatgtggt actggggccc ctccctgtac agcatcctct ctccctttct gcctctgctg 1260
ccaatcttct ttgcctgtg ggtgtacatc 1290

<210> 38
<211> 409
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 38
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser

165

170

175

Gln Ser Arg Glu Ser Gln Cys Met Glu Ser Thr Thr Ser Gly Phe Leu
 180 185 190

Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile
 195 200 205

Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe
 210 215 220

Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr
 225 230 235 240

Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg
 245 250 255

Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Cys Ile Leu Leu Leu
 260 265 270

Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro
 275 280 285

Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly Pro Cys
 290 295 300

Lys Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys
 305 310 315 320

Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro
 325 330 335

Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg
 340 345 350

Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly
 355 360 365

Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp
 370 375 380

Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro
385 390 395 400

Ile Phe Phe Cys Leu Trp Val Tyr Ile
405

<210> 39

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 39

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Gly Ser Gly Ala Thr Asn Phe Ser Leu
180 185 190

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Glu Ser Thr
195 200 205

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
210 215 220

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
225 230 235 240

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
245 250 255

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
260 265 270

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
275 280 285

Cys Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
290 295 300

Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr
305 310 315 320

Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser
325 330 335

Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp Gly Asn Cys Thr
340 345 350

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
355 360 365

Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
370 375 380

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp
385 390 395 400

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
405 410 415

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
420 425 430

<210> 40

<211> 409

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 40

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Met Glu Asn Ile Thr Ser Gly Phe Leu
180 185 190

Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile
195 200 205

Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe
210 215 220

Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser Pro Thr
225 230 235 240

Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg
245 250 255

Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu
260 265 270

Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro
275 280 285

Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly Pro Cys
290 295 300

Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr Pro Ser Cys

Leu Met Asn Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys Gly Ser Gly Ala Thr Asn Phe Ser Leu
180 185 190

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Glu Asn Ile
195 200 205

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
210 215 220

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
225 230 235 240

Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn
245 250 255

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
260 265 270

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
275 280 285

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
290 295 300

Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr
305 310 315 320

Ser Thr Gly Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser
325 330 335

Met Tyr Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr
340 345 350

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu
355 360 365

Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
370 375 380

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp
385 390 395 400

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe
405 410 415

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
420 425 430

<210> 42

<211> 90

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 42

Cys Ile Arg Ser Gln Phe Lys Gln Ser Arg Leu Gly Leu Gln Pro His
1 5 10 15

Gln Gly Pro Leu Ala Thr Ser Gln Ser Gly Arg Ser Gly Ser Ile Arg

20

25

30

Ala Arg Val His Ser Pro Thr Arg Arg Cys Phe Gly Val Glu Pro Ser
 35 40 45

Gly Ser Gly His Ile Gly His Ser Ala Ser Ser Ser Ser Ser Cys Leu
 50 55 60

His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser His Leu Ser Thr Ser
 65 70 75 80

Lys Arg Gln Ser Ser Ser Gly His Ala Val
 85 90

<210> 43

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 43

Ser Val Gly Pro Cys Ile Gln Asn Gln Leu Arg Lys Ser Arg Leu Gly
 1 5 10 15

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

Gly Ser Ile Arg Ala Arg Val His Pro Ser Pro Trp Gly Thr Val Gly
 35 40 45

Val Glu Pro Ser Gly Ser Gly His Ile His Asn Cys Ala Ser Asn Ser
 50 55 60

Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser His
 65 70 75 80

Ile Ser Thr Ser Lys Gly His Ser Ser Ser Gly His Ala Val
 85 90

<210> 44
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 44
Cys Ile Arg Ser Gln Leu Lys Gln Ser Arg Leu Gly Leu Gln Pro Gln
1 5 10 15

Gln Gly Ser Leu Ala Arg Ser Lys Ser Gly Arg Ser Gly Ser Ile Arg
20 25 30

Ala Arg Val His Pro Thr Thr Arg Gln Ser Phe Gly Val Glu Pro Ser
35 40 45

Gly Ser Gly His Ile Asp Asn Ser Ala Ser Ser Ala Ser Ser Cys Leu
50 55 60

His Gln Ser Ala Val Arg Lys Thr Ala Tyr Ser His Leu Ser Thr Ser
65 70 75 80

Lys Arg Gln Ser Ser Ser Gly His Ala Val
85 90

<210> 45
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 45
Ser Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu Gln Ser Gln
1 5 10 15

Gln Gly His Leu Ala Arg Arg Gln Gln Gly Arg Gly Trp Ser Ile Arg
20 25 30

Ala Gly Ile His Pro Thr Ala Arg Arg Pro Phe Gly Val Glu Pro Ser
35 40 45

Gly Ser Gly His Thr Ala Asn Leu Ala Ser Lys Ser Ala Ser Cys Leu
50 55 60

Tyr Gln Ser Ala Val Arg Lys Ala Ala Tyr Pro Val Val Ser Thr Phe
65 70 75 80

Lys Lys His Ser Ser Ser Gly His Ala Val
85 90

<210> 46

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 46

Arg Leu Val Ile Lys Thr Ser Gln Arg His Gly Asp Glu Pro Phe Cys
1 5 10 15

Ser Gln Pro Ser Gly Ile Leu Ser Arg Ser Ser Val Gly Pro Cys Ile
20 25 30

Arg Ser Gln Phe Lys Gln Ser Arg Leu Gly Leu Gln Pro His Gln Gly
35 40 45

Pro Leu Ala Thr Ser Gln Ser Gly Arg Ser Gly Ser Ile Arg Ala Arg
50 55 60

Val His Ser Pro Thr Arg Arg Cys Phe Gly Val Glu Pro Ser Gly Ser
65 70 75 80

Gly His Ile Gly His Ser Ala Ser Ser Ser Ser Ser Cys Leu His Gln
85 90 95

Ser Ala Val Arg Lys Ala Ala Tyr Ser His Leu Ser Thr Ser Lys Arg
100 105 110

Gln Ser Ser Ser Gly His Ala Val Glu Phe His Ser Phe Pro Pro Ser
115 120 125

Ser Ala Arg Ser Gln Ser Gln Gly Pro Val Phe Ser
130 135 140

<210> 47

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 47

Arg Leu Val Phe Gln Thr Ser Lys Arg His Gly Asp Lys Ser Phe Cys
1 5 10 15

Pro Gln Ser Pro Gly Ile Leu Pro Arg Ser Ser Val Gly Pro Cys Ile
20 25 30

Gln Asn Gln Leu Arg Lys Ser Arg Leu Gly Pro Gln Pro Ala Gln Gly
35 40 45

Gln Leu Ala Gly Arg Gln Gln Gly Gly Ser Gly Ser Ile Arg Ala Arg
50 55 60

Val His Pro Ser Pro Trp Gly Thr Val Gly Val Glu Pro Ser Gly Ser
65 70 75 80

Gly His Ile His Asn Cys Ala Ser Asn Ser Ser Ser Cys Leu His Gln
85 90 95

Ser Ala Val Arg Lys Ala Ala Tyr Ser His Ile Ser Thr Ser Lys Gly
100 105 110

His Ser Ser Ser Gly His Ala Val Glu Leu His His Phe Pro Pro Ser
115 120 125

Ser Ser Arg Ser Gln Ser Gln Gly Pro Val Leu Ser
130 135 140

<210> 48
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 48
Arg Leu Val Phe Gln Thr Ser Thr Arg His Gly Asp Glu Ser Phe Cys
1 5 10 15

Ser Gln Ser Ser Gly Ile Leu Ser Arg Ser Pro Val Gly Pro Cys Ile
20 25 30

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

Ser Leu Ala Arg Ser Lys Ser Gly Arg Ser Gly Ser Ile Arg Ala Arg
50 55 60

Val His Pro Thr Thr Arg Gln Ser Phe Gly Val Glu Pro Ser Gly Ser
65 70 75 80

Gly His Ile Asp Asn Ser Ala Ser Ser Ala Ser Ser Cys Leu His Gln
85 90 95

Ser Ala Val Arg Lys Thr Ala Tyr Ser His Leu Ser Thr Ser Lys Arg
100 105 110

Gln Ser Ser Ser Gly His Ala Val Glu Leu His Asn Phe Pro Pro Ser
115 120 125

Ser Ala Arg Ser Gln Ser Glu Gly Pro Leu Leu Ser
130 135 140

<210> 49
<211> 129
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 49

Ala Glu Ser Phe His Gln Gln Ser Ser Gly Ile Leu Ser Arg Pro Pro
1 5 10 15

Val Gly Ser Ser Leu Gln Ser Lys His Arg Lys Ser Arg Leu Gly Leu
20 25 30

Gln Ser Gln Gln Gly His Leu Ala Arg Arg Gln Gln Gly Arg Gly Trp
35 40 45

Ser Ile Arg Ala Gly Ile His Pro Thr Ala Arg Arg Pro Phe Gly Val
50 55 60

Glu Pro Ser Gly Ser Gly His Thr Ala Asn Leu Ala Ser Lys Ser Ala
65 70 75 80

Ser Cys Leu Tyr Gln Ser Ala Val Arg Lys Ala Ala Tyr Pro Val Val
85 90 95

Ser Thr Phe Lys Lys His Ser Ser Ser Gly His Ala Val Glu Leu His
100 105 110

Asn Leu Pro Pro Asn Ser Ala Arg Ser Gln Ser Glu Arg Pro Val Phe
115 120 125

Pro

<210> 50

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 50

Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp Glu

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

Gln Pro Ala Gln Gly Gln Leu Ala Gly Arg Gln Gln Gly Gly Ser Gly
225 230 235 240

Ser Ile Arg Ala Arg Val His Pro Ser Pro Trp Gly Thr Val Gly Val
245 250 255

Glu Pro Ser Gly Ser Gly His Ile His Asn Cys Ala Ser Asn Ser Ser
260 265 270

Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser His Ile
275 280 285

Ser Thr Ser Lys Gly His Ser Ser Ser Gly His Ala Val Glu Leu His
290 295 300

His Phe Pro Pro Ser
305

<210> 51
<211> 298
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 51
Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp Glu
1 5 10 15

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

Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val Ser
35 40 45

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

Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro Asn
65 70 75 80

Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val Gly
85 90 95

Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro Ala
100 105 110

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

Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe Gln Thr Arg
130 135 140

His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg Glu
145 150 155 160

Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu Gln
165 170 175

Glu Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser Ser Gly Ile
180 185 190

Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser Lys His Arg Lys
195 200 205

Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu Ala Arg Arg Gln
210 215 220

Gln Gly Arg Gly Trp Ser Ile Arg Ala Gly Ile His Pro Thr Ala Arg
225 230 235 240

Arg Pro Phe Gly Val Glu Pro Ser Gly Ser Gly His Thr Ala Asn Leu
245 250 255

Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Ala Val Arg Lys Ala
260 265 270

Ala Tyr Pro Val Val Ser Thr Phe Lys Lys His Ser Ser Ser Gly His
275 280 285

Ala Val Glu Leu His Asn Leu Pro Pro Asn
290 295

<210> 52

<211> 845

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 52

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

Glu Thr Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp
20 25 30

Glu Asp Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu
35 40 45

Asn Val Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu
50 55 60

Tyr Ser Ser Thr Val Pro Ile Phe Asn Pro Glu Trp Gln Thr Pro Ser
65 70 75 80

Phe Pro Lys Ile His Leu His Glu Asp Ile Ala Asn Arg Cys Gln Gln
85 90 95

Phe Val Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Arg Leu Ile
100 105 110

Met Pro Ala Arg Phe Tyr Pro Asn Ser Thr Lys Tyr Leu Pro Leu Asp
115 120 125

Lys Gly Ile Lys Pro Tyr Tyr Pro Asp His Val Val Asn His Tyr Phe
130 135 140

Gln Thr Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr
145 150 155 160

Lys Arg Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser
165 170 175

Trp Glu Gln Glu Leu His His Gly Arg Leu Val Ile Lys Thr Ser Gln
180 185 190

Arg His Gly Asp Glu Pro Phe Cys Ser Gln Pro Ser Gly Ile Leu Ser
195 200 205

Arg Ser Ser Val Gly Pro Cys Ile Arg Ser Gln Phe Lys Gln Ser Arg
210 215 220

Leu Gly Leu Gln Pro His Gln Gly Pro Leu Ala Thr Ser Gln Ser Gly
225 230 235 240

Arg Ser Gly Ser Ile Arg Ala Arg Val His Ser Pro Thr Arg Arg Cys
245 250 255

Phe Gly Val Glu Pro Ser Gly Ser Gly His Ile Gly His Ser Ala Ser
260 265 270

Ser Ser Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr
275 280 285

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

Glu Phe His Ser Phe Pro Pro Ser Ser Ala Arg Ser Gln Ser Gln Gly
305 310 315 320

Pro Val Phe Ser Cys Trp Trp Leu Gln Phe Arg Asn Thr Gln Pro Cys
325 330 335

Ser Lys Tyr Cys Leu Ser His Leu Val Asn Leu Leu Glu Asp Trp Gly
340 345 350

Pro Cys Asp Glu His Gly Glu His His Ile Arg Ile Pro Arg Thr Pro
355 360 365

Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn

370

375

380

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

Ile Thr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser
 405 410 415

Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val
 420 425 430

Ser Ala Ala Phe Tyr His Ile Pro Leu His Pro Ala Ala Met Pro His
 435 440 445

Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser
 450 455 460

Ser Asn Ser Arg Ile His Asn Asn Gln His Gly Thr Leu Gln Asn Leu
 465 470 475 480

His Asp Ser Cys Ser Arg Gln Leu Tyr Val Ser Leu Met Leu Leu Tyr
 485 490 495

Lys Thr Tyr Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu
 500 505 510

Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu
 515 520 525

Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro
 530 535 540

His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly Ala Lys
 545 550 555 560

Ser Val Gln His Leu Glu Ser Leu Tyr Thr Ala Val Thr Asn Phe Leu
 565 570 575

Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly
 580 585 590

Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu
595 600 605

Pro Gln Asp His Ile Val Gln Lys Ile Lys His Cys Phe Arg Lys Leu
610 615 620

Pro Ile Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly
625 630 635 640

Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu
645 650 655

Met Pro Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser
660 665 670

Pro Thr Tyr Lys Ala Phe Leu Ser Lys Gln Tyr Leu Asn Leu Tyr Pro
675 680 685

Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp Ala Thr
690 695 700

Pro Thr Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Thr
705 710 715 720

Phe Val Ala Pro Leu Pro Ile His Thr Ala His Leu Leu Ala Ala Cys
725 730 735

Phe Ala Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser
740 745 750

Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys
755 760 765

Thr Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser
770 775 780

Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr
785 790 795 800

Arg Pro Leu Leu Arg Leu Pro Tyr Arg Pro Thr Thr Gly Arg Thr Ser

805

810

815

Leu Tyr Ala Val Ser Pro Ser Val Pro Ser His Leu Pro Val Arg Val
 820 825 830

His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
 835 840 845

<210> 53

<211> 843

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 53

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
 1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
 35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro
 65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
 85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
 100 105 110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
 115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Val Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Ser Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Asp Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Lys Arg His
180 185 190

Gly Asp Lys Ser Phe Cys Pro Gln Ser Pro Gly Ile Leu Pro Arg Ser
195 200 205

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

Pro Gln Pro Ala Gln Gly Gln Leu Ala Gly Arg Gln Gln Gly Gly Ser
225 230 235 240

Gly Ser Ile Arg Ala Arg Val His Pro Ser Pro Trp Gly Thr Val Gly
245 250 255

Val Glu Pro Ser Gly Ser Gly His Ile His Asn Cys Ala Ser Asn Ser
260 265 270

Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Ala Ala Tyr Ser His
275 280 285

Ile Ser Thr Ser Lys Gly His Ser Ser Ser Gly His Ala Val Glu Leu
290 295 300

His His Phe Pro Pro Ser Ser Ser Arg Ser Gln Ser Gln Gly Pro Val
305 310 315 320

Leu Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Glu Pro Cys Ser Glu
325 330 335

Tyr Cys Leu Cys His Ile Val Asn Leu Ile Glu Asp Trp Gly Pro Cys
340 345 350

Thr Glu His Gly Glu His Arg Ile Arg Thr Pro Arg Thr Pro Ala Arg
355 360 365

Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Thr
370 375 380

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

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

Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala
420 425 430

Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu
435 440 445

Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Asn
450 455 460

Ser Arg Ile Ile Asn Asn Gln His Arg Thr Met Gln Asn Leu His Asp
465 470 475 480

Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met Leu Leu Tyr Lys Thr
485 490 495

Tyr Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe
500 505 510

Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln
515 520 525

Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys
530 535 540

Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly Ala Lys Ser Val
545 550 555 560

Gln His Leu Glu Ser Leu Tyr Ala Ala Val Thr Asn Phe Leu Leu Ser
565 570 575

Leu Gly Ile His Leu Asn Pro His Lys Thr Lys Arg Trp Gly Tyr Ser
580 585 590

Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln
595 600 605

Glu His Ile Val Gln Lys Ile Lys Met Cys Phe Arg Lys Leu Pro Val
610 615 620

Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu
625 630 635 640

Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro
645 650 655

Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr
660 665 670

Tyr Lys Ala Phe Leu Ser Lys Gln Tyr Leu His Leu Tyr Pro Val Ala
675 680 685

Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr
690 695 700

Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Arg Gly Ala Phe Val
705 710 715 720

Ser Pro Leu Pro Ile His Thr Ala His Leu Leu Ala Ala Cys Phe Ala
725 730 735

Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val
740 745 750

Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
755 760 765

Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu
770 775 780

Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro
785 790 795 800

Leu Leu Arg Leu Leu Tyr Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
805 810 815

Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro Asp Arg Val His Phe
820 825 830

Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
835 840

<210> 54

<211> 843

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 54

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Thr Pro Ser Phe Pro
65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro

100

105

110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
 115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Thr Val Asn His Tyr Phe Lys Thr
 130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
 145 150 155 160

Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
 165 170 175

Gln Glu Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Thr Arg His
 180 185 190

Gly Asp Glu Ser Phe Cys Ser Gln Ser Ser Gly Ile Leu Ser Arg Ser
 195 200 205

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

Leu Gln Pro Gln Gln Gly Ser Leu Ala Arg Ser Lys Ser Gly Arg Ser
 225 230 235 240

Gly Ser Ile Arg Ala Arg Val His Pro Thr Thr Arg Gln Ser Phe Gly
 245 250 255

Val Glu Pro Ser Gly Ser Gly His Ile Asp Asn Ser Ala Ser Ser Ala
 260 265 270

Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Thr Ala Tyr Ser His
 275 280 285

Leu Ser Thr Ser Lys Arg Gln Ser Ser Ser Gly His Ala Val Glu Leu
 290 295 300

His Asn Phe Pro Pro Ser Ser Ala Arg Ser Gln Ser Glu Gly Pro Leu
 305 310 315 320

Leu Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp
325 330 335

Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys
340 345 350

Thr Glu His Gly Glu His Asn Ile Arg Ile Pro Arg Thr Pro Ala Arg
355 360 365

Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Thr
370 375 380

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

His Val Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr
405 410 415

Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala
420 425 430

Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala Met Pro His Leu Leu
435 440 445

Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala Arg Leu Ser Ser Thr
450 455 460

Ser Arg Asn Ile Asn Tyr Gln His Gly Ala Met Gln Asp Leu His Asp
465 470 475 480

Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Leu Leu Leu Tyr Lys Thr
485 490 495

Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe
500 505 510

Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln
515 520 525

Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys

530

535

540

Leu Ala Phe Ser Tyr Met His Asp Val Val Leu Gly Ala Lys Ser Val
 545 550 555 560

Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr Asn Phe Leu Leu Ser
 565 570 575

Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser
 580 585 590

Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln
 595 600 605

Glu His Ile Val Leu Lys Ile Lys Gln Cys Phe Arg Lys Leu Pro Val
 610 615 620

Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu
 625 630 635 640

Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro
 645 650 655

Leu Tyr Ala Cys Ile Gln Ala Lys Gln Ala Phe Thr Phe Ser Pro Thr
 660 665 670

Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala
 675 680 685

Arg Gln Arg Ser Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr
 690 695 700

Gly Trp Gly Leu Ala Val Gly His Gln Arg Met Arg Gly Thr Phe Val
 705 710 715 720

Ser Pro Leu Pro Ile His Thr Ala His Leu Leu Ala Ala Cys Phe Ala
 725 730 735

Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val
 740 745 750

Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
755 760 765

Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu
770 775 780

Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro
785 790 795 800

Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
805 810 815

Ala Val Ser Pro Ser Val Pro Ser His Leu Pro Val Arg Val His Phe
820 825 830

Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
835 840

<210> 55

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 55

Met Pro Leu Ser Tyr Gln His Phe Arg Arg Leu Leu Leu Leu Asp Asp
1 5 10 15

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

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

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

Ser Thr Val Pro Val Phe Asn Pro His Trp Lys Thr Pro Ser Phe Pro
65 70 75 80

Asn Ile His Leu His Gln Asp Ile Ile Lys Lys Cys Glu Gln Phe Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Gln Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Val Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Leu Val Asn His Tyr Phe Gln Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr His Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Glu Leu Gln His Gly Ala Glu Ser Phe His Gln Gln Ser Ser Gly
180 185 190

Ile Leu Ser Arg Pro Pro Val Gly Ser Ser Leu Gln Ser Lys His Arg
195 200 205

Lys Ser Arg Leu Gly Leu Gln Ser Gln Gln Gly His Leu Ala Arg Arg
210 215 220

Gln Gln Gly Arg Gly Trp Ser Ile Arg Ala Gly Ile His Pro Thr Ala
225 230 235 240

Arg Arg Pro Phe Gly Val Glu Pro Ser Gly Ser Gly His Thr Ala Asn
245 250 255

Leu Ala Ser Lys Ser Ala Ser Cys Leu Tyr Gln Ser Ala Val Arg Lys
260 265 270

Ala Ala Tyr Pro Val Val Ser Thr Phe Lys Lys His Ser Ser Ser Gly
275 280 285

His Ala Val Glu Leu His Asn Leu Pro Pro Asn Ser Ala Arg Ser Gln
290 295 300

Ser Glu Arg Pro Val Phe Pro Cys Trp Trp Leu Gln Phe Arg Asn Ser
305 310 315 320

Lys Pro Cys Ser Asp Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu
325 330 335

Asp Trp Gly Pro Cys Ala Glu His Gly Glu His His Ile Arg Ile Pro
340 345 350

Arg Thr Pro Ala Arg Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn
355 360 365

Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln Phe
370 375 380

Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro Asn
385 390 395 400

Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser
405 410 415

Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala Ala
420 425 430

Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val Ala
435 440 445

Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn Tyr Gln His Gly Thr Met
450 455 460

Gln Asn Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu Met
465 470 475 480

Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro
485 490 495

Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro
500 505 510

Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg
515 520 525

Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met His Asp Val Val Leu
530 535 540

Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Phe Thr Ala Val Thr
545 550 555 560

Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys
565 570 575

Arg Trp Gly Tyr Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys Tyr
580 585 590

Gly Ser Leu Pro Gln Asp His Ile Ile Gln Lys Ile Lys Glu Cys Phe
595 600 605

Arg Lys Leu Pro Val Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg
610 615 620

Ile Val Gly Leu Leu Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr
625 630 635 640

Pro Ala Leu Met Pro Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe
645 650 655

Thr Phe Ser Pro Thr Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn
660 665 670

Leu Tyr Pro Val Ala Arg Gln Arg Pro Gly Leu Cys Gln Val Phe Ala
675 680 685

Asp Ala Thr Pro Thr Gly Trp Gly Leu Val Met Gly His Gln Arg Met
690 695 700

Arg Gly Thr Phe Lys Ala Pro Leu Pro Ile His Thr Ala His Leu Leu
705 710 715 720

Ala Ala Cys Phe Ala Arg Ser Arg Ser Gly Ala Asn Ile Leu Gly Thr
725 730 735

Asp Asn Ser Val Val Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu
740 745 750

Leu Gly Cys Ala Ala Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr
755 760 765

Val Pro Ser Ala Leu Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu
770 775 780

Gly Leu Tyr Arg Pro Leu Leu Arg Leu Pro Phe Arg Pro Thr Thr Gly
785 790 795 800

Arg Thr Ser Leu Tyr Ala Asp Ser Pro Ser Val Pro Ser His Leu Pro
805 810 815

Asp Arg Val His Phe Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
820 825 830

<210> 56
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 56
Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 57
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 57

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

Asp Val Glu Ser Asn Pro Gly Pro
20

<210> 58

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 58

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

Asn Pro Gly Pro
20

<210> 59

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 59

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 60

<211> 4

<212> PRT

<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
furin recognition/cleavage site"

<400> 60
Arg Ala Lys Arg
1

<210> 61
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
furin recognition/cleavage site"

<400> 61
Arg Glu Lys Arg
1

<210> 62
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
furin recognition/cleavage site"

<400> 62
Arg Arg Lys Arg
1

<210> 63
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 63
Gly Gly Gly Ser
1

<210> 64
<211> 185
<212> PRT
<213> Hepatitis B virus

<400> 64
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
145 150 155 160

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
165 170 175

Arg Ser Gln Ser Arg Glu Ser Gln Cys
180 185

<210> 65
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 65
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 66
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 66
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Asn Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

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

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 67
<211> 18
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
CSF2, GM-CSF sequence"

<400> 67
Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
1 5 10 15

Ser Val

<210> 68
<211> 23
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
PLAT, t-PA sequence"

<400> 68
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Ala Arg
20

<210> 69
<211> 16
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
CD74 sequence"

<400> 69
Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
1 5 10 15

<210> 70
<211> 17
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
serum albumin sequence"

<400> 70
Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala Tyr
1 5 10 15

Ser

<210> 71
<211> 31
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
beta-catenin sequence"

<400> 71
Met Arg Lys Ala Ala Val Ser His Trp Gln Gln Gln Ser Tyr Leu Asp
1 5 10 15

Ser Gly Ile His Ser Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser
20 25 30

<210> 72
<211> 107
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
CCL7, MCP-3 sequence"

<400> 72
Met Asn Pro Ser Ala Ala Val Ile Phe Cys Leu Ile Leu Leu Gly Leu
1 5 10 15

Ser Gly Thr Gln Gly Ile Leu Asp Met Ala Gln Pro Val Gly Ile Asn
20 25 30

Thr Ser Thr Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys
35 40 45

Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg
50 55 60

Glu Ala Val Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp
65 70 75 80

Pro Thr Gln Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys
85 90 95

Thr Gln Thr Pro Lys Leu Ala Ser Ala Gly Ala
100 105

<210> 73

<211> 76

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
ubiquitin sequence"

<400> 73

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

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

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly
65 70 75

<210> 74
<211> 17
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
calreticulin sequence"

<400> 74
Met Leu Leu Ser Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Val
1 5 10 15

Ala

<210> 75
<211> 16
<212> PRT
<213> Vesicular stomatitis virus

<400> 75
Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

<210> 76
<211> 21
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
CXCL10, IP-10 sequence"

<400> 76
Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
1 5 10 15

Ser Gly Ile Gln Gly
20

<210> 77
<211> 384
<212> PRT
<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
LAMP-1, N-terminal sequence"

<400> 77

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

Leu Leu Leu Gly Leu Met His Cys Ala Ser Ala Ala Met Phe Met Val
20 25 30

Lys Asn Gly Asn Gly Thr Ala Cys Ile Met Ala Asn Phe Ser Ala Ala
35 40 45

Phe Ser Val Asn Tyr Asp Thr Lys Ser Gly Pro Lys Asn Met Thr Leu
50 55 60

Asp Leu Pro Ser Asp Ala Thr Val Val Leu Asn Arg Ser Ser Cys Gly
65 70 75 80

Lys Glu Asn Thr Ser Asp Pro Ser Leu Val Ile Ala Phe Gly Arg Gly
85 90 95

His Thr Leu Thr Leu Asn Phe Thr Arg Asn Ala Thr Arg Tyr Ser Val
100 105 110

Gln Leu Met Ser Phe Val Tyr Asn Leu Ser Asp Thr His Leu Phe Pro
115 120 125

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

Arg Ala Asp Ile Asp Lys Lys Tyr Arg Cys Val Ser Gly Thr Gln Val
145 150 155 160

His Met Asn Asn Val Thr Val Thr Leu His Asp Ala Thr Ile Gln Ala
165 170 175

Tyr Leu Ser Asn Ser Ser Phe Ser Arg Gly Glu Thr Arg Cys Glu Gln
180 185 190

Asp Arg Pro Ser Pro Thr Thr Ala Pro Pro Ala Pro Pro Ser Pro Ser
195 200 205

Pro Ser Pro Val Pro Lys Ser Pro Ser Val Asp Lys Tyr Asn Val Ser
210 215 220

Gly Thr Asn Gly Thr Cys Leu Leu Ala Ser Met Gly Leu Gln Leu Asn
225 230 235 240

Leu Thr Tyr Glu Arg Lys Asp Asn Thr Thr Val Thr Arg Leu Leu Asn
245 250 255

Ile Asn Pro Asn Lys Thr Ser Ala Ser Gly Ser Cys Gly Ala His Leu
260 265 270

Val Thr Leu Glu Leu His Ser Glu Gly Thr Thr Val Leu Leu Phe Gln
275 280 285

Phe Gly Met Asn Ala Ser Ser Ser Arg Phe Phe Leu Gln Gly Ile Gln
290 295 300

Leu Asn Thr Leu Leu Pro Asp Ala Arg Asp Pro Ala Phe Lys Ala Ala
305 310 315 320

Asn Gly Ser Leu Arg Ala Leu Gln Ala Thr Val Gly Asn Ser Tyr Lys
325 330 335

Cys Asn Ala Glu Glu His Val Arg Val Thr Lys Ala Phe Ser Val Asn
340 345 350

Ile Phe Lys Val Trp Val Gln Ala Phe Lys Val Glu Gly Gly Gln Phe
355 360 365

Gly Ser Val Glu Glu Cys Leu Leu Asp Glu Asn Ser Leu Glu Asp Ile
370 375 380

<210> 78

<211> 39

<212> PRT

<213> Unknown

<220>

<221> source
<223> /note="Description of Unknown:
LAMP-1, C-terminal sequence"

<400> 78
Gly Ser Glu Phe Thr Leu Ile Pro Ile Ala Val Gly Gly Ala Leu Ala
1 5 10 15

Gly Leu Val Ile Val Leu Ile Ala Tyr Leu Val Gly Arg Lys Arg Ser
20 25 30

His Ala Gly Tyr Gln Thr Ile
35

<210> 79
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="T"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="A"

<220>
<221> VARIANT
<222> (19)..(19)
<223> /replace="G"

<220>
<221> VARIANT
<222> (24)..(24)
<223> /replace="G"

<220>
<221> VARIANT
<222> (29)..(29)
<223> /replace="S"

<220>

<221> VARIANT
<222> (31)..(31)
<223> /replace="T"

<220>
<221> VARIANT
<222> (32)..(32)
<223> /replace="I"

<220>
<221> VARIANT
<222> (36)..(36)
<223> /replace="P"

<220>
<221> VARIANT
<222> (39)..(39)
<223> /replace="V"

<220>
<221> VARIANT
<222> (41)..(41)
<223> /replace="H"

<220>
<221> VARIANT
<222> (42)..(42)
<223> /replace="I"

<220>
<221> VARIANT
<222> (47)..(47)
<223> /replace="A"

<220>
<221> VARIANT
<222> (53)..(53)
<223> /replace="V"

<220>
<221> VARIANT
<222> (54)..(54)
<223> /replace="M" or "P" or "T"

<220>
<221> SITE
<222> (1)..(55)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 79
Met Gln Trp Asn Ser Thr Ala Phe His Gln Thr Leu Gln Asp Pro Arg
1 5 10 15

Val Arg Ala Leu Tyr Phe Pro Ala Gly Gly Ser Ser Leu Gly Ala Val
20 25 30

Asn Pro Val Leu Thr Thr Ala Ser Pro Leu Ser Ser Ile Phe Ser Arg
35 40 45

Ile Gly Asp Pro Ala Leu Asn
50 55

<210> 80

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 80

Met Gln Trp Asn Ser Thr Ala Phe His Gln Ala Leu Gln Asp Pro Arg
1 5 10 15

Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
20 25 30

Asn Pro Ala Pro Asn Ile Ala Ser His Ile Ser Ser Ile Ser Ala Arg
35 40 45

Thr Gly Asp Pro Val Thr Asn
50 55

<210> 81

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 81

Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp Pro Arg
1 5 10 15

Val Arg Ala Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
20 25 30

Ser Pro Ala Gln Asn Thr Val Ser Ala Ile Ser Ser Ile Leu Ser Lys
35 40 45

Thr Gly Asp Pro Val Pro Asn
50 55

<210> 82

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 82

Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg
1 5 10 15

Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
20 25 30

Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
35 40 45

Thr Gly Asp Pro Ala Pro Asn
50 55

<210> 83

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 83

Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp Pro Arg
1 5 10 15

Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
20 25 30

Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
35 40 45

Ile Gly Asp Pro Ala Leu Asn
50 55

<210> 84
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (20)..(20)
<223> /replace="A"

<220>
<221> VARIANT
<222> (28)..(28)
<223> /replace="G" or "R"

<220>
<221> VARIANT
<222> (74)..(74)
<223> /replace="L"

<220>
<221> VARIANT
<222> (77)..(77)
<223> /replace="V"

<220>
<221> VARIANT
<222> (86)..(86)
<223> /replace="A"

<220>
<221> VARIANT
<222> (90)..(90)
<223> /replace="T"

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="D"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="T"

<220>
<221> VARIANT
<222> (119)..(119)
<223> /replace="A"

<220>
<221> VARIANT
<222> (127)..(127)
<223> /replace="G"

<220>
<221> VARIANT
<222> (132)..(132)
<223> /replace="G"

<220>
<221> VARIANT
<222> (137)..(137)
<223> /replace="S"

<220>
<221> VARIANT
<222> (139)..(139)
<223> /replace="T"

<220>
<221> VARIANT
<222> (140)..(140)
<223> /replace="I"

<220>
<221> VARIANT
<222> (144)..(144)
<223> /replace="P"

<220>
<221> VARIANT
<222> (147)..(147)
<223> /replace="V"

<220>
<221> VARIANT
<222> (149)..(149)

<223> /replace="H"

<220>

<221> VARIANT

<222> (150)..(150)

<223> /replace="I"

<220>

<221> VARIANT

<222> (155)..(155)

<223> /replace="A"

<220>

<221> VARIANT

<222> (161)..(161)

<223> /replace="V"

<220>

<221> VARIANT

<222> (162)..(162)

<223> /replace="M" or "P" or "T"

<220>

<221> SITE

<222> (1)..(163)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 84

Met	Gly	Gln	Asn	Leu	Ser	Thr	Ser	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp
1				5				10						15	

His	Gln	Leu	Asp	Pro	Ala	Phe	Arg	Ala	Asn	Thr	Ala	Asn	Pro	Asp	Trp
		20						25					30		

Asp	Phe	Asn	Pro	Asn	Lys	Asp	Thr	Trp	Pro	Asp	Ala	Asn	Lys	Val	Gly
		35					40					45			

Ala	Gly	Ala	Phe	Gly	Leu	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu
	50					55					60				

Gly	Trp	Ser	Pro	Gln	Ala	Gln	Gly	Ile	Ile	Gln	Thr	Leu	Pro	Ala	Asn
65				70						75					80

Pro	Pro	Pro	Ala	Ser	Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro
				85					90					95	

Leu Ser Pro Pro Leu Arg Asn Thr His Pro Gln Ala Met Gln Trp Asn
100 105 110

Ser Thr Ala Phe His Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu
115 120 125

Tyr Phe Pro Ala Gly Gly Ser Ser Leu Gly Ala Val Asn Pro Val Leu
130 135 140

Thr Thr Ala Ser Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro
145 150 155 160

Ala Leu Asn

<210> 85

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 85

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Ile
35 40 45

Lys Asp His Trp Pro Ala Ala Asn Gln Val Gly Val Gly Ala Phe Gly
50 55 60

Pro Gly Leu Thr Pro Pro His Gly Gly Ile Leu Gly Trp Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Ser Thr Ile Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Ala Phe His
115 120 125

Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Ala Pro Asn Ile Ala Ser His
145 150 155 160

Ile Ser Ser Ile Ser Ala Arg Thr Gly Asp Pro Val Thr Asn
165 170

<210> 86

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 86

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Lys Ala Asn Ser Glu Asn Pro Asp Trp Asp Leu Asn Pro His
35 40 45

Lys Asp Asn Trp Pro Asp Ala Asn Lys Val Gly Val Gly Ala Phe Gly
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65 70 75 80

Ala Gln Gly Leu Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu
100 105 110

Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Ser Pro Ala Gln Asn Thr Val Ser Ala
145 150 155 160

Ile Ser Ser Ile Leu Ser Lys Thr Gly Asp Pro Val Pro Asn
165 170

<210> 87

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 87

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp His Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser

85

90

95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn
 165 170

<210> 88

<211> 163

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 88

Met Gly Gln Asn Leu Ser Thr Ser Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Arg Ala Asn Thr Ala Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Thr Trp Pro Asp Ala Asn Lys Val Gly
 35 40 45

Ala Gly Ala Phe Gly Leu Gly Phe Thr Pro Pro His Gly Gly Leu Leu
 50 55 60

Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Gln Thr Leu Pro Ala Asn
 65 70 75 80

Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro
85 90 95

Leu Ser Pro Pro Leu Arg Asn Thr His Pro Gln Ala Met Gln Trp Asn
100 105 110

Ser Thr Thr Phe His Gln Thr Leu Gln Asp Pro Arg Val Arg Gly Leu
115 120 125

Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro
130 135 140

Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro
145 150 155 160

Ala Leu Asn

<210> 89

<211> 1603

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 89

atgtcttcaa gatccagag tcagggcct gtactttcct gctggtggct ccagttcagg 60

aacagtgagc cctgctccga atactgtctc tgccatatcg tcaatcttat cgaagactgg 120

ggaccctgta ccgaacatgg agaacatcgc atcaggactc ctaggacccc tgctcgtgtt 180

acaggcgggg tttttcttgt tgacaaaaat ctcacaata ccacagagtc tagactcgtg 240

gtggacttct ctcaattttc tagggggaac acccgtgtgt cttggccaaa attcgagtc 300

ccaaatctcc agtcactcac caacctgttg tcctccaatt tgtcctggtt atcgctggat 360

gtgtctgcgg cgttttatca tcttcctctg catcctgctg ctatgcctca tcttcttgtt 420

ggttcttctg gactatcaag gtatgttgcc cgtttgcct ctaattccag gatcatcaac 480

aaccagcacc ggaccatgca aaacctgcac gactcctgct caaggaacct ctatgtttcc 540

ctcatgttgc tgtacaaaac ctacggacgg aaactgcact tgtattccca tcccatcatc 600

ttgggctttc gcaaaattcc tatgggagtg ggcctcagtc cgtttctctt ggctcagttt	660
actagtgcc a tttgttcagt ggttcgtagg gctttccccc actgtctggc tttcagttat	720
atgcatgatg tggtaattggg ggccaagtct gtacaacatc ttgagtcctt ttatgccgct	780
gttaccaatt ttcttttgtc tttgggtata catttaaacc ctcaaaaac aaaaagatgg	840
ggatattccc ttaacttcat gggatatgta attgggagtt ggggcacatt gccgcaggaa	900
catattgtac aaaaaatcaa aatgtgtttt aggaaacttc ctgtaaaccg gcctattgat	960
tggaaagtat gtcaacgaat tgtgggtctt ttggggtttg ccgcccctt cagcaatgt	1020
ggatattcctg ctttaatgcc tttatatgca tgtatacaag caaaacaggc ttttactttc	1080
tcgccaactt acaaggcctt cctaagtaaa cagtatctgc acctttacc cgttgctcgg	1140
caacggcctg gtctgtgcc a gtgttttgct gacgcaacc ccactggttg gggcttggcc	1200
ataggccatc agcgcatgcg tggagccttc gtgtctctc tgccgatcca tactgcgcat	1260
ctcctggccg cttgttttgc tcgcagcagg tctggggcaa aatcatcgg gactgacaat	1320
tctgtcgtgc tctccgcaa gtatacatcc tttccatggc tgctaggctg tgctgccaac	1380
tggatcctgc gcgggacgtc ctttgtttac gtcccgtcgg cgctgaatcc cgcggacgac	1440
ccctcccggg gccgcttggg gctctaccgc ccgcttctcc gcttgttgta ccgaccgact	1500
acggggcgca cctctctcta cgcggactcc ccgtctgtgc cttctcatct gccggaccgt	1560
gtgcacttcg cttcacctct gcacgtcgca tggagaccac cgt	1603

<210> 90

<211> 1602

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 90

atgtcatcca gatcccagag tcagggccct gtcctttcct gttggtggct ccagttcagg	60
aacagtgagc cctgttctga gtactgtctc tgccacattg tcaatctgat tgaggactgg	120
ggcccctgca cagagcatgg tgaacacagg atcaggactc ccaggacccc tgccagggtg	180
actggtgggg ttttccttgt tgacaaaaat ctcacaaca ccacagagtc aaggcttgtg	240

gtggacttct ctcaattttc aagggggaac acaagggtgt cttggcccaa atttgcagtc	300
ccaaatctcc agtctctgac caacctgttg tcctccaatt tgtcctggtt gtctctggat	360
gtctctgctg ctttttatca tcttcctctc catcctgctg ccatgcctca tcttcttggt	420
ggttcttctg gcctctctag gtatgttgcc agattgtcct ccaattccag gatcatcaac	480
aaccagcaca ggaccatgca aaacctgcat gactcctgct ccagaaacct ctatgtttct	540
ctcatgttgc tgtacaaaac ctatggcagg aaactgcatt tgtattccca tcccatcatc	600
ttgggcttca ggaaaattcc catgggagtg ggcctcagtc ccttcctctt ggctcagttc	660
accagtgcc tttgttctgt tgtcaggagg gctttccccc actgtcttgc tttcagttac	720
atgcatgatg tggctcttggg ggccaagtct gtccaacatc ttgagtcact ttatgctgct	780
gtgaccaact ttcttttgtc tttgggcatc cttttgaacc ctacaaaaac caaaagatgg	840
ggctattccc tcaatttcat gggctatgtc attgggagtt ggggcacttt gccccaggaa	900
cacattgtgc aaaaaatcaa gatgtgtttc aggaaacttc ctgtgaacag gccaatgac	960
tggaaagtct gtcagagaat tgtgggtctt ttgggggttg cagctccttt cacccaatgt	1020
ggctatcctg ctttgatgcc cttgtatgcc tgcattcagg ccaaacaggc tttcactttc	1080
tccccactt acaaggcctt cctcagcaaa cagtatctcc acctttacc tgttgcaagg	1140
cagaggcctg gtctgtgcca agtgtttgct gatgcaacct cactgggtg gggcttggcc	1200
attggccatc agagaatgag aggtgccttt gtgtctcctc tccccatcca cactgctcat	1260
ctcctggcag cttgctttgc aaggagcagg tctggagcca aactcatagg gactgacaat	1320
tctgtgggtc tctccagaaa gtacacctcc tttccttggc tgctgggctg tgcagccaac	1380
tggatcctga gggggacttc ctttgtttat gtcccctctg ccctgaatcc tgcagatgac	1440
ccctccaggg gcaggttggg gctctacaga ccccttctca gggtgttgta cagaccaaca	1500
acagggagga cctctctcta tgcagattcc ccctctgttc cttctcatct tccagacaga	1560
gtgcactttg cttctcctct gcatgtggct tggagacctc cc	1602

<210> 91

<211> 1602

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 91

atgtctagca gaagccagtc ccagggacct gtgctgtctt gttggtggct tcagtttcgg	60
aatagcgagc catgtagcga gtattgcctg tgtcacatcg tgaatctgat tgaggattgg	120
ggaccatgca cagagcacgg agagcaccgg atcagaacct ctaggacacc agcccgcgtg	180
acaggaggcg tgttcctggg ggataagaac ccccataata caacagagag cagactgggtg	240
gtggattttt ctgagttttc tcggggcaat acaagagtgt cctggccaaa gtttgccgtg	300
cccaatctcc agagcctgac aaacctgctg tcttctaata tgagctggct gtccttgagc	360
gtgtccgccg ctttttacca cctgccactg caccctgccg ccatgcccc cctgctgggtg	420
ggcagctccg gactgagcag atacgtggca aggctgtcta gcaattctag aattattaat	480
aatcagcaca gaacaatgca gaatctgcat gattcttgta gcaggaatct gtacgtgagc	540
ctgatgctgc tgtataagac atatggacgc aagctgcacc tgtatttctca ccctattatt	600
ctgggcttcc ggaagatccc tatgggcgtg ggactgtccc cattcctgct ggcccagttt	660
acctccgcc tctgctctgt ggtgcggaga gccttccac attgtctggc cttttcttac	720
atgcacgatg tggtgctggg cgccaaatcc gtgcagcacc tggagtctct gtatgccgcc	780
gtgacaaact tcctgctgag cctgggcatc cacctgaatc cacataagac aaagcgggtg	840
ggctattctc tgaattttat gggctatgtg atcggcagct ggggaaccct gccacaggag	900
cacattgtgc agaagatcaa gatgtgcttt cgcaagctgc ccgtgaatcg gcctatcgat	960
tggaagggtg gccagaggat cgtgggactg ctgggattcg cagcaccctt taccagtg	1020
ggctaccag ccctgatgcc actgtatgcc tgtatccagg ccaaacaggc cttcaccttt	1080
tcccctacat ataaggcttt tctgtctaag cagtacctgc atctgtatcc agtggcaagg	1140
cagaggccag gactgtgcca ggtgtttgca gatgcaacac caacaggatg gggactggca	1200
atcggacacc agaggatgag aggagccttc gtgagcccac tgccaattca caccgcccac	1260
ctgctggcag catgctttgc aaggtccgc tctggagcaa agctgattgg caccgataac	1320
agcgtgggtg tgtccagaaa atacaccagc ttcccctggc tgctgggatg tgcagcaaat	1380
tggattctga ggggcaccag cttcgtgtat gtgccttccg ccctgaatcc tgccgatgat	1440
ccatctcgag gcagactggg actgtatagg cactgctga gactgctgta taggcctacc	1500

acaggcagaa catccctgta tgccgacagc ccatccgtgc cctctcacct gccagataga	1560
gtgcatttcg caagcccact gcatgtggca tggaggccac cc	1602

<210> 92
 <211> 1602
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 92	
atgtcttcaa gatcccagag tcagggccct gtactttcct gctggtggct ccagttcagg	60
aacagtgagc cctgctctga atactgtctc tgccatattg tcaatcttat agaagactgg	120
ggaccctgta ctgaacatgg agaacatagg atcaggactc ctaggacccc tgctagagtt	180
acagggggggg tttttcttgt tgacaaaaat cctcacaata ccacagagtc tagacttgtg	240
gtggacttct ctcaattttc taggggggaac accagggtgt cttggccaaa atttgcagtc	300
ccaaatctcc agtcactcac caacctgttg tcctccaatt tgtcctggtt atccctggat	360
gtgtctgcag ccttttatca tcttcctctg catcctgctg ctatgcctca tcttcttgtt	420
ggttcttctg gactatcaag gtatgttgcc aggttgtcct ctaattccag gatcatcaac	480
aaccagcaca ggaccatgca aaacctgcat gactcctgct caaggaacct ctatgtttcc	540
ctcatgttgc tgtacaaaac ctatggaagg aaactgcact tgtattcca tcccatcatc	600
ttgggcttta gaaaaattcc tatgggagtg ggcctcagtc cttttctctt ggctcagttt	660
actagtgcc a tttgttcagt ggtagaagg gctttccccc actgtctggc tttcagttat	720
atgcatgatg tggatattggg ggccaagtct gtacaacatc ttgagtcctt ttatgctgct	780
gttaccaatt ttcttttgtc tttgggtata catttaaacc ctcaaaaac aaaaagatgg	840
ggatattccc ttaacttcat gggatatgta attgggagtt ggggcacatt gcctcaggaa	900
catattgtac aaaaaatcaa aatgtgtttt aggaaacttc ctgtaaacag gcctattgat	960
tggaaagtat gtcaaagaat tgtgggtctt ttggggtttg cagccccttt cacccaatgt	1020
ggatatcctg ctttaatgcc tttatatgca tgtatacaag caaaacaggc ttttactttc	1080
tccccaactt acaaggcctt cctaagtaaa cagtatctgc acctttacc tgttgctagg	1140

caaaggcctg gtctgtgcca agtgtttgct gatgcaaccc ccactggttg gggcttggcc	1200
ataggccatc agaggatgag gggagccttt gtgtctcctc tgcctatcca tactgccc	1260
ctcctggcag cttgttttgc taggagcagg tctggggcaa aactcattgg gactgacaat	1320
tctgttgtgc tctccagaaa gtatacatcc tttccatggc tgctaggctg tgctgccaac	1380
tggatcctga gggggacatc ctttgtttat gtcccttcag cactgaatcc tgctgatgac	1440
ccctccaggg gcagattggg gctctacagg ccccttctca gggttgttgta cagaccact	1500
actgggagaa cctctctcta tgcagactcc ccctctgtgc cttctcatct gcctgacagg	1560
gtgcactttg cttcacctct gcatgttgca tggagaccac ct	1602

<210> 93

<211> 1602

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 93

atgagttccc gatcacagag tcaggggccc gtcctttcat gttggtggct tcagtttcga	60
aactccgagc catgtttctga gtattgtctc tgccacattg tgaatcttat tgaagactgg	120
ggcccctgca ccgagcacgg cgagcaccga atacggacac ctcgaacgcc agcaagagtg	180
acgggcggag tgttcctcgt cgacaagaat ccacacaaca cgacggagag tagattggtc	240
gttgatttca gtcaattttc aagaggcaat acacgagttt cttggccgaa attcgccgta	300
ccgaatctgc aatccttgac aaatttgctt agttctaatt tgtcttggct ttctctcgat	360
gtttccgccg ctttctatca cttgcccctt caccagccg cgatgccgca tctcttgggtg	420
ggcagctctg gacttagtag atacgtagct agactcagtt ctaactcacg gataataaat	480
aaccaacatc gcactatgca gaacctgcat gattcttggt cccggaactt gtatgtctcc	540
ttgatgttgt tgtataaaac ttatgggcga aagcttcac tgtatagcca tccgattata	600
ttgggtttta ggaaaattcc tatgggtggt ggcttgagcc cttttctgct ggcgcaattt	660
acttcagcta tctgctcagt agtacgccgg gcgtttcccc attgtcttgc tttctcatac	720
atgcatgatg tagtacttgg ggccaagtct gtacaacacc ttgagagttt gtatgccgcc	780

gtaactaatt tccttctctc tctcgggatc catcttaacc ctcaaaaaac gaagaggtgg	840
ggttattctc tgaatttcat gggatatgtt atcgggtctt ggggaacgct gcctcaggaa	900
cacatcgtcc agaaaatcaa gatgtgtttc agaaagttgc cagtgaacag accgatagat	960
tggaaggttt gccaaagaat tgttggcttg ttgggattcg cagccccatt cacacagtgc	1020
gggtatccgg ctttgatgcc cttttatgct tgtatccagg caaaacaggc attcaccttt	1080
tcaccgactt acaaagcatt tctttctaag cagtatctcc atctttaccc tgctgctcga	1140
cagcggccgg ggctttgcca ggttttcgca gacgcaacc caactggttg gggctttgctg	1200
atcggccacc agaggatgcg cgggtgcattc gtgtccccgc tccaatcca tacggcccac	1260
ttgctggcgg cgtgcttcgc tcgaagtaga agcggggcta aattgatcgg cacggacaat	1320
tcagtcgtgt tgtcacgcaa atatacctcc tttccctggt tgctcggttg cgcagcaaac	1380
tggatacttc ggggaactag tttcgtttat gtgccctctg ctctcaacc cgccgacgat	1440
ccttcacgag ggaggctggg tctttaccgc ccattgctca ggctgcttta ccggcctacc	1500
actgggagaa caagcttgta cgccgacagc ccgagcgtcc cgtctcatct gcccgacaga	1560
gttcactttg cgagtccatt gcacgtcgct tggcgcccg c	1602

<210> 94

<211> 1602

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 94

atgagttcca gatcacagag tcaggggcct gtcctttcat gttggtggct tcagtttaga	60
aactcagagc catgttctga gtattgtctc tgccacattg tgaatcttat tgaagactgg	120
ggcccctgca cagagcatgg agagcacaga ataaggacac ctagaacccc agcaagagtg	180
acaggtggag tgttcctggt agacaagaat ccacacaaca caactgagag tagattgggtg	240
gttgatttca gtcaattttc aagaggcaat acaagagttt cttggccaaa atttgctgta	300
cccaatctgc aatccttgac aaatttgctt agttctaatt tgtcttggtt ttctctagat	360
gtttctgcag ctttctatca cttgcccctt caccagcag ctatgcctca tctcttggtg	420

ggcagctctg gacttagtag atatgtagct agactcagtt ctaactcaag gataataaat	480
aaccaacata ggactatgca gaacctgcat gattcttggt ccaggaactt gtatgtctcc	540
ttgatgttgt tgtataaaac ttatgggaga aagcttcac tgtatagcca tcctattata	600
ttgggtttta ggaaaattcc tatgggtggt ggcttgagcc cttttctgct ggcccaattt	660
acttcagcta tctgctcagt agtaaggagg gcctttcccc attgtcttgc tttctcatac	720
atgcatgatg tagtacttgg ggccaagtct gtacaacacc ttgagagttt gtatgcagca	780
gtaactaatt tccttctctc tcttgggata catcttaacc ctcaaaaac caagaggtgg	840
ggttattctc tgaatttcat gggatatgtt atagggtctt gggaaccct gcctcaggaa	900
cacattgtcc agaaaatcaa gatgtgtttc agaaagttgc cagtgaacag accaatagat	960
tggaaggttt gccaaagaat tgttggcttg ttgggatttg cagccccatt cacacagtgt	1020
gggtatcctg ctttgatgcc cttttatgct tgtatccagg caaacaggc attcaccttt	1080
tcacccactt acaaagcatt tctttctaag cagtatctcc atctttacc tgtggctaga	1140
cagaggccag ggctttgcca ggtttttgca gatgcaacc caactggttg gggctttgca	1200
attggccacc agaggatgag aggtgcattt gtgtccccac tccaatcca tactgcccac	1260
ttgctggcag cttgctttgc tagaagtaga agtggggcta aattgattgg cacagacaat	1320
tcagtttgtt tgtcaaggaa atatacctcc tttccctggt tgcttggttg tgcagcaaac	1380
tggatactta ggggaactag ttttgtttat gtgccctctg ctctcaacc tgcagatgat	1440
ccttcaagag ggaggctggg tctttacagg ccattgctca ggctgcttta caggcctacc	1500
actgggagaa caagcttgta tgcagacagc cccagtgtcc cctctcatct gcctgacaga	1560
gttcactttg caagtcatt gcatgttgct tggagacctc ca	1602

<210> 95
 <211> 6
 <212> PRT
 <213> Hepatitis B virus

<400> 95
 Ser Ala Arg Ser Gln Ser
 1 5

<210> 96
 <211> 6

<212> PRT
<213> Hepatitis B virus

<400> 96
Ser Ser Arg Ser Gln Ser
1 5

<210> 97
<211> 4
<212> PRT
<213> Hepatitis B virus

<400> 97
Tyr Met Asp Asp
1

<210> 98
<211> 4
<212> PRT
<213> Hepatitis B virus

<400> 98
Ala Glu Leu Leu
1

<210> 99
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 99
Tyr Met His Asp
1

<210> 100
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 100

Ala His Leu Leu
1

<210> 101
<211> 8
<212> PRT
<213> Hepatitis B virus

<400> 101
Met Gly Leu Lys Phe Arg Gln Leu
1 5

<210> 102
<211> 8
<212> PRT
<213> Hepatitis B virus

<400> 102
Met Gly Leu Lys Ile Arg Gln Leu
1 5