

SEQUENCE LISTING

<110> WEREWOLF THERAPEUTICS, INC.

<120> ACTIVATABLE INTERLEUKIN-2 POLYPEPTIDES AND METHODS OF USE THEREOF

<130> 105365-0021

<140>

<141>

<150> 62/756,507

<151> 2018-11-06

<150> 62/756,504

<151> 2018-11-06

<150> 62/671,225

<151> 2018-05-14

<160> 137

<170> PatentIn version 3.5

<210> 1

<211> 153

<212> PRT

<213> Homo sapiens

<400> 1

Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu
1				5					10					15	

Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu
			20					25					30		

Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile
		35					40					45			

Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe
		50				55					60				

Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu
65					70					75					80

Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys
				85					90					95	

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
100 105 110

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
115 120 125

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

Cys Gln Ser Ile Ile Ser Thr Leu Thr
145 150

<210> 2
<211> 609
<212> PRT
<213> Homo sapiens

<400> 2
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
20 25 30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
35 40 45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
100 105 110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115 120 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
130 135 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165 170 175

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
195 200 205

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

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225 230 235 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
245 250 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
290 295 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305 310 315 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Gly Ser
325 330 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
340 345 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
355 360 365

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

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385 390 395 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
405 410 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
420 425 430

Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
435 440 445

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
450 455 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Cys Leu Ser Val Phe
465 470 475 480

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
485 490 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Gly Arg Pro Cys Phe
500 505 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
515 520 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
530 535 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545 550 555 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
565 570 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
580 585 590

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
595 600 605

Leu

<210> 3
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP7 cleavage domain sequence"

<400> 3
Lys Arg Ala Leu Gly Leu Pro Gly
1 5

<210> 4
<211> 40
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP7 cleavage domain sequence"

<400> 4
Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp Glu
1 5 10 15

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

Asp Arg Asp Arg Asp Arg Asp Arg
35 40

<210> 5
<211> 5
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP9 cleavage domain sequence"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Ile"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Thr"

<220>
<221> SITE
<222> (1)..(5)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 5
Pro Arg Ser Leu Ser
1 5

<210> 6
<211> 5
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP9 cleavage domain sequence"

<400> 6
Leu Glu Ala Thr Ala
1 5

<210> 7

<211> 10
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP11 cleavage domain sequence"

<400> 7
Gly Gly Ala Ala Asn Leu Val Arg Gly Gly
1 5 10

<210> 8
<211> 10
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP14 cleavage domain sequence"

<400> 8
Ser Gly Arg Ile Gly Phe Leu Arg Thr Ala
1 5 10

<210> 9
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP cleavage domain sequence"

<400> 9
Pro Leu Gly Leu Ala Gly
1 5

<210> 10
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP cleavage domain sequence"

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<400> 10
Pro Leu Gly Leu Ala Xaa
1 5

<210> 11
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP cleavage domain sequence"

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Cys(me)

<400> 11
Pro Leu Gly Xaa Ala Gly
1 5

<210> 12
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
MMP cleavage domain sequence"

<400> 12
Glu Ser Pro Ala Tyr Tyr Thr Ala
1 5

<210> 13
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source

<223> /note="Description of Unknown:
MMP cleavage domain sequence"

<400> 13

Arg Leu Gln Leu Lys Leu
1 5

<210> 14

<211> 7

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
MMP cleavage domain sequence"

<400> 14

Arg Leu Gln Leu Lys Ala Cys
1 5

<210> 15

<211> 7

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
MMP2, MMP9, MMP14 cleavage domain sequence"

<220>

<221> MOD_RES

<222> (3)..(3)

<223> Cit

<220>

<221> MOD_RES

<222> (5)..(5)

<223> Hof

<400> 15

Glu Pro Xaa Gly Xaa Tyr Leu
1 5

<210> 16

<211> 5

<212> PRT

<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Urokinase plasminogen activator (uPA) cleavage domain
sequence"

<400> 16
Ser Gly Arg Ser Ala
1 5

<210> 17
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Urokinase plasminogen activator (uPA) cleavage domain
sequence"

<400> 17
Asp Ala Phe Lys
1

<210> 18
<211> 5
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Urokinase plasminogen activator (uPA) cleavage domain
sequence"

<400> 18
Gly Gly Gly Arg Arg
1 5

<210> 19
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Lysosomal Enzyme cleavage domain sequence"

<400> 19

Gly Phe Leu Gly
1

<210> 20
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Lysosomal Enzyme cleavage domain sequence"

<400> 20
Ala Leu Ala Leu
1

<210> 21
<211> 2
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Lysosomal Enzyme cleavage domain sequence"

<400> 21
Phe Lys
1

<210> 22
<211> 3
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Cathepsin B cleavage domain sequence"

<400> 22
Asn Leu Leu
1

<210> 23
<211> 5
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Cathepsin D cleavage domain sequence"

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Cys(et)

<400> 23
Pro Ile Xaa Phe Phe
1 5

<210> 24
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Cathepsin K cleavage domain sequence"

<400> 24
Gly Gly Pro Arg Gly Leu Pro Gly
1 5

<210> 25
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Prostate Specific Antigen cleavage domain sequence"

<400> 25
His Ser Ser Lys Leu Gln
1 5

<210> 26
<211> 7
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:

Prostate Specific Antigen cleavage domain sequence"

<400> 26

His Ser Ser Lys Leu Gln Leu

1 5

<210> 27

<211> 9

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:

Prostate Specific Antigen cleavage domain sequence"

<400> 27

His Ser Ser Lys Leu Gln Glu Asp Ala

1 5

<210> 28

<211> 10

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:

Herpes Simplex Virus Protease cleavage domain
sequence"

<400> 28

Leu Val Leu Ala Ser Ser Ser Phe Gly Tyr

1 5 10

<210> 29

<211> 10

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:

HIV Protease cleavage domain sequence"

<400> 29

Gly Val Ser Gln Asn Tyr Pro Ile Val Gly

1 5 10

<210> 30

<211> 10
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
CMV Protease cleavage domain sequence"

<400> 30
Gly Val Val Gln Ala Ser Cys Arg Leu Ala
1 5 10

<210> 31
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Thrombin cleavage domain sequence"

<220>
<221> MOD_RES
<222> (2)..(2)
<223> 2-carboxy piperidine

<400> 31
Phe Xaa Arg Ser
1

<210> 32
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Thrombin cleavage domain sequence"

<400> 32
Asp Pro Arg Ser Phe Leu
1 5

<210> 33
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Thrombin cleavage domain sequence"

<400> 33
Pro Pro Arg Ser Phe Leu
1 5

<210> 34
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Caspase-3 cleavage domain sequence"

<400> 34
Asp Glu Val Asp
1

<210> 35
<211> 5
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Caspase-3 cleavage domain sequence"

<400> 35
Asp Glu Val Asp Pro
1 5

<210> 36
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Caspase-3 cleavage domain sequence"

<400> 36
Lys Gly Ser Gly Asp Val Glu Gly
1 5

<210> 37
<211> 6
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Interleukin 1-Beta converting enzyme cleavage domain
sequence"

<400> 37
Gly Trp Glu His Asp Gly
1 5

<210> 38
<211> 7
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Enterokinase cleavage domain sequence"

<400> 38
Glu Asp Asp Asp Asp Lys Ala
1 5

<210> 39
<211> 9
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
FAP cleavage domain sequence"

<400> 39
Lys Gln Glu Gln Asn Pro Gly Ser Thr
1 5

<210> 40
<211> 6
<212> PRT
<213> Unknown

<220>

<221> source
<223> /note="Description of Unknown:
Kallikrein 2 cleavage domain sequence"

<400> 40
Gly Lys Ala Phe Arg Arg
1 5

<210> 41
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Plasmin cleavage domain sequence"

<400> 41
Asp Ala Phe Lys
1

<210> 42
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Plasmin cleavage domain sequence"

<400> 42
Asp Val Leu Lys
1

<210> 43
<211> 4
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Plasmin cleavage domain sequence"

<400> 43
Asp Ala Phe Lys
1

<210> 44
<211> 7
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
TOP cleavage domain sequence"

<400> 44
Ala Leu Leu Leu Ala Leu Leu
1 5

<210> 45
<211> 652
<212> PRT
<213> Artificial Sequence

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

<400> 45
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp
20 25 30

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn
85 90 95

Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
130 135 140

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
145 150 155 160

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
165 170 175

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
180 185 190

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
195 200 205

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
210 215 220

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
225 230 235 240

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
245 250 255

Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
260 265 270

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
275 280 285

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
290 295 300

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

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
325 330 335

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
340 345 350

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
355 360 365

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
405 410 415

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
420 425 430

Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro
435 440 445

Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr
450 455 460

Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn
465 470 475 480

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
485 490 495

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp
500 505 510

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
515 520 525

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
530 535 540

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

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln
565 570 575

Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe
580 585 590

Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
595 600 605

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
610 615 620

Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly
625 630 635 640

Thr Lys Val Glu Ile Lys His His His His His His
645 650

<210> 46

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 46

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp
20 25 30

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn
85 90 95

Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
130 135 140

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
145 150 155 160

Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
165 170 175

Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val
180 185 190

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
195 200 205

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
210 215 220

Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr
225 230 235 240

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
260 265 270

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln

275

280

285

Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 290 295 300

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 325 330 335

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
 340 345 350

Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 355 360 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 370 375 380

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser
 385 390 395 400

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly
 405 410 415

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 420 425 430

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu
 450 455 460

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
 465 470 475 480

Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val
 485 490 495

Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
500 505 510

Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
515 520 525

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
530 535 540

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
545 550 555 560

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
565 570 575

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

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
595 600 605

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
610 615 620

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

Ile Ile Ser Thr Leu Thr His His His His His His
645 650

<210> 47

<211> 553

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 47

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn
145 150 155 160

Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
165 170 175

Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr
210 215 220

Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly
225 230 235 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
245 250 255

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly Gly
260 265 270

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser
275 280 285

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
290 295 300

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
305 310 315 320

Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
325 330 335

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
340 345 350

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
355 360 365

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
370 375 380

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
385 390 395 400

Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu
405 410 415

Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
420 425 430

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
435 440 445

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
450 455 460

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
465 470 475 480

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
485 490 495

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
500 505 510

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
515 520 525

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
530 535 540

Val Ser Ser His His His His His His
545 550

<210> 48
<211> 553
<212> PRT
<213> Artificial Sequence

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

<400> 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg

50

55

60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr
 100 105 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn
 145 150 155 160

Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 165 170 175

Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser
 180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr
 210 215 220

Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly
 225 230 235 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 245 250 255

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 260 265 270

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
275 280 285

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
290 295 300

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
305 310 315 320

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
325 330 335

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
340 345 350

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
355 360 365

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
385 390 395 400

Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro
405 410 415

Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu
420 425 430

Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro
435 440 445

Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala
450 455 460

Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu
465 470 475 480

Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro

485

490

495

Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
500 505 510

Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile
515 520 525

Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser
530 535 540

Thr Leu Thr His His His His His His
545 550

<210> 49

<211> 553

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 49

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
130 135 140

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

Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
165 170 175

Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
180 185 190

Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr
195 200 205

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

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

Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly
245 250 255

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
260 265 270

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
275 280 285

Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
290 295 300

Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
305 310 315 320

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
325 330 335

Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly Lys Gly
340 345 350

Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro
355 360 365

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

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
385 390 395 400

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly
405 410 415

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
420 425 430

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
435 440 445

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
450 455 460

Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro
465 470 475 480

Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser
485 490 495

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
500 505 510

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
515 520 525

Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val
530 535 540

Glu Ile Lys His His His His His His
545 550

<210> 50

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 50

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp
20 25 30

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn
85 90 95

Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
130 135 140

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
145 150 155 160

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
165 170 175

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
180 185 190

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
195 200 205

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
210 215 220

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
225 230 235 240

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
245 250 255

Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
260 265 270

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
275 280 285

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
290 295 300

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

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
325 330 335

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
340 345 350

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

355

360

365

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
 370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 385 390 395 400

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 405 410 415

Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
 420 425 430

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 435 440 445

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 450 455 460

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

Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser
 485 490 495

Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 500 505 510

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 515 520 525

Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp
 530 535 540

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 545 550 555 560

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 565 570 575

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
580 585 590

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys
595 600 605

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
625 630 635 640

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
645 650 655

Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
660 665 670

Val Glu Ile Lys His His His His His His
675 680

<210> 51

<211> 667

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 51

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp
20 25 30

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn
85 90 95

Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
130 135 140

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
145 150 155 160

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
165 170 175

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
180 185 190

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
195 200 205

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
210 215 220

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
225 230 235 240

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
245 250 255

Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
260 265 270

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
275 280 285

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
290 295 300

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

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
325 330 335

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
340 345 350

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
355 360 365

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
405 410 415

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
420 425 430

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
435 440 445

Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly
450 455 460

Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr
465 470 475 480

Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
485 490 495

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
500 505 510

Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr
515 520 525

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ser Gly Gly Pro Gly
530 535 540

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Asp Ile Gln Met Thr Gln
545 550 555 560

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
565 570 575

Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln
580 585 590

Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg
595 600 605

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
610 615 620

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
625 630 635 640

Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr
645 650 655

Lys Val Glu Ile Lys His His His His His His
660 665

<210> 52

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 52

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
130 135 140

Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
165 170 175

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
180 185 190

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
195 200 205

Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
210 215 220

Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr
225 230 235 240

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

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
260 265 270

Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly
275 280 285

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
305 310 315 320

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
325 330 335

Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys
340 345 350

Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val
355 360 365

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
370 375 380

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
385 390 395 400

Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
405 410 415

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

420

425

430

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
 435 440 445

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
 450 455 460

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 465 470 475 480

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
 485 490 495

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
 500 505 510

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 515 520 525

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
 530 535 540

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 545 550 555 560

Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
 565 570 575

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser
 580 585 590

Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu
 595 600 605

Leu Val Ala Arg Ile Thr Arg Gly Gly Thr Ile Ser Tyr Asp Asp Ser
 610 615 620

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
 625 630 635 640

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr
645 650 655

Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val
660 665 670

Thr Val Ser Ser His His His His His His
675 680

<210> 53
<211> 393
<212> PRT
<213> Artificial Sequence

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

<400> 53
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
130 135 140

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
165 170 175

Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly Lys Gly
180 185 190

Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro
195 200 205

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

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225 230 235 240

Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly
245 250 255

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
260 265 270

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
275 280 285

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
290 295 300

Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro
305 310 315 320

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
340 345 350

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
355 360 365

Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val
370 375 380

Glu Ile Lys His His His His His His
385 390

<210> 54

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 54

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
130 135 140

Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
165 170 175

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
180 185 190

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
195 200 205

Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
210 215 220

Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr
225 230 235 240

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

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
260 265 270

Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly
275 280 285

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
305 310 315 320

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser

325

330

335

Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys
 340 345 350

Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val
 355 360 365

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 370 375 380

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 385 390 395 400

Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 405 410 415

Lys His His His His His His
 420

<210> 55

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 55

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
 20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
 35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
 50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
130 135 140

Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
165 170 175

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
180 185 190

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
195 200 205

Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
210 215 220

Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr
225 230 235 240

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

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
260 265 270

Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly
275 280 285

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
305 310 315 320

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
325 330 335

Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys
340 345 350

Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val
355 360 365

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
370 375 380

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
385 390 395 400

Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
405 410 415

Lys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
420 425 430

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
435 440 445

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
450 455 460

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
465 470 475 480

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
485 490 495

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
500 505 510

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
515 520 525

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
530 535 540

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
545 550 555 560

Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
565 570 575

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser
580 585 590

Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu
595 600 605

Leu Val Ala Arg Ile Thr Arg Gly Gly Thr Ile Ser Tyr Asp Asp Ser
610 615 620

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
625 630 635 640

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr
645 650 655

Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val
660 665 670

Thr Val Ser Ser His His His His His His
675 680

<210> 56

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 56

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Ala Gly Gly
1 5 10 15

Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Asn Ser
20 25 30

Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Lys Gln Arg Glu Phe Val
35 40 45

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Val Cys Asn
85 90 95

Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
115 120 125

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
130 135 140

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
145 150 155 160

Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
165 170 175

Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val
180 185 190

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

195

200

205

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 210 215 220

Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr
 225 230 235 240

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
 260 265 270

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
 275 280 285

Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 290 295 300

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 325 330 335

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
 340 345 350

Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 355 360 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly
 385 390 395 400

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln
 405 410 415

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

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

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
450 455 460

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
465 470 475 480

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
485 490 495

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
500 505 510

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
515 520 525

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala
530 535 540

Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
545 550 555 560

Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
565 570 575

Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys
580 585 590

Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro
595 600 605

Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg
610 615 620

Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys

625		630		635		640									
Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr
				645					650					655	

Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile
		660						665					670		

Ser	Thr	Leu	Thr	His	His	His	His	His	His
		675						680	

<210> 57
 <211> 393
 <212> PRT
 <213> Artificial Sequence

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

<400> 57															
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5						10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
		20						25					30		

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

Ala	Ala	Ile	Asp	Ser	Ser	Ser	Tyr	Thr	Tyr	Ser	Pro	Asp	Thr	Val	Arg
	50					55				60					

Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu
65					70					75				80	

Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
			85						90					95	

Arg	Asp	Ser	Asn	Trp	Asp	Ala	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn
145 150 155 160

Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
165 170 175

Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr
210 215 220

Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser
225 230 235 240

Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro
245 250 255

Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu
260 265 270

Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro
275 280 285

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

Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu
305 310 315 320

Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro
325 330 335

Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
340 345 350

Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile
355 360 365

Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser
370 375 380

Thr Leu Thr His His His His His His
385 390

<210> 58

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Ser Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr

100

105

110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 130 135 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn
 145 150 155 160

Val Gly Thr Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 165 170 175

Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser
 180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 195 200 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr
 210 215 220

Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly
 225 230 235 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 245 250 255

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly
 260 265 270

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser
 275 280 285

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 290 295 300

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 305 310 315 320

Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
325 330 335

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
340 345 350

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
355 360 365

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
370 375 380

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
385 390 395 400

Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu
405 410 415

Thr His His His His His His
420

<210> 59

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 59

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp
20 25 30

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn
85 90 95

Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
130 135 140

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
145 150 155 160

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
165 170 175

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
180 185 190

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
195 200 205

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
210 215 220

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
225 230 235 240

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
245 250 255

Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
260 265 270

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
275 280 285

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
290 295 300

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

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
325 330 335

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
340 345 350

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
355 360 365

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
405 410 415

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

Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp
435 440 445

Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asn
450 455 460

Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala
465 470 475 480

Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
485 490 495

Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala Arg Trp Arg
500 505 510

Gly Asp Gly Tyr Tyr Ala Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
515 520 525

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
530 535 540

Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
545 550 555 560

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
565 570 575

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
580 585 590

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
595 600 605

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
610 615 620

Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
625 630 635 640

Gln Gln Ser Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
645 650 655

Glu Ile Lys His His His His His His Glu Pro Glu Ala
660 665

<210> 60

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 60

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp
20 25 30

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

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

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn
85 90 95

Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val
100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
130 135 140

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
145 150 155 160

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
165 170 175

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
180 185 190

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
195 200 205

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
210 215 220

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
225 230 235 240

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
245 250 255

Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
260 265 270

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
275 280 285

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
290 295 300

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

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
325 330 335

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
340 345 350

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
355 360 365

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu
405 410 415

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr

420

425

430

Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr
 435 440 445

Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 450 455 460

Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly
 465 470 475 480

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

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Tyr
 500 505 510

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 515 520 525

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln
 530 535 540

Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Val Ser Cys
 545 550 555 560

Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
 565 570 575

Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Pro Gly
 580 585 590

Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
 595 600 605

Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
 610 615 620

Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala Arg Trp Arg Gly Asp
 625 630 635 640

Gly Tyr Tyr Ala Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr
645 650 655

Val Ser Ser His His His His His His Glu Pro Glu Ala
660 665

<210> 61

<211> 689

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 61

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
130 135 140

Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln
165 170 175

Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys
180 185 190

Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu
195 200 205

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile
210 215 220

Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys
225 230 235 240

Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
245 250 255

Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala Arg Trp
260 265 270

Arg Gly Asp Gly Tyr Tyr Ala Tyr Phe Asp Val Trp Gly Ala Gly Thr
275 280 285

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
290 295 300

Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
305 310 315 320

Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln
325 330 335

Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys
340 345 350

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu
355 360 365

Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
370 375 380

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
385 390 395 400

Cys Gln Gln Ser Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys
405 410 415

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
420 425 430

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
435 440 445

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

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
465 470 475 480

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
485 490 495

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

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
515 520 525

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
530 535 540

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
545 550 555 560

Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu
565 570 575

Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg
580 585 590

Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly Lys
595 600 605

Gln Arg Glu Leu Val Ala Arg Ile Thr Arg Gly Gly Thr Ile Ser Tyr
610 615 620

Asp Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
625 630 635 640

Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly
645 650 655

Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly
660 665 670

Thr Gln Val Thr Val Ser Ser His His His His His His Glu Pro Glu
675 680 685

Ala

<210> 62

<211> 689

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 62

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys

35

40

45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
 50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
 65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
 85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
 115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
 130 135 140

Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
 165 170 175

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 180 185 190

Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser
 195 200 205

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 210 215 220

Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser
 225 230 235 240

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu
 245 250 255

Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro
260 265 270

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly
275 280 285

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
290 295 300

Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Val Ser
305 310 315 320

Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val
325 330 335

Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Pro
340 345 350

Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr
355 360 365

Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser
370 375 380

Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala Arg Trp Arg Gly
385 390 395 400

Asp Gly Tyr Tyr Ala Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val
405 410 415

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
420 425 430

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
435 440 445

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

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

465		470		475		480
Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala						
		485		490		495
Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr						
		500		505		510
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val						
		515		520		525
Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr						
		530		535		540
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser						
545		550		555		560
Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu						
		565		570		575
Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg						
		580		585		590
Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly Lys						
		595		600		605
Gln Arg Glu Leu Val Ala Arg Ile Thr Arg Gly Gly Thr Ile Ser Tyr						
		610		615		620
Asp Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys						
625		630		635		640
Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly						
		645		650		655
Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly						
		660		665		670
Thr Gln Val Thr Val Ser Ser His His His His His Glu Pro Glu						
		675		680		685

Ala

<210> 63

<211> 272

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
IL2Ra sequence"

<400> 63

Met Asp Ser Tyr Leu Leu Met Trp Gly Leu Leu Thr Phe Ile Met Val
1 5 10 15

Pro Gly Cys Gln Ala Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro
20 25 30

His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn
35 40 45

Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr
50 55 60

Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys
65 70 75 80

Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro
85 90 95

Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro
100 105 110

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

Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val
130 135 140

Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His
145 150 155 160

Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg
165 170 175

Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser Gln
180 185 190

Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro Glu
195 200 205

Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln Thr
210 215 220

Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr Gln
225 230 235 240

Val Ala Val Ala Gly Cys Val Phe Leu Leu Ile Ser Val Leu Leu Leu
245 250 255

Ser Gly Leu Thr Trp Gln Arg Arg Gln Arg Lys Ser Arg Arg Thr Ile
260 265 270

<210> 64

<211> 551

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
IL2Rb sequence"

<400> 64

Met Ala Ala Pro Ala Leu Ser Trp Arg Leu Pro Leu Leu Ile Leu Leu
1 5 10 15

Leu Pro Leu Ala Thr Ser Trp Ala Ser Ala Ala Val Asn Gly Thr Ser
20 25 30

Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp
35 40 45

Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp

50

55

60

Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser
65 70 75 80

Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln
85 90 95

Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu
100 105 110

Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu
115 120 125

Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu
130 135 140

Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr
145 150 155 160

Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His
165 170 175

Thr Trp Glu Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp
180 185 190

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

Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser
210 215 220

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

Ile Pro Trp Leu Gly His Leu Leu Val Gly Leu Ser Gly Ala Phe Gly
245 250 255

Phe Ile Ile Leu Val Tyr Leu Leu Ile Asn Cys Arg Asn Thr Gly Pro
260 265 270

Trp Leu Lys Lys Val Leu Lys Cys Asn Thr Pro Asp Pro Ser Lys Phe
275 280 285

Phe Ser Gln Leu Ser Ser Glu His Gly Gly Asp Val Gln Lys Trp Leu
290 295 300

Ser Ser Pro Phe Pro Ser Ser Ser Phe Ser Pro Gly Gly Leu Ala Pro
305 310 315 320

Glu Ile Ser Pro Leu Glu Val Leu Glu Arg Asp Lys Val Thr Gln Leu
325 330 335

Leu Leu Gln Gln Asp Lys Val Pro Glu Pro Ala Ser Leu Ser Ser Asn
340 345 350

His Ser Leu Thr Ser Cys Phe Thr Asn Gln Gly Tyr Phe Phe Phe His
355 360 365

Leu Pro Asp Ala Leu Glu Ile Glu Ala Cys Gln Val Tyr Phe Thr Tyr
370 375 380

Asp Pro Tyr Ser Glu Glu Asp Pro Asp Glu Gly Val Ala Gly Ala Pro
385 390 395 400

Thr Gly Ser Ser Pro Gln Pro Leu Gln Pro Leu Ser Gly Glu Asp Asp
405 410 415

Ala Tyr Cys Thr Phe Pro Ser Arg Asp Asp Leu Leu Leu Phe Ser Pro
420 425 430

Ser Leu Leu Gly Gly Pro Ser Pro Pro Ser Thr Ala Pro Gly Gly Ser
435 440 445

Gly Ala Gly Glu Glu Arg Met Pro Pro Ser Leu Gln Glu Arg Val Pro
450 455 460

Arg Asp Trp Asp Pro Gln Pro Leu Gly Pro Pro Thr Pro Gly Val Pro
465 470 475 480

Asp Leu Val Asp Phe Gln Pro Pro Pro Glu Leu Val Leu Arg Glu Ala

485

490

495

Gly Glu Glu Val Pro Asp Ala Gly Pro Arg Glu Gly Val Ser Phe Pro
 500 505 510

Trp Ser Arg Pro Pro Gly Gln Gly Glu Phe Arg Ala Leu Asn Ala Arg
 515 520 525

Leu Pro Leu Asn Thr Asp Ala Tyr Leu Ser Leu Gln Glu Leu Gln Gly
 530 535 540

Gln Asp Pro Thr His Leu Val
 545 550

<210> 65

<211> 369

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 IL2Rg sequence"

<400> 65

Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1 5 10 15

Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
 20 25 30

Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
 35 40 45

Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
 50 55 60

Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
 65 70 75 80

Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
 85 90 95

Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
100 105 110

Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
115 120 125

Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
130 135 140

Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145 150 155 160

Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
165 170 175

Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
180 185 190

Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
195 200 205

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

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

Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe
245 250 255

Leu Phe Ala Leu Glu Ala Val Val Ile Ser Val Gly Ser Met Gly Leu
260 265 270

Ile Ile Ser Leu Leu Cys Val Tyr Phe Trp Leu Glu Arg Thr Met Pro
275 280 285

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

Gly Asn Phe Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser
305 310 315 320

Leu Gln Pro Asp Tyr Ser Glu Arg Leu Cys Leu Val Ser Glu Ile Pro
325 330 335

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

Gln His Ser Pro Tyr Trp Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu
355 360 365

Thr

<210> 66

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 66

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

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

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
50 55 60

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

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

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp

100

105

110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Val Gly Ala Phe Arg Pro Tyr
 115 120 125

Arg Lys His Glu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Arg Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser
 145 150 155 160

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

Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp
 180 185 190

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

Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser
 210 215 220

Gly Asn Thr Ala Ser Leu Thr Thr Thr Gly Ala Gln Ala Glu Asp Glu
 225 230 235 240

Ala Asp Tyr Tyr Cys Asn Ser Ser Pro Phe Glu His Asn Leu Val Val
 245 250 255

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu His His His His His His
 260 265 270

Glu Pro Glu Ala
 275

<210> 67

<211> 674

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 67

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu
165 170 175

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
180 185 190

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg
195 200 205

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

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

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
245 250 255

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp
260 265 270

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
275 280 285

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
290 295 300

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
305 310 315 320

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly
325 330 335

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser
340 345 350

Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
355 360 365

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
370 375 380

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe
385 390 395 400

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
420 425 430

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
435 440 445

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
450 455 460

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
465 470 475 480

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
485 490 495

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
500 505 510

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
515 520 525

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
530 535 540

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
545 550 555 560

Ser Gly Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys
565 570 575

Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg
580 585 590

Gln Ala Pro Gly Lys Gln Arg Glu Leu Val Ala Arg Ile Thr Arg Gly
595 600 605

Gly Thr Ile Ser Tyr Asp Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
610 615 620

Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys
625 630 635 640

Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp
645 650 655

Tyr Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser His His His His
660 665 670

His His

<210> 68

<211> 674

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 68

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

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys

115

120

125

Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
 130 135 140

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

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
 165 170 175

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
 180 185 190

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

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 210 215 220

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

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

Ser Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
 260 265 270

Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser
 275 280 285

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

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln
 305 310 315 320

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

Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg
340 345 350

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
355 360 365

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala
370 375 380

Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
405 410 415

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
420 425 430

Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp
435 440 445

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala
450 455 460

Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
465 470 475 480

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
485 490 495

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

Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Pro Gly Pro Ala Gly
515 520 525

Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
530 535 540

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu

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

<210> 69
 <211> 425
 <212> PRT
 <213> Artificial Sequence

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

<400> 69
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

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

Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu
35 40 45

Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu
50 55 60

Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln
65 70 75 80

Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr
85 90 95

Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser
100 105 110

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

Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val
130 135 140

Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu
145 150 155 160

His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr
165 170 175

Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu Thr Ser
180 185 190

Gln Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly Arg Pro
195 200 205

Glu Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln Ile Gln
210 215 220

Thr Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr Glu Tyr
225 230 235 240

Gln Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
260 265 270

Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro
275 280 285

Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu
290 295 300

Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro
305 310 315 320

Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala
325 330 335

Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu
340 345 350

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

Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
370 375 380

Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile
385 390 395 400

Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser
405 410 415

Thr Leu Thr His His His His His His
420 425

<210> 70

<211> 425

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 70

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly
165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
180 185 190

Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro Pro
195 200 205

Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr
210 215 220

Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly
225 230 235 240

Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp
245 250 255

Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln
260 265 270

Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met
275 280 285

Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys
290 295 300

Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His
305 310 315 320

Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg
325 330 335

Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly
340 345 350

Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu
355 360 365

Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly
370 375 380

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

Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr
405 410 415

Glu Tyr Gln His His His His His His

420

425

<210> 71

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 71

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

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

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

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
 50 55 60

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

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 90 95

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
 100 105 110

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

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro Pro
 145 150 155 160

Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr
165 170 175

Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly
180 185 190

Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp
195 200 205

Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln
210 215 220

Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met
225 230 235 240

Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys
245 250 255

Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His
260 265 270

Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg
275 280 285

Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly
290 295 300

Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu
305 310 315 320

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

Arg Pro Glu Ser Glu Thr Ser Cys Leu Val Thr Thr Thr Asp Phe Gln
340 345 350

Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr
355 360 365

Glu Tyr Gln Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
385 390 395 400

Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
405 410 415

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
420 425 430

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
435 440 445

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
450 455 460

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
465 470 475 480

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

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
500 505 510

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
515 520 525

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
530 535 540

Ile Ser Thr Leu Thr His His His His His His
545 550 555

<210> 72

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 72

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly
165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
180 185 190

Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro Pro
195 200 205

Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr
210 215 220

Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly
225 230 235 240

Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp
245 250 255

Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln
260 265 270

Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met
275 280 285

Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys
290 295 300

Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His
305 310 315 320

Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg
325 330 335

Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly
340 345 350

Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu
355 360 365

Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly
370 375 380

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

Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr
405 410 415

Glu Tyr Gln Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

420

425

430

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 435 440 445

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

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 465 470 475 480

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
 485 490 495

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
 515 520 525

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
 530 535 540

Val Thr Val Ser Ser His His His His His His
 545 550 555

<210> 73

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 73

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
 20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly
165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
180 185 190

Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Cys Asp Asp Asp Pro Pro
195 200 205

Glu Ile Pro His Ala Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr
210 215 220

Met Leu Asn Cys Glu Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly
225 230 235 240

Ser Leu Tyr Met Leu Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp
245 250 255

Asn Gln Cys Gln Cys Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln
260 265 270

Val Thr Pro Gln Pro Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met
275 280 285

Gln Ser Pro Met Gln Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys
290 295 300

Arg Glu Pro Pro Pro Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His
305 310 315 320

Phe Val Val Gly Gln Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg
325 330 335

Ala Leu His Arg Gly Pro Ala Glu Ser Val Cys Lys Met Thr His Gly
340 345 350

Lys Thr Arg Trp Thr Gln Pro Gln Leu Ile Cys Thr Gly Glu Met Glu
355 360 365

Thr Ser Gln Phe Pro Gly Glu Glu Lys Pro Gln Ala Ser Pro Glu Gly
370 375 380

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

Ile Gln Thr Glu Met Ala Ala Thr Met Glu Thr Ser Ile Phe Thr Thr
405 410 415

Glu Tyr Gln Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
420 425 430

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
435 440 445

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

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
465 470 475 480

Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu
485 490 495

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
515 520 525

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
530 535 540

Val Thr Val Ser Ser His His His His His His
545 550 555

<210> 74

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 74

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

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

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

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
50 55 60

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

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
100 105 110

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala
130 135 140

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

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

Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala
180 185 190

Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr
195 200 205

Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp
210 215 220

Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
225 230 235 240

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
275 280 285

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr

290

295

300

Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr
 305 310 315 320

Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser
 325 330 335

Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 340 345 350

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 355 360 365

Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly
 370 375 380

Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
 385 390 395 400

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 405 410 415

Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
 420 425 430

Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
 435 440 445

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
 450 455 460

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
 465 470 475 480

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
 485 490 495

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
 500 505 510

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
515 520 525

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
530 535 540

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
545 550 555 560

Cys Gln Ser Ile Ile Ser Thr Leu Thr His His His His His His
565 570 575

<210> 75

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 75

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly
165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
180 185 190

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
195 200 205

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
210 215 220

Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala
225 230 235 240

Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr
245 250 255

Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp
260 265 270

Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
275 280 285

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu
290 295 300

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ser Gly Gly
305 310 315 320

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Asp Ile Gln Met
325 330 335

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

Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr
355 360 365

Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser
370 375 380

Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
385 390 395 400

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
405 410 415

Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly
420 425 430

Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
435 440 445

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
450 455 460

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
465 470 475 480

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
485 490 495

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
500 505 510

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
515 520 525

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
530 535 540

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
545 550 555 560

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
580 585 590

Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
595 600 605

Ser Gly Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala
610 615 620

Pro Gly Lys Gln Arg Glu Leu Val Ala Arg Ile Thr Arg Gly Gly Thr
625 630 635 640

Ile Ser Tyr Asp Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
645 650 655

Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu
660 665 670

Asp Thr Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp
675 680 685

Gly Lys Gly Thr Gln Val Thr Val Ser Ser His His His His His His
690 695 700

<210> 76

<211> 689

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 76

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp

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

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
290 295 300

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

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
325 330 335

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
340 345 350

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
355 360 365

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
420 425 430

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

435

440

445

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
 450 455 460

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp
 465 470 475 480

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp
 485 490 495

Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr
 500 505 510

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
 515 520 525

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn
 530 535 540

Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 545 550 555 560

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 565 570 575

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 580 585 590

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 595 600 605

Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
 610 615 620

Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 625 630 635 640

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 645 650 655

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr
660 665 670

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His
675 680 685

His

<210> 77

<211> 545

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 77

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu
165 170 175

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
180 185 190

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg
195 200 205

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

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

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
245 250 255

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp
260 265 270

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
275 280 285

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
290 295 300

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
305 310 315 320

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly
325 330 335

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser
340 345 350

Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
355 360 365

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
370 375 380

Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe
385 390 395 400

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
420 425 430

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
435 440 445

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
450 455 460

Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg
465 470 475 480

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
485 490 495

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
500 505 510

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val
515 520 525

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His
530 535 540

His
545

<210> 78

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 78

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Ser Gly

165

170

175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 180 185 190

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 195 200 205

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 210 215 220

Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala
 225 230 235 240

Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr
 245 250 255

Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp
 260 265 270

Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 275 280 285

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu
 290 295 300

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 305 310 315 320

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
 325 330 335

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

Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr
 355 360 365

Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser
 370 375 380

Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
385 390 395 400

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
405 410 415

Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly
420 425 430

Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
435 440 445

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
450 455 460

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
465 470 475 480

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
485 490 495

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
500 505 510

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
515 520 525

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
530 535 540

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
545 550 555 560

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
565 570 575

<210> 79

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 79

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

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

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

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
50 55 60

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

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
100 105 110

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala
130 135 140

Gly Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys
145 150 155 160

Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile
165 170 175

Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu
180 185 190

Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
195 200 205

Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu
210 215 220

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

Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met
245 250 255

Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg
260 265 270

Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly
275 280 285

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu
290 295 300

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

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
325 330 335

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
340 345 350

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
355 360 365

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
370 375 380

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
385 390 395 400

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His
405 410 415

His His His His His
420

<210> 80
<211> 806
<212> PRT
<213> Artificial Sequence

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

<400> 80
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Ser Gly Ser Gly Ser Gly Ser
130 135 140

Gly Ser Gly Ser Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly

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

Lys Pro Glu Asp Thr Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr
370 375 380

Asp Tyr Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser Gly Ser Gly
385 390 395 400

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Val Gln
405 410 415

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
420 425 430

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala
435 440 445

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile
450 455 460

Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe
465 470 475 480

Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
485 490 495

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser
500 505 510

Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
515 520 525

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
545 550 555 560

Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr
565 570 575

Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu

590

Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
785 790 795 800

His His His His His His
805

<210> 81
<211> 676
<212> PRT
<213> Artificial Sequence

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

<400> 81
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Ser Gly Ser Gly Ser Gly Ser
130 135 140

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

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
165 170 175

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
180 185 190

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

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
210 215 220

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

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

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Gly Ser Gly
260 265 270

Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Glu Val Gln Leu Val
275 280 285

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
290 295 300

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val
305 310 315 320

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser
325 330 335

Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile
340 345 350

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
355 360 365

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp
370 375 380

Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
385 390 395 400

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
405 410 415

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

Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val
435 440 445

Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr
450 455 460

Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
465 470 475 480

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
485 490 495

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr
500 505 510

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Pro Gly Pro
515 520 525

Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr
530 535 540

Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met
545 550 555 560

Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met
565 570 575

Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His
580 585 590

Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
595 600 605

Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
610 615 620

Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
625 630 635 640

Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn
645 650 655

Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr His His
660 665 670

His His His His
675

<210> 82

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 82

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

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

65

70

75

80

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Ser Gly Ser Gly Ser Gly Ser
130 135 140

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

Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala
165 170 175

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
180 185 190

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

Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
210 215 220

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

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

Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly
260 265 270

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser
275 280 285

Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln
290 295 300

Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg
305 310 315 320

Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys
325 330 335

His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
340 345 350

Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile
355 360 365

Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr
370 375 380

Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu
385 390 395 400

Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr His
405 410 415

His His His His His
420

<210> 83
<211> 420
<212> PRT
<213> Artificial Sequence

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

<400> 83
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
130 135 140

Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
195 200 205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
210 215 220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
290 295 300

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

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
325 330 335

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
340 345 350

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
355 360 365

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His
405 410 415

His His His His
420

<210> 84

<211> 550

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 84

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

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

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

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
165 170 175

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
180 185 190

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp

195

200

205

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 210 215 220

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

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

Ser Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
 260 265 270

Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr
 275 280 285

Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met
 290 295 300

Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met
 305 310 315 320

Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His
 325 330 335

Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
 340 345 350

Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
 355 360 365

Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
 370 375 380

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

Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly
 405 410 415

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln
420 425 430

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
435 440 445

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
450 455 460

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile
465 470 475 480

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
485 490 495

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
500 505 510

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
515 520 525

Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
530 535 540

His His His His His His
545 550

<210> 85
<211> 420
<212> PRT
<213> Artificial Sequence

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

<400> 85
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
195 200 205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
210 215 220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
290 295 300

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

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
325 330 335

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
340 345 350

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
355 360 365

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His
405 410 415

His His His His
420

<210> 86

<211> 290

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 86

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

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln

195

200

205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
 210 215 220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
 245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
 260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr His His His His
 275 280 285

His His
 290

<210> 87

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 87

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
 20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
 35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
 50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu
165 170 175

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
180 185 190

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
195 200 205

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

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
245 250 255

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

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His
275 280 285

His His His
290

<210> 88
<211> 689
<212> PRT
<213> Artificial Sequence

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

<400> 88
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
130 135 140

Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys

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

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
420 425 430

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
435 440 445

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
450 455 460

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp
465 470 475 480

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp
485 490 495

Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr
500 505 510

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
515 520 525

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn
530 535 540

Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
545 550 555 560

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
565 570 575

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

580

585

590

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
 595 600 605

Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
 610 615 620

Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 625 630 635 640

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 645 650 655

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr
 660 665 670

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His
 675 680 685

His

<210> 89

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 89

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
 20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
 35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly
165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
180 185 190

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
195 200 205

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
210 215 220

Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala
225 230 235 240

Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr
245 250 255

Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp
260 265 270

Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
275 280 285

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu
290 295 300

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
305 310 315 320

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
325 330 335

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

Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr
355 360 365

Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser
370 375 380

Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
385 390 395 400

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
405 410 415

Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly
420 425 430

Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
435 440 445

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
450 455 460

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
465 470 475 480

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
485 490 495

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
500 505 510

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
515 520 525

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
530 535 540

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
545 550 555 560

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
580 585 590

Gly Gly Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala
595 600 605

Ser Gly Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr
610 615 620

Pro Gly Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser
625 630 635 640

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

Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu
660 665 670

Asp Thr Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp
675 680 685

Gly Gln Gly Thr Gln Val Thr Val Ser Ser His His His His His His
690 695 700

<210> 90

<211> 674

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 90

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

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

Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly
50 55 60

Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser Thr Asn
65 70 75 80

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr
100 105 110

Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Ala Pro Thr Ser Ser Ser Thr Lys
130 135 140

Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile
145 150 155 160

Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu

165

170

175

Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
 180 185 190

Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu
 195 200 205

Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn
 210 215 220

Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met
 225 230 235 240

Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg
 245 250 255

Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly
 260 265 270

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu
 275 280 285

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
 290 295 300

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
 305 310 315 320

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
 325 330 335

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe
 340 345 350

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
 355 360 365

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
 370 375 380

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly
385 390 395 400

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
420 425 430

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
435 440 445

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala
450 455 460

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile
465 470 475 480

Asp Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe
485 490 495

Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
500 505 510

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser
515 520 525

Asn Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
530 535 540

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
545 550 555 560

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
565 570 575

Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr
580 585 590

Asn Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu

595

600

605

Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser
 610 615 620

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
 625 630 635 640

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro
 645 650 655

Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His
 660 665 670

His His

<210> 91

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 91

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

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

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 35 40 45

Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly
 50 55 60

Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr
 65 70 75 80

Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

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

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
145 150 155 160

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
165 170 175

Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln
180 185 190

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

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr
245 250 255

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
290 295 300

Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
305 310 315 320

Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
325 330 335

Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met
340 345 350

Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
355 360 365

Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe
370 375 380

His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
385 390 395 400

Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
405 410 415

Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
420 425 430

Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly Pro Ala Gly Met
435 440 445

Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
450 455 460

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
465 470 475 480

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
485 490 495

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
500 505 510

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
515 520 525

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
530 535 540

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
545 550 555 560

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
580 585 590

Gly Gly Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala
595 600 605

Ser Gly Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr
610 615 620

Pro Gly Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser
625 630 635 640

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

Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu
660 665 670

Asp Thr Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp
675 680 685

Gly Gln Gly Thr Gln Val Thr Val Ser Ser His His His His His His
690 695 700

<210> 92

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 92

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

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

Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly
50 55 60

Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser Thr Asn
65 70 75 80

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr
100 105 110

Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

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

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
165 170 175

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
180 185 190

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp

195

200

205

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 210 215 220

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

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

Ser Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro
 260 265 270

Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser
 275 280 285

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

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln
 305 310 315 320

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

Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg
 340 345 350

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
 355 360 365

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala
 370 375 380

Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
 385 390 395 400

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
 405 410 415

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
420 425 430

Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp
435 440 445

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala
450 455 460

Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
465 470 475 480

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
485 490 495

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

Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly
515 520 525

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
530 535 540

Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
545 550 555 560

Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
565 570 575

Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
580 585 590

Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
595 600 605

Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
610 615 620

Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser

625		630		635		640									
Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val
				645					650					655	

Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr
			660					665					670		

Ala	Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr
		675					680					685			

Phe	Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr	His	His	His	His	His	His
	690					695				700					

<210> 93
 <211> 689
 <212> PRT
 <213> Artificial Sequence

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

<400> 93															
Met	Asp	Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp
1				5				10						15	

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

Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly
		35					40					45			

Phe	Thr	Phe	Ser	Ser	Tyr	Thr	Leu	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly
	50					55					60				

Lys	Gly	Leu	Glu	Trp	Val	Ala	Ala	Ile	Asp	Ser	Ser	Ser	Tyr	Thr	Tyr
65					70					75					80

Ser	Pro	Asp	Thr	Val	Arg	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala
				85					90					95	

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

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

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
145 150 155 160

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
165 170 175

Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln
180 185 190

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

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
210 215 220

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
225 230 235 240

Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr
245 250 255

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
260 265 270

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
275 280 285

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
290 295 300

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
305 310 315 320

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
325 330 335

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

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
355 360 365

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

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
385 390 395 400

Leu Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
405 410 415

Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
420 425 430

Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
435 440 445

Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
450 455 460

Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
465 470 475 480

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

Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
500 505 510

Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
515 520 525

Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
530 535 540

Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser Gly
545 550 555 560

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser
565 570 575

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

Ala Ser Gly Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln
595 600 605

Thr Pro Gly Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly
610 615 620

Ser Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
625 630 635 640

Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro
645 650 655

Glu Asp Thr Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr
660 665 670

Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser His His His His His
675 680 685

His

<210> 94

<211> 700

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 94

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

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
195 200 205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala

210

215

220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
 245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
 260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
 275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Arg Gly Glu Thr Gly
 290 295 300

Pro Ala Ala Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
 305 310 315 320

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 325 330 335

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
 340 345 350

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr
 355 360 365

Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 370 375 380

Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp
 385 390 395 400

Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser
 405 410 415

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 420 425 430

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
450 455 460

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
465 470 475 480

Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro
485 490 495

Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr
500 505 510

Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn
515 520 525

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
530 535 540

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp Ala Leu Asp
545 550 555 560

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
580 585 590

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
595 600 605

Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln
610 615 620

Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe
625 630 635 640

Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr

645

650

655

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 660 665 670

Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly
 675 680 685

Thr Lys Val Glu Ile Lys His His His His His His
 690 695 700

<210> 95

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 95

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

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

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 35 40 45

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
 50 55 60

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

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

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Val Gly Ala Phe Arg Pro Tyr
115 120 125

Arg Lys His Glu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Arg Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser
145 150 155 160

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

Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp
180 185 190

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

Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser
210 215 220

Gly Asn Thr Ala Ser Leu Thr Thr Thr Gly Ala Gln Ala Glu Asp Glu
225 230 235 240

Ala Asp Tyr Tyr Cys Asn Ser Ser Pro Phe Glu His Asn Leu Val Val
245 250 255

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu His His His His His His
260 265 270

Glu Pro Glu Ala
275

<210> 96

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 96

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

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

Leu Val Arg Pro Gly Thr Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Pro Gly Ser Gly Gly Thr
65 70 75 80

Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp
100 105 110

Ser Ala Val Tyr Phe Cys Ala Arg Trp Arg Gly Asp Gly Tyr Tyr Ala
115 120 125

Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
145 150 155 160

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

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

Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
195 200 205

Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe

210

215

220

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

Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp
 245 250 255

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys His His His
 260 265 270

His His His Glu Pro Glu Ala
 275

<210> 97

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 97

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

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

Leu Val Arg Pro Gly Thr Ser Val Lys Val Ser Cys Lys Ala Ser Gly
 35 40 45

Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly
 50 55 60

Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Pro Gly Ser Gly Gly Thr
 65 70 75 80

Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp
100 105 110

Ser Ala Val Tyr Phe Cys Ala Arg Trp Arg Gly Asp Gly Tyr Tyr Ala
115 120 125

Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ser
130 135 140

Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Asp Ile
145 150 155 160

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

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

Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
195 200 205

Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe
210 215 220

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

Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp
245 250 255

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys His His His
260 265 270

His His His Glu Pro Glu Ala
275

<210> 98

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 98

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

Leu Arg Gly Ala Arg Cys Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
20 25 30

Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
35 40 45

Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln
50 55 60

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

Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
100 105 110

Tyr Cys Gln Gln Ser Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr
115 120 125

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

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

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

Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly
180 185 190

Leu Glu Trp Ile Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr

195

200

205

Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
 210 215 220

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

Val Tyr Phe Cys Ala Arg Trp Arg Gly Asp Gly Tyr Tyr Ala Tyr Phe
 245 250 255

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser His His His
 260 265 270

His His His Glu Pro Glu Ala
 275

<210> 99

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 99

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

Leu Arg Gly Ala Arg Cys Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
 20 25 30

Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
 35 40 45

Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln
 50 55 60

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

Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
100 105 110

Tyr Cys Gln Gln Ser Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly
130 135 140

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

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

Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly
180 185 190

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

Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
210 215 220

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

Val Tyr Phe Cys Ala Arg Trp Arg Gly Asp Gly Tyr Tyr Ala Tyr Phe
245 250 255

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser His His His
260 265 270

His His His Glu Pro Glu Ala
275

<210> 100

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 100

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser
145 150 155 160

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

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys

180

185

190

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
 195 200 205

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

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
 225 230 235 240

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
 245 250 255

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

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His His
 275 280 285

His His His Glu Pro Glu Ala
 290 295

<210> 101

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 101

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
 20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
 35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Gly Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala His Lys Ser Glu
165 170 175

Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu
180 185 190

Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp
195 200 205

His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val
210 215 220

Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe
225 230 235 240

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

Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe
260 265 270

Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro
275 280 285

Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe
290 295 300

Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr
305 310 315 320

Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr
325 330 335

Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu
340 345 350

Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu
355 360 365

Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp
370 375 380

Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu
385 390 395 400

Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys
405 410 415

His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys
420 425 430

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

Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu
450 455 460

Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val
465 470 475 480

Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe
485 490 495

Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser
500 505 510

Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu
515 520 525

Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe
530 535 540

Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln
545 550 555 560

Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala
565 570 575

Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr
580 585 590

Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys
595 600 605

Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser
610 615 620

Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser
625 630 635 640

Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro
645 650 655

Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe
660 665 670

Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu
675 680 685

Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys
690 695 700

His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp
705 710 715 720

Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
725 730 735

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala
740 745 750

Leu Gly Leu His His His His His His Glu Pro Glu Ala
755 760 765

<210> 102

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 102

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn

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

Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr
325 330 335

Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu
340 345 350

Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu
355 360 365

Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp
370 375 380

Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu
385 390 395 400

Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys
405 410 415

His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys
420 425 430

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

Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu
450 455 460

Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val
465 470 475 480

Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe
485 490 495

Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser
500 505 510

Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu
515 520 525

Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe

530

535

540

Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln
 545 550 555 560

Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala
 565 570 575

Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr
 580 585 590

Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys
 595 600 605

Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser
 610 615 620

Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser
 625 630 635 640

Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro
 645 650 655

Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe
 660 665 670

Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu
 675 680 685

Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys
 690 695 700

His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp
 705 710 715 720

Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
 725 730 735

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala
 740 745 750

Leu Gly Leu His His His His His His Glu Pro Glu Ala
755 760 765

<210> 103

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 103

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Asp Ala His Lys Ser Glu
165 170 175

Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu
180 185 190

Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp
195 200 205

His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val
210 215 220

Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe
225 230 235 240

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

Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe
260 265 270

Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro
275 280 285

Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe
290 295 300

Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr
305 310 315 320

Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr
325 330 335

Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu
340 345 350

Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu
355 360 365

Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp
370 375 380

Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu
385 390 395 400

Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys
405 410 415

His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys
420 425 430

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

Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu
450 455 460

Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val
465 470 475 480

Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe
485 490 495

Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser
500 505 510

Val Val Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu
515 520 525

Lys Cys Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe
530 535 540

Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln
545 550 555 560

Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala
565 570 575

Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr
580 585 590

Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys
595 600 605

Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser
610 615 620

Val Val Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser
625 630 635 640

Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro
645 650 655

Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe
660 665 670

Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu
675 680 685

Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys
690 695 700

His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp
705 710 715 720

Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr
725 730 735

Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala
740 745 750

Leu Gly Leu His His His His His His Glu Pro Glu Ala
755 760 765

<210> 104

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 104

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu
165 170 175

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
180 185 190

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
195 200 205

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

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
245 250 255

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

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly
305 310 315 320

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu
325 330 335

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
340 345 350

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg
355 360 365

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser
370 375 380

Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser
385 390 395 400

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
405 410 415

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp

420

425

430

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 450 455 460

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 465 470 475 480

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly
 485 490 495

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser
 500 505 510

Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 515 520 525

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 530 535 540

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

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
 565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
 580 585 590

Gly Gly Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala
 595 600 605

Ser Gly Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr
 610 615 620

Pro Gly Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser
 625 630 635 640

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

Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu
660 665 670

Asp Thr Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp
675 680 685

Gly Gln Gly Thr Gln Val Thr Val Ser Ser His His His His His His
690 695 700

Glu Pro Glu Ala
705

<210> 105

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 105

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

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

Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly
50 55 60

Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser Thr Asn
65 70 75 80

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr
100 105 110

Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
195 200 205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
210 215 220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
290 295 300

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

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
325 330 335

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
340 345 350

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
355 360 365

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
420 425 430

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro
435 440 445

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

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val
485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser
500 505 510

Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp
545 550 555 560

Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
580 585 590

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
595 600 605

Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val
610 615 620

Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr
625 630 635 640

Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
645 650 655

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
660 665 670

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr
675 680 685

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His His
690 695 700

Glu Pro Glu Ala
705

<210> 106

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 106

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

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

Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly
50 55 60

Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser Thr Asn
65 70 75 80

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr
100 105 110

Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
130 135 140

Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
195 200 205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
210 215 220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
290 295 300

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

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
325 330 335

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
340 345 350

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
355 360 365

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly

405

410

415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 420 425 430

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro
 435 440 445

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

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
 465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val
 485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser
 500 505 510

Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile
 515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
 530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp
 545 550 555 560

Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 580 585 590

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 595 600 605

Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val
 610 615 620

Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr
625 630 635 640

Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
645 650 655

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
660 665 670

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr
675 680 685

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His His
690 695 700

Glu Pro Glu Ala
705

<210> 107
<211> 161
<212> PRT
<213> Artificial Sequence

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

<400> 107
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr His His His His His
145 150 155 160

His

<210> 108

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 108

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly
305 310 315 320

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu
325 330 335

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
340 345 350

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg
355 360 365

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser
370 375 380

Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser
385 390 395 400

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
405 410 415

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp
420 425 430

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
450 455 460

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
465 470 475 480

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly
485 490 495

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser

500

505

510

Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
515 520 525

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
530 535 540

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

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly
580 585 590

Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
595 600 605

Ser Gly Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala
610 615 620

Pro Gly Lys Gln Arg Glu Leu Val Ala Arg Ile Thr Arg Gly Gly Thr
625 630 635 640

Ile Ser Tyr Asp Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
645 650 655

Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu
660 665 670

Asp Thr Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp
675 680 685

Gly Lys Gly Thr Gln Val Thr Val Ser Ser His His His His His His
690 695 700

Glu Pro Glu Ala
705

<210> 109
<211> 708
<212> PRT
<213> Artificial Sequence

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

<400> 109
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly
50 55 60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
195 200 205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
210 215 220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
290 295 300

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

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
325 330 335

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
340 345 350

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
355 360 365

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
420 425 430

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro
435 440 445

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

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val
485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser
500 505 510

Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp
545 550 555 560

Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
580 585 590

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
595 600 605

Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val
610 615 620

Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr
625 630 635 640

Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
645 650 655

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
660 665 670

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr
675 680 685

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His His
690 695 700

Glu Pro Glu Ala
705

<210> 110
<211> 708
<212> PRT
<213> Artificial Sequence

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

<400> 110
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

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

Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly

50

55

60

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

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

Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110

Gly Val Tyr Tyr Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys
115 120 125

Gly Thr Gln Val Thr Val Ser Ser Ser Gly Gly Pro Gly Pro Ala Gly
130 135 140

Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys
145 150 155 160

Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
165 170 175

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
180 185 190

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
195 200 205

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
210 215 220

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

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
245 250 255

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
260 265 270

Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro
275 280 285

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
290 295 300

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

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
325 330 335

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
340 345 350

Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr
355 360 365

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
370 375 380

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
385 390 395 400

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
420 425 430

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro
435 440 445

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

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val

485

490

495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser
500 505 510

Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile
515 520 525

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
530 535 540

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp
545 550 555 560

Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
580 585 590

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
595 600 605

Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val
610 615 620

Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr
625 630 635 640

Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
645 650 655

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
660 665 670

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr
675 680 685

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His His
690 695 700

Glu Pro Glu Ala
705

<210> 111
<211> 579
<212> PRT
<213> Artificial Sequence

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

<400> 111
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Gly
145 150 155 160

Pro Ala Gly Leu Tyr Ala Gln Pro Gly Ser Glu Val Gln Leu Val Glu
165 170 175

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
180 185 190

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
195 200 205

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

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
245 250 255

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

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly
305 310 315 320

Pro Ala Gly Leu Tyr Ala Gln Pro Gly Ser Glu Val Gln Leu Val Glu
325 330 335

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
340 345 350

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg
355 360 365

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser
370 375 380

Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser
385 390 395 400

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
405 410 415

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp
420 425 430

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
450 455 460

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
465 470 475 480

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly
485 490 495

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser
500 505 510

Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
515 520 525

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
530 535 540

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

Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His His Glu
565 570 575

Pro Glu Ala

<210> 112
<211> 579
<212> PRT
<213> Artificial Sequence

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

<400> 112
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Pro
145 150 155 160

Gly Gly Pro Ala Gly Ile Gly Pro Gly Ser Glu Val Gln Leu Val Glu

165

170

175

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
 180 185 190

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
 195 200 205

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

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
 225 230 235 240

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
 245 250 255

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

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 290 295 300

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Pro
 305 310 315 320

Gly Gly Pro Ala Gly Ile Gly Pro Gly Ser Glu Val Gln Leu Val Glu
 325 330 335

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 340 345 350

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg
 355 360 365

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser
 370 375 380

Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser
385 390 395 400

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
405 410 415

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp
420 425 430

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
450 455 460

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
465 470 475 480

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly
485 490 495

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser
500 505 510

Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
515 520 525

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
530 535 540

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

Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His His Glu
565 570 575

Pro Glu Ala

<211> 579
<212> PRT
<213> Artificial Sequence

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

<400> 113
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Ala
145 150 155 160

Leu Phe Lys Ser Ser Phe Pro Pro Gly Ser Glu Val Gln Leu Val Glu
165 170 175

Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys
180 185 190

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
195 200 205

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

Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile
225 230 235 240

Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu
245 250 255

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

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Ala
305 310 315 320

Leu Phe Lys Ser Ser Phe Pro Pro Gly Ser Glu Val Gln Leu Val Glu
325 330 335

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
340 345 350

Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg
355 360 365

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser
370 375 380

Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser
385 390 395 400

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
405 410 415

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn Trp Asp
420 425 430

Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
450 455 460

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
465 470 475 480

Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly
485 490 495

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser
500 505 510

Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
515 520 525

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
530 535 540

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

Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His His Glu
565 570 575

Pro Glu Ala

<210> 114

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 114

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Pro
145 150 155 160

Leu Ala Gln Lys Leu Lys Ser Ser Pro Gly Ser Glu Val Gln Leu Val
165 170 175

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser
180 185 190

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
195 200 205

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
210 215 220

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

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
245 250 255

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

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
290 295 300

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro
305 310 315 320

Pro Leu Ala Gln Lys Leu Lys Ser Ser Pro Gly Ser Glu Val Gln Leu
325 330 335

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
340 345 350

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp
355 360 365

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

Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr
385 390 395 400

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser

405

410

415

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Asn
420 425 430

Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
435 440 445

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
450 455 460

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
465 470 475 480

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
485 490 495

Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
500 505 510

Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
515 520 525

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
530 535 540

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr
545 550 555 560

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His
565 570 575

His Glu Pro Glu Ala
580

<210> 115

<211> 613

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 115

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

Leu Arg Gly Ala Arg Cys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr
20 25 30

Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn
35 40 45

Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
50 55 60

Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys
65 70 75 80

Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln
85 90 95

Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn
100 105 110

Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
115 120 125

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

Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr Ser Gly Gly Pro Pro
145 150 155 160

Gly Gly Pro Ala Gly Ile Gly Ala Leu Phe Lys Ser Ser Phe Pro Pro
165 170 175

Leu Ala Gln Lys Leu Lys Ser Ser Pro Gly Ser Glu Val Gln Leu Val
180 185 190

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser
195 200 205

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
210 215 220

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
225 230 235 240

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

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
260 265 270

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
275 280 285

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
290 295 300

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
305 310 315 320

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro
325 330 335

Pro Gly Gly Pro Ala Gly Ile Gly Ala Leu Phe Lys Ser Ser Phe Pro
340 345 350

Pro Leu Ala Gln Lys Leu Lys Ser Ser Pro Gly Ser Glu Val Gln Leu
355 360 365

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
370 375 380

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp
385 390 395 400

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Asp
405 410 415

Ser Ser Ser Tyr Thr Tyr Ser Pro Asp Thr Val Arg Gly Arg Phe Thr
420 425 430

Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser
435 440 445

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

Trp Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
465 470 475 480

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
485 490 495

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
500 505 510

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

Val Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
530 535 540

Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
545 550 555 560

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
565 570 575

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr
580 585 590

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys His His His His His
595 600 605

His Glu Pro Glu Ala
610

<210> 116

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 116

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
 20 25 30

Gly Met Ser Trp Val Arg Gln Gly Gly Gly Gly Gly Leu Asp Gly Asn
 35 40 45

Glu Glu Pro Gly Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
 50 55 60

Arg Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
65 70 75 80

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 85 90 95

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
 100 105 110

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

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

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

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
 165 170 175

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu

180

185

190

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
 195 200 205

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

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
 225 230 235 240

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly
 245 250 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
 260 265 270

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
 275 280 285

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val
 290 295 300

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
 305 310 315 320

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg
 325 330 335

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
 340 345 350

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
 355 360 365

Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
 370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 385 390 395 400

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
405 410 415

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

Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
435 440 445

Val Val Ala Ile Asn Trp Ala Ser Gly Ser Thr Tyr Tyr Ala Asp Ser
450 455 460

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
465 470 475 480

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
485 490 495

Cys Ala Ala Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp
500 505 510

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
515 520 525

His His His His His His
530

<210> 117

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 117

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
20 25 30

Gly Met Ser Trp Val Arg Gln Gly Gly Gly Gly Gly Leu Asp Gly Asn
35 40 45

Glu Glu Pro Gly Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
50 55 60

Arg Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
65 70 75 80

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
85 90 95

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
100 105 110

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Val Val Gly Gly Gly Gly Thr Gln
130 135 140

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

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
165 170 175

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
180 185 190

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
195 200 205

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

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
225 230 235 240

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
260 265 270

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
275 280 285

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val
290 295 300

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
305 310 315 320

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg
325 330 335

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
340 345 350

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
355 360 365

Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
405 410 415

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

Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
435 440 445

Val Val Ala Ile Asn Trp Ala Ser Gly Ser Thr Tyr Tyr Ala Asp Ser
450 455 460

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
465 470 475 480

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
485 490 495

Cys Ala Ala Gly Tyr Gln Ile Asn Ser Gly Asn Tyr Asn Phe Lys Asp
500 505 510

Tyr Glu Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
515 520 525

His His His His His His
530

<210> 118
<211> 398
<212> PRT
<213> Artificial Sequence

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

<400> 118
Val Val Gly Gly Gly Gly Thr Gln Thr Val Val Thr Gln Glu Pro Ser
1 5 10 15

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
20 25 30

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
35 40 45

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
50 55 60

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
65 70 75 80

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr

85

90

95

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
 100 105 110

Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 130 135 140

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 145 150 155 160

Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 165 170 175

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

Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
 195 200 205

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

Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile
 225 230 235 240

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
 260 265 270

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala
 275 280 285

Ala Ser Gly Arg Thr Phe Ser Ser Tyr Ala Met Gly Trp Phe Arg Gln
 290 295 300

Ala Pro Gly Lys Glu Arg Glu Phe Val Val Ala Ile Asn Trp Ala Ser
305 310 315 320

Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
325 330 335

Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
340 345 350

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly Tyr Gln Ile Asn
355 360 365

Ser Gly Asn Tyr Asn Phe Lys Asp Tyr Glu Tyr Asp Tyr Trp Gly Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser His His His His His His
385 390 395

<210> 119
<211> 518
<212> PRT
<213> Artificial Sequence

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

<400> 119
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
20 25 30

Gly Met Ser Trp Val Arg Gln Gly Gly Gly Gly Gly Leu Asp Gly Asn
35 40 45

Glu Glu Pro Gly Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
50 55 60

Arg Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
65 70 75 80

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
85 90 95

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
100 105 110

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

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

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

Val Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Ser Gly Asn
165 170 175

Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu
180 185 190

Ile Gly Gly Thr Lys Phe Leu Val Pro Gly Thr Pro Ala Arg Phe Ser
195 200 205

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

Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu Trp Tyr Ser Asn Arg
225 230 235 240

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly
245 250 255

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
260 265 270

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser
275 280 285

Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr Ala Ile Asn Trp Val
290 295 300

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser
305 310 315 320

Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Gln Val Lys Asp Arg
325 330 335

Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met
340 345 350

Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His
355 360 365

Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
405 410 415

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

Tyr His Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
435 440 445

Val Ser Thr Ile Asn Pro Ala Gly Thr Thr Asp Tyr Ala Glu Ser Val
450 455 460

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
465 470 475 480

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
485 490 495

Asp Ser Tyr Gly Tyr Arg Gly Gln Gly Thr Gln Val Thr Val Ser Ser
500 505 510

His His His His His His
515

<210> 120
<211> 518
<212> PRT
<213> Artificial Sequence

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

<400> 120
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
20 25 30

Gly Met Ser Trp Val Arg Gln Gly Gly Gly Gly Gly Leu Asp Gly Asn
35 40 45

Glu Glu Pro Gly Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
50 55 60

Arg Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
65 70 75 80

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
85 90 95

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
100 105 110

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Val Val Gly Gly Gly Gly Thr Gln
130 135 140

Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr

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

Ala Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln
370 375 380

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
405 410 415

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

Tyr His Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
435 440 445

Val Ser Thr Ile Asn Pro Ala Gly Thr Thr Asp Tyr Ala Glu Ser Val
450 455 460

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
465 470 475 480

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
485 490 495

Asp Ser Tyr Gly Tyr Arg Gly Gln Gly Thr Gln Val Thr Val Ser Ser
500 505 510

His His His His His
515

<210> 121
<211> 382
<212> PRT
<213> Artificial Sequence

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

<400> 121
Val Val Gly Gly Gly Gly Thr Gln Thr Val Val Thr Gln Glu Pro Ser
1 5 10 15

Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser
20 25 30

Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys
35 40 45

Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val
50 55 60

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
65 70 75 80

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
85 90 95

Cys Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
100 105 110

Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
130 135 140

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
145 150 155 160

Asn Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
165 170 175

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

Tyr Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
195 200 205

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

Ala Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile
225 230 235 240

Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
260 265 270

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala
275 280 285

Ala Ser Arg Phe Met Ile Ser Glu Tyr His Met His Trp Val Arg Gln
290 295 300

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Thr Ile Asn Pro Ala Gly
305 310 315 320

Thr Thr Asp Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
325 330 335

Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro
340 345 350

Glu Asp Thr Ala Val Tyr Tyr Cys Asp Ser Tyr Gly Tyr Arg Gly Gln
355 360 365

Gly Thr Gln Val Thr Val Ser Ser His His His His His His
370 375 380

<210> 122

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 122

Gln Val Gln Leu Val Glu Ser Gly Gly Ala Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Val Asn Arg Tyr
20 25 30

Ser Met Arg Trp Tyr Arg Gln Ala Pro Gly Lys Glu Arg Glu Trp Val
35 40 45

Ala Gly Met Ser Ser Ala Gly Asp Arg Ser Ser Tyr Glu Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Arg Asn Thr Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Val Asn Val Gly Phe Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu
115 120 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
165 170 175

Gly Ser Gly Arg Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn
195 200 205

Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly
210 215 220

Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser Gly

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

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
450 455 460

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Thr Leu
465 470 475 480

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
485 490 495

Leu His His His His His His
500

<210> 123

<211> 509

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 123

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65 70 75 80

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

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Val
115 120 125

Val Gly Gly Gly Gly Thr Gln Thr Val Val Thr Gln Glu Pro Ser Leu
130 135 140

Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Ala Ser Ser Thr
145 150 155 160

Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro
165 170 175

Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Val Pro
180 185 190

Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala
195 200 205

Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys
210 215 220

Thr Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
245 250 255

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
260 265 270

Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn
275 280 285

Lys Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
290 295 300

Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr
305 310 315 320

Ala Asp Gln Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
325 330 335

Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala
340 345 350

Val Tyr Tyr Cys Val Arg His Ala Asn Phe Gly Asn Ser Tyr Ile Ser
355 360 365

Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
385 390 395 400

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala
405 410 415

Ser Arg Phe Met Ile Ser Glu Tyr His Met His Trp Val Arg Gln Ala
420 425 430

Pro Gly Lys Gly Leu Glu Trp Val Ser Thr Ile Asn Pro Ala Gly Thr
435 440 445

Thr Asp Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
450 455 460

Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu
465 470 475 480

Asp Thr Ala Val Tyr Tyr Cys Asp Ser Tyr Gly Tyr Arg Gly Gln Gly
485 490 495

Thr Gln Val Thr Val Ser Ser His His His His His His
500 505

<210> 124

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 124

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

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

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Leu Ala Trp Val Arg Gln Ala Pro Gly
50 55 60

Lys Gly Leu Glu Trp Val Ala Ala Ile Asp Ser Ser Ser Tyr Thr Tyr
65 70 75 80

Ser Pro Asp Thr Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

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

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
145 150 155 160

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
165 170 175

Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Gly Trp Tyr Gln Gln
180 185 190

Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile Tyr Ser Ala Ser Phe Arg

195

200

205

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 210 215 220

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 225 230 235 240

Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr
 245 250 255

Lys Val Glu Ile Lys His His His His His His
 260 265

<210> 125
 <211> 5
 <212> PRT
 <213> Unknown

<220>
 <221> source
 <223> /note="Description of Unknown:
 Sortase A cleavage site"

<220>
 <221> MOD_RES
 <222> (3)..(3)
 <223> Any amino acid

<400> 125
 Leu Pro Xaa Thr Gly
 1 5

<210> 126
 <211> 25
 <212> PRT
 <213> Artificial Sequence

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

<220>
 <221> SITE
 <222> (1)..(25)

<223> /note="This sequence may encompass 1-5 'Gly Gly Gly Gly Ser' repeating units"

<400> 126

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 127

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<220>

<221> SITE

<222> (1)..(20)

<223> /note="This sequence may encompass 1-5 'Gly Gly Gly Ser' repeating units"

<400> 127

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

Gly Gly Gly Ser
20

<210> 128

<211> 7

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown: Protease-cleavable sequence"

<400> 128

Gly Pro Leu Gly Val Arg Gly
1 5

<210> 129

<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Protease-cleavable sequence"

<400> 129
Ile Pro Val Ser Leu Arg Ser Gly
1 5

<210> 130
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Protease-cleavable sequence"

<400> 130
Val Pro Leu Ser Leu Tyr Ser Gly
1 5

<210> 131
<211> 10
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Protease-cleavable sequence"

<400> 131
Ser Gly Glu Ser Pro Ala Tyr Tyr Thr Ala
1 5 10

<210> 132
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 132
Gly Gly Gly Gly Ser
1 5

<210> 133
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 133
Gly Ser Gly Ser Gly Ser
1 5

<210> 134
<211> 13
<212> PRT
<213> Artificial Sequence

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

<400> 134
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Thr
1 5 10

<210> 135
<211> 15
<212> PRT
<213> Artificial Sequence

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

<400> 135
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 136
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
6xHis tag"

<400> 136
His His His His His His
1 5

<210> 137
<211> 124
<212> PRT
<213> Artificial Sequence

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

<400> 137
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
20 25 30

Gly Met Ser Trp Val Arg Gln Gly Gly Gly Gly Gly Leu Asp Gly Asn
35 40 45

Glu Glu Pro Gly Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly
50 55 60

Arg Asp Thr Leu Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
65 70 75 80

Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
85 90 95

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser
100 105 110

Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser
115 120