

SEQUENCE LISTING

<110> WEREWOLF THERAPEUTICS, INC.

<120> ACTIVATABLE CYTOKINE POLYPEPTIDES AND METHODS OF USE THEREOF

<130> 105365-0020

<140>

<141>

<150> 62/756,507

<151> 2018-11-06

<150> 62/756,515

<151> 2018-11-06

<150> 62/756,504

<151> 2018-11-06

<150> 62/671,225

<151> 2018-05-14

<160> 205

<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>
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 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

<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 piperdine

<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 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 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 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 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
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
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 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 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> 520

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 66

Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

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

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
115 120 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145 150 155 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
165 170 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
180 185 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
195 200 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
210 215 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
225 230 235 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
245 250 255

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

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
275 280 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
290 295 300

Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
305 310 315 320

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

Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu
340 345 350

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

Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu
370 375 380

Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr
385 390 395 400

Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr
405 410 415

Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu
420 425 430

Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile
435 440 445

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

Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu
465 470 475 480

Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala
485 490 495

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

Ser Ala His His His His His His
515 520

<210> 67
<211> 524
<212> PRT
<213> Artificial Sequence

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

<400> 67
Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

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

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
115 120 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145 150 155 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala

165

170

175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
 180 185 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
 195 200 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
 210 215 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
 225 230 235 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
 245 250 255

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

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
 275 280 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
 290 295 300

Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 305 310 315 320

Ser Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys
 325 330 335

Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln
 340 345 350

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

Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys
 370 375 380

Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu
385 390 395 400

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

Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met
420 425 430

Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro
435 440 445

Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu
450 455 460

Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser
465 470 475 480

Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile
485 490 495

Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met
500 505 510

Ser Tyr Leu Asn Ala Ser His His His His His His
515 520

<210> 68
<211> 940
<212> PRT
<213> Artificial Sequence

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

<400> 68
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg Tyr Thr
85 90 95

His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
115 120 125

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

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

His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Phe
165 170 175

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

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

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

His Gly Ser His Asp Asn Trp Gly Gln Gly Thr Met Val Thr Val Ser
225 230 235 240

Ser 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 Ile Trp
275 280 285

Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr Pro Asp
290 295 300

Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu Glu Asp
305 310 315 320

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

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

Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu Leu Leu
355 360 365

His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Asp Gln
370 375 380

Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn Tyr
385 390 395 400

Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp Leu
405 410 415

Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln Gly Val
420 425 430

Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly Asp Asn
435 440 445

Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala Cys Pro
450 455 460

Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala Val His
465 470 475 480

Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp Ile
485 490 495

Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu Lys Asn
500 505 510

Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp Ser Thr
515 520 525

Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln Gly Lys
530 535 540

Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr Ser Ala
545 550 555 560

Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala Gln Asp
565 570 575

Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro Cys Ser
580 585 590

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
595 600 605

Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu Ser Gln Ser Arg Asn
610 615 620

Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu Lys Leu
625 630 635 640

Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp Ile Thr
645 650 655

Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu Leu His
660 665 670

Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr Thr Arg
675 680 685

Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr Leu Cys
690 695 700

Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu Phe Gln
705 710 715 720

Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile Ile Leu
725 730 735

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

His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu Ala Asp
755 760 765

Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala Phe Ser
770 775 780

Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser Ser Ala
785 790 795 800

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu
805 810 815

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser
820 825 830

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly
835 840 845

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
850 855 860

Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys
865 870 875 880

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu
885 890 895

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
900 905 910

Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val
915 920 925

Ser Ser His His His His His His Glu Pro Glu Ala
930 935 940

<210> 69

<211> 1069

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 69

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg Tyr Thr
85 90 95

His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val

115

120

125

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

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

His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Phe
 165 170 175

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

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

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

His Gly Ser His Asp Asn Trp Gly Gln Gly Thr Met Val Thr Val Ser
 225 230 235 240

Ser 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 Ile Trp
 275 280 285

Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr Pro Asp
 290 295 300

Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu Glu Asp
 305 310 315 320

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

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

Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu Leu Leu
355 360 365

His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Asp Gln
370 375 380

Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn Tyr
385 390 395 400

Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp Leu
405 410 415

Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln Gly Val
420 425 430

Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly Asp Asn
435 440 445

Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala Cys Pro
450 455 460

Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala Val His
465 470 475 480

Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp Ile
485 490 495

Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu Lys Asn
500 505 510

Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp Ser Thr
515 520 525

Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln Gly Lys
530 535 540

Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr Ser Ala

545		550		555		560									
Thr	Val	Ile	Cys	Arg	Lys	Asn	Ala	Ser	Ile	Ser	Val	Arg	Ala	Gln	Asp
				565					570					575	
Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Glu	Trp	Ala	Ser	Val	Pro	Cys	Ser
			580					585					590		
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg
			595					600					605		
Val	Ile	Pro	Val	Ser	Gly	Pro	Ala	Arg	Cys	Leu	Ser	Gln	Ser	Arg	Asn
	610					615						620			
Leu	Leu	Lys	Thr	Thr	Asp	Asp	Met	Val	Lys	Thr	Ala	Arg	Glu	Lys	Leu
625					630					635					640
Lys	His	Tyr	Ser	Cys	Thr	Ala	Glu	Asp	Ile	Asp	His	Glu	Asp	Ile	Thr
				645					650					655	
Arg	Asp	Gln	Thr	Ser	Thr	Leu	Lys	Thr	Cys	Leu	Pro	Leu	Glu	Leu	His
			660					665					670		
Lys	Asn	Glu	Ser	Cys	Leu	Ala	Thr	Arg	Glu	Thr	Ser	Ser	Thr	Thr	Arg
		675					680					685			
Gly	Ser	Cys	Leu	Pro	Pro	Gln	Lys	Thr	Ser	Leu	Met	Met	Thr	Leu	Cys
	690					695					700				
Leu	Gly	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Thr	Glu	Phe	Gln
705					710					715					720
Ala	Ile	Asn	Ala	Ala	Leu	Gln	Asn	His	Asn	His	Gln	Gln	Ile	Ile	Leu
			725						730					735	
Asp	Lys	Gly	Met	Leu	Val	Ala	Ile	Asp	Glu	Leu	Met	Gln	Ser	Leu	Asn
			740					745					750		
His	Asn	Gly	Glu	Thr	Leu	Arg	Gln	Lys	Pro	Pro	Val	Gly	Glu	Ala	Asp
		755					760					765			

Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala Phe Ser
770 775 780

Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser Ser Ala
785 790 795 800

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu
805 810 815

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser
820 825 830

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly
835 840 845

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
850 855 860

Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys
865 870 875 880

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu
885 890 895

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
900 905 910

Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val
915 920 925

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
930 935 940

Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Ala Gly
945 950 955 960

Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Asn
965 970 975

Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Lys Gln Arg Glu Phe

980

985

990

Val Ala Ile Ile Asn Ser Val Gly Ser Thr Asn Tyr Ala Asp Ser Val
 995 1000 1005

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
 1010 1015 1020

Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr
 1025 1030 1035

Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr
 1040 1045 1050

Gln Val Thr Val Ser Ser His His His His His His Glu Pro Glu
 1055 1060 1065

Ala

<210> 70

<211> 1069

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 70

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

Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly
130 135 140

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

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

Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe
180 185 190

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
195 200 205

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg Tyr
210 215 220

Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu
225 230 235 240

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

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
260 265 270

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly
275 280 285

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
290 295 300

Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
305 310 315 320

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
325 330 335

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Lys
340 345 350

Thr His Gly Ser His Asp Asn Trp Gly Gln Gly Thr Met Val Thr Val
355 360 365

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

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

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

Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr Pro
420 425 430

Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu Glu
435 440 445

Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly Ser
450 455 460

Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln
465 470 475 480

Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu Leu
485 490 495

Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Asp
500 505 510

Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn
515 520 525

Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp
530 535 540

Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln Gly
545 550 555 560

Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly Asp
565 570 575

Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala Cys
580 585 590

Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala Val
595 600 605

His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp
610 615 620

Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu Lys
625 630 635 640

Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp Ser
645 650 655

Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln Gly
660 665 670

Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr Ser
675 680 685

Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala Gln
690 695 700

Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro Cys
705 710 715 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
725 730 735

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

Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu Lys
755 760 765

Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp Ile
770 775 780

Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu Leu
785 790 795 800

His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr Thr
805 810 815

Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr Leu
820 825 830

Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu Phe
835 840 845

Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile Ile
850 855 860

Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu Leu Met Gln Ser Leu
865 870 875 880

Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu Ala
885 890 895

Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala Phe
900 905 910

Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser Ser
915 920 925

Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
930 935 940

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
945 950 955 960

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
965 970 975

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
980 985 990

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
995 1000 1005

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
1010 1015 1020

Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
1025 1030 1035

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
1040 1045 1050

Leu Val Thr Val Ser Ser His His His His His His Glu Pro Glu
1055 1060 1065

Ala

<210> 71

<211> 940

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 71

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 Glu 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 Gly
115 120 125

Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro
130 135 140

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

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

Leu Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg
180 185 190

Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly
195 200 205

Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg
210 215 220

Tyr Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val

225		230		235		240									
Leu	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
				245					250					255	
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
			260						265					270	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
		275					280					285			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	290						295				300				
Ala	Phe	Ile	Arg	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
305					310					315					320
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
				325					330					335	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			340					345					350		
Lys	Thr	His	Gly	Ser	His	Asp	Asn	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr
		355					360					365			
Val	Ser	Ser	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	
Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	Tyr
			420					425					430		
Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	Asp	Thr	Pro	Glu
		435					440					445			

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
450 455 460

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

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
485 490 495

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
500 505 510

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
515 520 525

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
530 535 540

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
545 550 555 560

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
565 570 575

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
580 585 590

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
595 600 605

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
610 615 620

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
625 630 635 640

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
645 650 655

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln

660

665

670

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
 675 680 685

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
 690 695 700

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
 705 710 715 720

Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 725 730 735

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

Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu
 755 760 765

Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp
 770 775 780

Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu
 785 790 795 800

Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr
 805 810 815

Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr
 820 825 830

Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu
 835 840 845

Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile
 850 855 860

Ile Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu Leu Met Gln Ser
 865 870 875 880

Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu
885 890 895

Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala
900 905 910

Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser
915 920 925

Ser Ala His His His His His His Glu Pro Glu Ala
930 935 940

<210> 72

<211> 940

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 72

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

Gly Ser Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp
130 135 140

Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr
145 150 155 160

Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val
165 170 175

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

Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser
195 200 205

Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile
210 215 220

Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu
225 230 235 240

Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile
245 250 255

Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp
260 265 270

Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val
275 280 285

Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp
290 295 300

Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val
305 310 315 320

Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe
325 330 335

Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys
340 345 350

Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp
355 360 365

Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln
370 375 380

Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp
385 390 395 400

Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val
405 410 415

Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser
420 425 430

Val Pro Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
435 440 445

Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu Ser
450 455 460

Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala
465 470 475 480

Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His
485 490 495

Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro
500 505 510

Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser
515 520 525

Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met
530 535 540

Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln
545 550 555 560

Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln
565 570 575

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

Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val
595 600 605

Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu
610 615 620

His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr
625 630 635 640

Leu Ser Ser Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu
645 650 655

Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
660 665 670

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
675 680 685

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

Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Ser
705 710 715 720

Asn Thr Val Lys Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
725 730 735

Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe
740 745 750

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
755 760 765

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg Tyr
770 775 780

Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu
785 790 795 800

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
805 810 815

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
820 825 830

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly
835 840 845

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
850 855 860

Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
865 870 875 880

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
885 890 895

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Lys
900 905 910

Thr His Gly Ser His Asp Asn Trp Gly Gln Gly Thr Met Val Thr Val
915 920 925

Ser Ser His His His His His His Glu Pro Glu Ala
930 935 940

<210> 73

<211> 940

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 73

Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
20 25 30

Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
65 70 75 80

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

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

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
115 120 125

Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
145 150 155 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
165 170 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
180 185 190

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

195

200

205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
 210 215 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
 225 230 235 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
 245 250 255

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

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
 275 280 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
 290 295 300

Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 305 310 315 320

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

Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu
 340 345 350

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

Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu
 370 375 380

Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr
 385 390 395 400

Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr
 405 410 415

Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu
420 425 430

Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile
435 440 445

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

Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu
465 470 475 480

Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala
485 490 495

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

Ser Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
515 520 525

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
530 535 540

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
545 550 555 560

Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg
565 570 575

Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Ser Asn Thr
580 585 590

Val Lys Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile
595 600 605

Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly
610 615 620

Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala

625					630						635					640
Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Arg	Tyr	Thr	His	
				645					650					655		
Pro	Ala	Leu	Leu	Phe	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Gly	
			660					665					670			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	
		675					680					685				
Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	
	690						695				700					
Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	His	
705					710					715					720	
Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Phe	Ile	
				725					730					735		
Arg	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	
			740					745					750			
Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	
		755					760					765				
Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Lys	Thr	His	
	770					775					780					
Gly	Ser	His	Asp	Asn	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	
785					790					795					800	
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	
				805					810					815		
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Asn	Ser	
			820					825					830			
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Lys	Phe	Gly	
	835						840					845				

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
850 855 860

Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys
865 870 875 880

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu
885 890 895

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr
900 905 910

Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val
915 920 925

Ser Ser His His His His His His Glu Pro Glu Ala
930 935 940

<210> 74
<211> 328
<212> PRT
<213> Homo sapiens

<400> 74
Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser

305 310 315 320

 Glu Trp Ala Ser Val Pro Cys Ser
 325

 <210> 75
 <211> 215
 <212> PRT
 <213> Mus musculus

 <400> 75
 Met Cys Gln Ser Arg Tyr Leu Leu Phe Leu Ala Thr Leu Ala Leu Leu
 1 5 10 15

 Asn His Leu Ser Leu Ala Arg Val Ile Pro Val Ser Gly Pro Ala Arg
 20 25 30

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

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

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

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

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

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

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

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

 Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys

165

170

175

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

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

Met Gly Tyr Leu Ser Ser Ala
 210 215

<210> 76

<211> 862

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 IL12Rb-2 sequence"

<400> 76

Met Ala His Thr Phe Arg Gly Cys Ser Leu Ala Phe Met Phe Ile Ile
 1 5 10 15

Thr Trp Leu Leu Ile Lys Ala Lys Ile Asp Ala Cys Lys Arg Gly Asp
 20 25 30

Val Thr Val Lys Pro Ser His Val Ile Leu Leu Gly Ser Thr Val Asn
 35 40 45

Ile Thr Cys Ser Leu Lys Pro Arg Gln Gly Cys Phe His Tyr Ser Arg
 50 55 60

Arg Asn Lys Leu Ile Leu Tyr Lys Phe Asp Arg Arg Ile Asn Phe His
 65 70 75 80

His Gly His Ser Leu Asn Ser Gln Val Thr Gly Leu Pro Leu Gly Thr
 85 90 95

Thr Leu Phe Val Cys Lys Leu Ala Cys Ile Asn Ser Asp Glu Ile Gln
 100 105 110

Ile Cys Gly Ala Glu Ile Phe Val Gly Val Ala Pro Glu Gln Pro Gln
115 120 125

Asn Leu Ser Cys Ile Gln Lys Gly Glu Gln Gly Thr Val Ala Cys Thr
130 135 140

Trp Glu Arg Gly Arg Asp Thr His Leu Tyr Thr Glu Tyr Thr Leu Gln
145 150 155 160

Leu Ser Gly Pro Lys Asn Leu Thr Trp Gln Lys Gln Cys Lys Asp Ile
165 170 175

Tyr Cys Asp Tyr Leu Asp Phe Gly Ile Asn Leu Thr Pro Glu Ser Pro
180 185 190

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

Ser Ser Ser Leu Pro Ser Thr Phe Thr Phe Leu Asp Ile Val Arg Pro
210 215 220

Leu Pro Pro Trp Asp Ile Arg Ile Lys Phe Gln Lys Ala Ser Val Ser
225 230 235 240

Arg Cys Thr Leu Tyr Trp Arg Asp Glu Gly Leu Val Leu Leu Asn Arg
245 250 255

Leu Arg Tyr Arg Pro Ser Asn Ser Arg Leu Trp Asn Met Val Asn Val
260 265 270

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

Glu Tyr Glu Phe Gln Ile Ser Ser Lys Leu His Leu Tyr Lys Gly Ser
290 295 300

Trp Ser Asp Trp Ser Glu Ser Leu Arg Ala Gln Thr Pro Glu Glu Glu
305 310 315 320

Pro Thr Gly Met Leu Asp Val Trp Tyr Met Lys Arg His Ile Asp Tyr
325 330 335

Ser Arg Gln Gln Ile Ser Leu Phe Trp Lys Asn Leu Ser Val Ser Glu
340 345 350

Ala Arg Gly Lys Ile Leu His Tyr Gln Val Thr Leu Gln Glu Leu Thr
355 360 365

Gly Gly Lys Ala Met Thr Gln Asn Ile Thr Gly His Thr Ser Trp Thr
370 375 380

Thr Val Ile Pro Arg Thr Gly Asn Trp Ala Val Ala Val Ser Ala Ala
385 390 395 400

Asn Ser Lys Gly Ser Ser Leu Pro Thr Arg Ile Asn Ile Met Asn Leu
405 410 415

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

Gly Met Asp Asn Ile Leu Val Thr Trp Gln Pro Pro Arg Lys Asp Pro
435 440 445

Ser Ala Val Gln Glu Tyr Val Val Glu Trp Arg Glu Leu His Pro Gly
450 455 460

Gly Asp Thr Gln Val Pro Leu Asn Trp Leu Arg Ser Arg Pro Tyr Asn
465 470 475 480

Val Ser Ala Leu Ile Ser Glu Asn Ile Lys Ser Tyr Ile Cys Tyr Glu
485 490 495

Ile Arg Val Tyr Ala Leu Ser Gly Asp Gln Gly Gly Cys Ser Ser Ile
500 505 510

Leu Gly Asn Ser Lys His Lys Ala Pro Leu Ser Gly Pro His Ile Asn
515 520 525

Ala Ile Thr Glu Glu Lys Gly Ser Ile Leu Ile Ser Trp Asn Ser Ile
530 535 540

Pro Val Gln Glu Gln Met Gly Cys Leu Leu His Tyr Arg Ile Tyr Trp
545 550 555 560

Lys Glu Arg Asp Ser Asn Ser Gln Pro Gln Leu Cys Glu Ile Pro Tyr
565 570 575

Arg Val Ser Gln Asn Ser His Pro Ile Asn Ser Leu Gln Pro Arg Val
580 585 590

Thr Tyr Val Leu Trp Met Thr Ala Leu Thr Ala Ala Gly Glu Ser Ser
595 600 605

His Gly Asn Glu Arg Glu Phe Cys Leu Gln Gly Lys Ala Asn Trp Met
610 615 620

Ala Phe Val Ala Pro Ser Ile Cys Ile Ala Ile Ile Met Val Gly Ile
625 630 635 640

Phe Ser Thr His Tyr Phe Gln Gln Lys Val Phe Val Leu Leu Ala Ala
645 650 655

Leu Arg Pro Gln Trp Cys Ser Arg Glu Ile Pro Asp Pro Ala Asn Ser
660 665 670

Thr Cys Ala Lys Lys Tyr Pro Ile Ala Glu Glu Lys Thr Gln Leu Pro
675 680 685

Leu Asp Arg Leu Leu Ile Asp Trp Pro Thr Pro Glu Asp Pro Glu Pro
690 695 700

Leu Val Ile Ser Glu Val Leu His Gln Val Thr Pro Val Phe Arg His
705 710 715 720

Pro Pro Cys Ser Asn Trp Pro Gln Arg Glu Lys Gly Ile Gln Gly His
725 730 735

Gln Ala Ser Glu Lys Asp Met Met His Ser Ala Ser Ser Pro Pro Pro
740 745 750

Pro Arg Ala Leu Gln Ala Glu Ser Arg Gln Leu Val Asp Leu Tyr Lys
755 760 765

Val Leu Glu Ser Arg Gly Ser Asp Pro Lys Pro Glu Asn Pro Ala Cys
770 775 780

Pro Trp Thr Val Leu Pro Ala Gly Asp Leu Pro Thr His Asp Gly Tyr
785 790 795 800

Leu Pro Ser Asn Ile Asp Asp Leu Pro Ser His Glu Ala Pro Leu Ala
805 810 815

Asp Ser Leu Glu Glu Leu Glu Pro Gln His Ile Ser Leu Ser Val Phe
820 825 830

Pro Ser Ser Ser Leu His Pro Leu Thr Phe Ser Cys Gly Asp Lys Leu
835 840 845

Thr Leu Asp Gln Leu Lys Met Arg Cys Asp Ser Leu Met Leu
850 855 860

<210> 77

<211> 662

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
IL12Rb-1 sequence"

<400> 77

Met Glu Pro Leu Val Thr Trp Val Val Pro Leu Leu Phe Leu Phe Leu
1 5 10 15

Leu Ser Arg Gln Gly Ala Ala Cys Arg Thr Ser Glu Cys Cys Phe Gln
20 25 30

Asp Pro Pro Tyr Pro Asp Ala Asp Ser Gly Ser Ala Ser Gly Pro Arg
35 40 45

Asp Leu Arg Cys Tyr Arg Ile Ser Ser Asp Arg Tyr Glu Cys Ser Trp
50 55 60

Gln Tyr Glu Gly Pro Thr Ala Gly Val Ser His Phe Leu Arg Cys Cys

65

70

75

80

Leu Ser Ser Gly Arg Cys Cys Tyr Phe Ala Ala Gly Ser Ala Thr Arg
 85 90 95

Leu Gln Phe Ser Asp Gln Ala Gly Val Ser Val Leu Tyr Thr Val Thr
 100 105 110

Leu Trp Val Glu Ser Trp Ala Arg Asn Gln Thr Glu Lys Ser Pro Glu
 115 120 125

Val Thr Leu Gln Leu Tyr Asn Ser Val Lys Tyr Glu Pro Pro Leu Gly
 130 135 140

Asp Ile Lys Val Ser Lys Leu Ala Gly Gln Leu Arg Met Glu Trp Glu
 145 150 155 160

Thr Pro Asp Asn Gln Val Gly Ala Glu Val Gln Phe Arg His Arg Thr
 165 170 175

Pro Ser Ser Pro Trp Lys Leu Gly Asp Cys Gly Pro Gln Asp Asp Asp
 180 185 190

Thr Glu Ser Cys Leu Cys Pro Leu Glu Met Asn Val Ala Gln Glu Phe
 195 200 205

Gln Leu Arg Arg Arg Gln Leu Gly Ser Gln Gly Ser Ser Trp Ser Lys
 210 215 220

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

Val Arg Phe Ser Val Glu Gln Leu Gly Gln Asp Gly Arg Arg Arg Leu
 245 250 255

Thr Leu Lys Glu Gln Pro Thr Gln Leu Glu Leu Pro Glu Gly Cys Gln
 260 265 270

Gly Leu Ala Pro Gly Thr Glu Val Thr Tyr Arg Leu Gln Leu His Met
 275 280 285

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

Lys Met Pro Tyr Leu Ser Gly Ala Ala Tyr Asn Val Ala Val Ile Ser
305 310 315 320

Ser Asn Gln Phe Gly Pro Gly Leu Asn Gln Thr Trp His Ile Pro Ala
325 330 335

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

Gly Thr Thr Met Tyr Trp Pro Ala Arg Ala Gln Ser Met Thr Tyr Cys
355 360 365

Ile Glu Trp Gln Pro Val Gly Gln Asp Gly Gly Leu Ala Thr Cys Ser
370 375 380

Leu Thr Ala Pro Gln Asp Pro Asp Pro Ala Gly Met Ala Thr Tyr Ser
385 390 395 400

Trp Ser Arg Glu Ser Gly Ala Met Gly Gln Glu Lys Cys Tyr Tyr Ile
405 410 415

Thr Ile Phe Ala Ser Ala His Pro Glu Lys Leu Thr Leu Trp Ser Thr
420 425 430

Val Leu Ser Thr Tyr His Phe Gly Gly Asn Ala Ser Ala Ala Gly Thr
435 440 445

Pro His His Val Ser Val Lys Asn His Ser Leu Asp Ser Val Ser Val
450 455 460

Asp Trp Ala Pro Ser Leu Leu Ser Thr Cys Pro Gly Val Leu Lys Glu
465 470 475 480

Tyr Val Val Arg Cys Arg Asp Glu Asp Ser Lys Gln Val Ser Glu His
485 490 495

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

500

505

510

Gly Val Ala Tyr Thr Val Gln Val Arg Ala Asp Thr Ala Trp Leu Arg
 515 520 525

Gly Val Trp Ser Gln Pro Gln Arg Phe Ser Ile Glu Val Gln Val Ser
 530 535 540

Asp Trp Leu Ile Phe Phe Ala Ser Leu Gly Ser Phe Leu Ser Ile Leu
 545 550 555 560

Leu Val Gly Val Leu Gly Tyr Leu Gly Leu Asn Arg Ala Ala Arg His
 565 570 575

Leu Cys Pro Pro Leu Pro Thr Pro Cys Ala Ser Ser Ala Ile Glu Phe
 580 585 590

Pro Gly Gly Lys Glu Thr Trp Gln Trp Ile Asn Pro Val Asp Phe Gln
 595 600 605

Glu Glu Ala Ser Leu Gln Glu Ala Leu Val Val Glu Met Ser Trp Asp
 610 615 620

Lys Gly Glu Arg Thr Glu Pro Leu Glu Lys Thr Glu Leu Pro Glu Gly
 625 630 635 640

Ala Pro Glu Leu Ala Leu Asp Thr Glu Leu Ser Leu Glu Asp Gly Asp
 645 650 655

Arg Cys Lys Ala Lys Met
 660

<210> 78

<211> 328

<212> PRT

<213> Homo sapiens

<400> 78

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

Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val

20

25

30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Trp Ala Ser Val Pro Cys Ser
325

<210> 79
<211> 335
<212> PRT
<213> Mus musculus

<400> 79
Met Cys Pro Gln Lys Leu Thr Ile Ser Trp Phe Ala Ile Val Leu Leu
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr Tyr Asn

305 310 315 320

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

<210> 80

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 80

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

Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr
130 135 140

Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp
145 150 155 160

Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser
165 170 175

Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn
180 185 190

Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr
195 200 205

Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile
210 215 220

Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn
225 230 235 240

Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg
245 250 255

Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met
260 265 270

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser His His His His His His
385 390 395

<210> 81

<211> 547

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 81

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

Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr

130

135

140

Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp
 145 150 155 160

Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser
 165 170 175

Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn
 180 185 190

Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr
 195 200 205

Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile
 210 215 220

Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn
 225 230 235 240

Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg
 245 250 255

Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met
 260 265 270

Lys Gly Leu Pro Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser
 275 280 285

Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser
 290 295 300

Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys
 305 310 315 320

Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val
 325 330 335

Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser
 340 345 350

His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala
355 360 365

Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg
370 375 380

Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu
385 390 395 400

Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro Gly
405 410 415

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

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

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
450 455 460

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

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

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

Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu
515 520 525

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

His His His
545

<211> 547
<212> PRT
<213> Artificial Sequence

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

<400> 82
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 Glu 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 Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
115 120 125

Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr
130 135 140

Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp
145 150 155 160

Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser
165 170 175

Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn
180 185 190

Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr
195 200 205

Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile
210 215 220

Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn
225 230 235 240

Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg
245 250 255

Lys Arg Lys Arg Ser Arg Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly
260 265 270

Ser Gly Gly Gly Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser
275 280 285

Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser
290 295 300

Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys
305 310 315 320

Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val
325 330 335

Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser
340 345 350

His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala
355 360 365

Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg
370 375 380

Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu
385 390 395 400

Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro Gly
405 410 415

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

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

Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg
450 455 460

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

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

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

Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu
515 520 525

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

His His His
545

<210> 83
<211> 166
<212> PRT
<213> Homo sapiens

<400> 83
Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160

Gly Arg Arg Ala Ser Gln
165

<210> 84
<211> 155
<212> PRT
<213> Mus musculus

<400> 84
Met Asn Ala Thr His Cys Ile Leu Ala Leu Gln Leu Phe Leu Met Ala
1 5 10 15

Val Ser Gly Cys Tyr Cys His Gly Thr Val Ile Glu Ser Leu Glu Ser
20 25 30

Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser
35 40 45

Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys
50 55 60

Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val
65 70 75 80

Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser
85 90 95

His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala
100 105 110

Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg
115 120 125

Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu
130 135 140

Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys
145 150 155

<210> 85
<211> 699
<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys 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 Ser
405 410 415

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

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

Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn
450 455 460

Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser
465 470 475 480

Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser

485

490

495

Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser
 500 505 510

Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu
 515 520 525

Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg
 530 535 540

Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg
 545 550 555 560

Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
 565 570 575

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 580 585 590

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

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 610 615 620

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
 660 665 670

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
 675 680 685

Val Thr Val Ser Ser His His His His His His
 690 695

<210> 86
<211> 436
<212> PRT
<213> Artificial Sequence

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

<400> 86
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 Glu 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 Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
115 120 125

Gly Ser Cys Asp Leu Pro Gln Thr His Asn Leu Arg Asn Lys Arg Ala
130 135 140

Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser Pro Leu Ser Cys Leu
145 150 155 160

Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu Lys Val Asp Ala Gln
165 170 175

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

Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser Ser Ala Ala Trp Asn
195 200 205

Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu His Gln Gln Leu Asn
210 215 220

Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly Val Gln Glu Phe Pro
225 230 235 240

Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg Lys Tyr Phe His Arg
245 250 255

Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser Pro Cys Ala Trp Glu
260 265 270

Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser Ser Ser Ala Asn Val
275 280 285

Leu Gly Arg Leu Arg Glu Glu Lys Ser Gly Gly Pro Gly Pro Ala Gly
290 295 300

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

Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser
325 330 335

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

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
355 360 365

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

Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
385 390 395 400

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
405 410 415

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

Glu Pro Glu Ala
435

<210> 87

<211> 428

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 87

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

Gly Ser Cys Asp Leu Pro Gln Thr His Asn Leu Arg Asn Lys Arg Ala
130 135 140

Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser Pro Leu Ser Cys Leu
145 150 155 160

Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu Lys Val Asp Ala Gln
165 170 175

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

Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser Ser Ala Ala Trp Asn
195 200 205

Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu His Gln Gln Leu Asn
210 215 220

Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly Val Gln Glu Phe Pro
225 230 235 240

Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg Lys Tyr Phe His Arg
245 250 255

Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser Pro Cys Ala Trp Glu
260 265 270

Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser Ser Ser Ala Asn Val
275 280 285

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

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

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly

325

330

335

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 340 345 350

Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys
 355 360 365

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

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

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

Ser Ser His His His His His His Glu Pro Glu Ala
 420 425

<210> 88

<211> 489

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 IFNgR1 sequence"

<400> 88

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

Ala Glu Met Gly Thr Ala Asp Leu Gly Pro Ser Ser Val Pro Thr Pro
 20 25 30

Thr Asn Val Thr Ile Glu Ser Tyr Asn Met Asn Pro Ile Val Tyr Trp
 35 40 45

Glu Tyr Gln Ile Met Pro Gln Val Pro Val Phe Thr Val Glu Val Lys
 50 55 60

Asn Tyr Gly Val Lys Asn Ser Glu Trp Ile Asp Ala Cys Ile Asn Ile
65 70 75 80

Ser His His Tyr Cys Asn Ile Ser Asp His Val Gly Asp Pro Ser Asn
85 90 95

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

Tyr Ala Lys Ser Glu Glu Phe Ala Val Cys Arg Asp Gly Lys Ile Gly
115 120 125

Pro Pro Lys Leu Asp Ile Arg Lys Glu Glu Lys Gln Ile Met Ile Asp
130 135 140

Ile Phe His Pro Ser Val Phe Val Asn Gly Asp Glu Gln Glu Val Asp
145 150 155 160

Tyr Asp Pro Glu Thr Thr Cys Tyr Ile Arg Val Tyr Asn Val Tyr Val
165 170 175

Arg Met Asn Gly Ser Glu Ile Gln Tyr Lys Ile Leu Thr Gln Lys Glu
180 185 190

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

Leu Asn Ser Gln Tyr Cys Val Ser Ala Glu Gly Val Leu His Val Trp
210 215 220

Gly Val Thr Thr Glu Lys Ser Lys Glu Val Cys Ile Thr Ile Phe Asn
225 230 235 240

Ser Ser Ile Lys Gly Ser Leu Trp Ile Pro Val Val Ala Ala Leu Leu
245 250 255

Leu Phe Leu Val Leu Ser Leu Val Phe Ile Cys Phe Tyr Ile Lys Lys
260 265 270

Ile Asn Pro Leu Lys Glu Lys Ser Ile Ile Leu Pro Lys Ser Leu Ile
275 280 285

Ser Val Val Arg Ser Ala Thr Leu Glu Thr Lys Pro Glu Ser Lys Tyr
290 295 300

Val Ser Leu Ile Thr Ser Tyr Gln Pro Phe Ser Leu Glu Lys Glu Val
305 310 315 320

Val Cys Glu Glu Pro Leu Ser Pro Ala Thr Val Pro Gly Met His Thr
325 330 335

Glu Asp Asn Pro Gly Lys Val Glu His Thr Glu Glu Leu Ser Ser Ile
340 345 350

Thr Glu Val Val Thr Thr Glu Glu Asn Ile Pro Asp Val Val Pro Gly
355 360 365

Ser His Leu Thr Pro Ile Glu Arg Glu Ser Ser Ser Pro Leu Ser Ser
370 375 380

Asn Gln Ser Glu Pro Gly Ser Ile Ala Leu Asn Ser Tyr His Ser Arg
385 390 395 400

Asn Cys Ser Glu Ser Asp His Ser Arg Asn Gly Phe Asp Thr Asp Ser
405 410 415

Ser Cys Leu Glu Ser His Ser Ser Leu Ser Asp Ser Glu Phe Pro Pro
420 425 430

Asn Asn Lys Gly Glu Ile Lys Thr Glu Gly Gln Glu Leu Ile Thr Val
435 440 445

Ile Lys Ala Pro Thr Ser Phe Gly Tyr Asp Lys Pro His Val Leu Val
450 455 460

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

Pro Thr Glu Asp Ser Lys Glu Phe Ser
485

<210> 89
<211> 337
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
IFNgR2 sequence"

<400> 89
Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe
1 5 10 15

Ala Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
20 25 30

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
35 40 45

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Gln
50 55 60

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
65 70 75 80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
85 90 95

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
115 120 125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
145 150 155 160

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr
165 170 175

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
180 185 190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
195 200 205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
210 215 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
225 230 235 240

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
245 250 255

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys
260 265 270

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

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
290 295 300

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val
305 310 315 320

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr
325 330 335

Leu

<210> 90

<211> 528

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 90

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

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

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
165 170 175

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
180 185 190

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

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

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
225 230 235 240

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

Pro Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn Asn
260 265 270

Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu
275 280 285

Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln
290 295 300

Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp
305 310 315 320

Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile
325 330 335

Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser
340 345 350

Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe
355 360 365

Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu Ser Ser Leu
370 375 380

Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly
385 390 395 400

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

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

Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro
435 440 445

Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
450 455 460

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

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

Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser
500 505 510

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

<210> 91
<211> 658
<212> PRT
<213> Artificial Sequence

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

<400> 91
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 Glu Ser Val
50 55 60

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

80

95

110

125

140

160

175

190

205

240

255

270

285

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

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

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

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

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

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

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

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

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

Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala
435 440 445

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

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

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

Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val

500

505

510

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

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

Ser Gly Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys
 545 550 555 560

Ala Ala Ser Gly Arg Ile Phe Ser Ile Asp Ile Met Ser Trp Tyr Arg
 565 570 575

Gln Ala Pro Gly Lys Gln Arg Glu Leu Val Ala Arg Ile Thr Arg Gly
 580 585 590

Gly Thr Ile Ser Tyr Asp Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 595 600 605

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

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

Tyr Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser His His His His
 645 650 655

His His

<210> 92

<211> 1337

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 92

Glu Ala His Lys Ser Glu Ile Ala His Arg Tyr Asn Asp Leu Gly Glu
1 5 10 15

Gln His Phe Lys Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln
20 25 30

Lys Cys Ser Tyr Asp Glu His Ala Lys Leu Val Gln Glu Val Thr Asp
35 40 45

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

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu
65 70 75 80

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

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

Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala Met Cys Thr Ser Phe Lys
115 120 125

Glu Asn Pro Thr Thr Phe Met Gly His Tyr Leu His Glu Val Ala Arg
130 135 140

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

Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala Glu Ala Asp Lys Glu Ser
165 170 175

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

Ser Val Arg Gln Arg Met Lys Cys Ser Ser Met Gln Lys Phe Gly Glu
195 200 205

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

Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu Ala Thr Asp Leu Thr Lys
225 230 235 240

Val Asn Lys Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

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

Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro Leu Leu Lys Lys Ala His
275 280 285

Cys Leu Ser Glu Val Glu His Asp Thr Met Pro Ala Asp Leu Pro Ala
290 295 300

Ile Ala Ala Asp Phe Val Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala
305 310 315 320

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

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

Tyr Glu Ala Thr Leu Glu Lys Cys Cys Ala Glu Ala Asn Pro Pro Ala
355 360 365

Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln Pro Leu Val Glu Glu Pro
370 375 380

Lys Asn Leu Val Lys Thr Asn Cys Asp Leu Tyr Glu Lys Leu Gly Glu
385 390 395 400

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

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

Val Gly Thr Lys Cys Cys Thr Leu Pro Glu Asp Gln Arg Leu Pro Cys
435 440 445

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

Glu Lys Thr Pro Val Ser Glu His Val Thr Lys Cys Cys Ser Gly Ser
465 470 475 480

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

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

Ile Cys Thr Leu Pro Glu Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala
515 520 525

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

Lys Thr Val Met Asp Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys
545 550 555 560

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

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

Met Lys Gly Leu Pro Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu
595 600 605

Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys
610 615 620

Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met
625 630 635 640

Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu
645 650 655

Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu
660 665 670

Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp
675 680 685

Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln
690 695 700

Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro
705 710 715 720

Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro
725 730 735

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Ala His Lys Ser
740 745 750

Glu Ile Ala His Arg Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly
755 760 765

Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp
770 775 780

Glu His Ala Lys Leu Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys
785 790 795 800

Val Ala Asp Glu Ser Ala Ala Asn Cys Asp Lys Ser Leu His Thr Leu
805 810 815

Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly
820 825 830

Glu Leu Ala Asp Cys Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys
835 840 845

Phe Leu Gln His Lys Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg
850 855 860

Pro Glu Ala Glu Ala Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr
865 870 875 880

Phe Met Gly His Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe
885 890 895

Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu
900 905 910

Thr Gln Cys Cys Ala Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys
915 920 925

Leu Asp Gly Val Lys Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg
930 935 940

Met Lys Cys Ser Ser Met Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala
945 950 955 960

Trp Ala Val Ala Arg Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala
965 970 975

Glu Ile Thr Lys Leu Ala Thr Asp Leu Thr Lys Val Asn Lys Glu Cys
980 985 990

Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala
995 1000 1005

Lys Tyr Met Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln
1010 1015 1020

Thr Cys Cys Asp Lys Pro Leu Leu Lys Lys Ala His Cys Leu Ser
1025 1030 1035

Glu Val Glu His Asp Thr Met Pro Ala Asp Leu Pro Ala Ile Ala
1040 1045 1050

Ala Asp Phe Val Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala Glu
1055 1060 1065

Ala Lys Asp Val Phe Leu Gly Thr Phe Leu Tyr Glu Tyr Ser Arg
1070 1075 1080

Arg His Pro Asp Tyr Ser Val Ser Leu Leu Leu Arg Leu Ala Lys
1085 1090 1095

Lys Tyr Glu Ala Thr Leu Glu Lys Cys Cys Ala Glu Ala Asn Pro
1100 1105 1110

Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln Pro Leu Val
1115 1120 1125

Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu Tyr Glu
1130 1135 1140

Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Ile Leu Val Arg Tyr
1145 1150 1155

Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala
1160 1165 1170

Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro
1175 1180 1185

Glu Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala Ile
1190 1195 1200

Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu
1205 1210 1215

His Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro
1220 1225 1230

Cys Phe Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu
1235 1240 1245

Phe Lys Ala Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu
1250 1255 1260

Pro Glu Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu
1265 1270 1275

Leu Val Lys His Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr
1280 1285 1290

Val Met Asp Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys Ala
1295 1300 1305

Ala Asp Lys Asp Thr Cys Phe Ser Thr Glu Gly Pro Asn Leu Val
1310 1315 1320

Thr Arg Cys Lys Asp Ala Leu Ala His His His His His His
1325 1330 1335

<210> 93

<211> 1485

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 93

Glu Ala His Lys Ser Glu Ile Ala His Arg Tyr Asn Asp Leu Gly Glu
1 5 10 15

Gln His Phe Lys Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln
20 25 30

Lys Cys Ser Tyr Asp Glu His Ala Lys Leu Val Gln Glu Val Thr Asp
35 40 45

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

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu
65 70 75 80

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

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

Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala Met Cys Thr Ser Phe Lys
115 120 125

Glu Asn Pro Thr Thr Phe Met Gly His Tyr Leu His Glu Val Ala Arg
130 135 140

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

Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala Glu Ala Asp Lys Glu Ser
165 170 175

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

Ser Val Arg Gln Arg Met Lys Cys Ser Ser Met Gln Lys Phe Gly Glu
195 200 205

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

Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu Ala Thr Asp Leu Thr Lys
225 230 235 240

Val Asn Lys Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

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

Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro Leu Leu Lys Lys Ala His
275 280 285

Cys Leu Ser Glu Val Glu His Asp Thr Met Pro Ala Asp Leu Pro Ala
290 295 300

Ile Ala Ala Asp Phe Val Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Thr Phe Leu Tyr Glu Tyr Ser Arg

325

330

335

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

Tyr Glu Ala Thr Leu Glu Lys Cys Cys Ala Glu Ala Asn Pro Pro Ala
 355 360 365

Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln Pro Leu Val Glu Glu Pro
 370 375 380

Lys Asn Leu Val Lys Thr Asn Cys Asp Leu Tyr Glu Lys Leu Gly Glu
 385 390 395 400

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

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

Val Gly Thr Lys Cys Cys Thr Leu Pro Glu Asp Gln Arg Leu Pro Cys
 435 440 445

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

Glu Lys Thr Pro Val Ser Glu His Val Thr Lys Cys Cys Ser Gly Ser
 465 470 475 480

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

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

Ile Cys Thr Leu Pro Glu Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala
 515 520 525

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

Lys Thr Val Met Asp Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys
545 550 555 560

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

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

Met Lys Gly Leu Pro Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu
595 600 605

Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys
610 615 620

Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met
625 630 635 640

Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu
645 650 655

Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu
660 665 670

Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp
675 680 685

Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln
690 695 700

Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro
705 710 715 720

Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Gly Gly Gly Gly
725 730 735

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Gly Thr Val Ile
740 745 750

Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp

755

760

765

Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys
 770 775 780

Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu
 785 790 795 800

Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile
 805 810 815

Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys
 820 825 830

Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn
 835 840 845

Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His
 850 855 860

Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys
 865 870 875 880

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu
 885 890 895

Ala His Lys Ser Glu Ile Ala His Arg Tyr Asn Asp Leu Gly Glu Gln
 900 905 910

His Phe Lys Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln Lys
 915 920 925

Cys Ser Tyr Asp Glu His Ala Lys Leu Val Gln Glu Val Thr Asp Phe
 930 935 940

Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Ala Asn Cys Asp Lys Ser
 945 950 955 960

Leu His Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu Arg
 965 970 975

Glu Asn Tyr Gly Glu Leu Ala Asp Cys Cys Thr Lys Gln Glu Pro Glu
980 985 990

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Ser Leu Pro
995 1000 1005

Pro Phe Glu Arg Pro Glu Ala Glu Ala Met Cys Thr Ser Phe Lys
1010 1015 1020

Glu Asn Pro Thr Thr Phe Met Gly His Tyr Leu His Glu Val Ala
1025 1030 1035

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala
1040 1045 1050

Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala Glu Ala Asp
1055 1060 1065

Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys Glu Lys
1070 1075 1080

Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser Met
1085 1090 1095

Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
1100 1105 1110

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys
1115 1120 1125

Leu Ala Thr Asp Leu Thr Lys Val Asn Lys Glu Cys Cys His Gly
1130 1135 1140

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys Tyr
1145 1150 1155

Met Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys
1160 1165 1170

Cys Asp Lys Pro Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val

1175

1180

1185

Glu His Asp Thr Met Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp
1190 1195 1200

Phe Val Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala Glu Ala Lys
1205 1210 1215

Asp Val Phe Leu Gly Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His
1220 1225 1230

Pro Asp Tyr Ser Val Ser Leu Leu Leu Arg Leu Ala Lys Lys Tyr
1235 1240 1245

Glu Ala Thr Leu Glu Lys Cys Cys Ala Glu Ala Asn Pro Pro Ala
1250 1255 1260

Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln Pro Leu Val Glu Glu
1265 1270 1275

Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu Tyr Glu Lys Leu
1280 1285 1290

Gly Glu Tyr Gly Phe Gln Asn Ala Ile Leu Val Arg Tyr Thr Gln
1295 1300 1305

Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala Ala Arg
1310 1315 1320

Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu Asp
1325 1330 1335

Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala Ile Leu Asn
1340 1345 1350

Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu His Val
1355 1360 1365

Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro Cys Phe
1370 1375 1380

Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys
1385 1390 1395

Ala Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu
1400 1405 1410

Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val
1415 1420 1425

Lys His Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met
1430 1435 1440

Asp Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp
1445 1450 1455

Lys Asp Thr Cys Phe Ser Thr Glu Gly Pro Asn Leu Val Thr Arg
1460 1465 1470

Cys Lys Asp Ala Leu Ala His His His His His His
1475 1480 1485

<210> 94

<211> 698

<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 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 His Gly Thr Val Ile Glu Ser
275 280 285

Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu
290 295 300

Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly
305 310 315 320

Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu
325 330 335

Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val
340 345 350

Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys
355 360 365

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

Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu
385 390 395 400

Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Gly Gly
405 410 415

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Gly Thr
420 425 430

Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly
435 440 445

Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp
450 455 460

Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe
465 470 475 480

Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn
485 490 495

Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn
500 505 510

Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val
515 520 525

Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val
530 535 540

Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser
545 550 555 560

Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
565 570 575

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
580 585 590

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

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
610 615 620

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
625 630 635 640

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

Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
660 665 670

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
675 680 685

Thr Val Ser Ser His His His His His His
690 695

<210> 95
<211> 699
<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
260 265 270

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

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
610 615 620

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
660 665 670

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
675 680 685

Val Thr Val Ser Ser His His His His His His
690 695

<210> 96

<211> 554

<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 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 His Gly Thr Val Ile Glu Ser
275 280 285

Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu
290 295 300

Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly
305 310 315 320

Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu
325 330 335

Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val
340 345 350

Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys
355 360 365

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

Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu
385 390 395 400

Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys 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 Glu Pro Glu Ala
545 550

<210> 97

<211> 554

<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 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 His Gly Thr Val Ile Glu Ser Leu
 145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
 165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
 195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
 210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
 225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
 245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
 260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys 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 Gly
405 410 415

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

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

Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Asn Ser Val Met
450 455 460

Ala Trp Tyr Arg Gln Thr Pro Gly Lys Gln Arg Glu Phe Val Ala Ile
465 470 475 480

Ile Asn Ser Val Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg
485 490 495

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met
500 505 510

Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Val Cys Asn Arg Asn
515 520 525

Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
530 535 540

His His His His His His Glu Pro Glu Ala

545

550

<210> 98

<211> 702

<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly
275 280 285

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

Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile
305 310 315 320

Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln
325 330 335

Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr
340 345 350

Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn
355 360 365

Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser
370 375 380

Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn
385 390 395 400

Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val
405 410 415

His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg
420 425 430

Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
435 440 445

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
450 455 460

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
465 470 475 480

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
485 490 495

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
515 520 525

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
530 535 540

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

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
565 570 575

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

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

Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu
610 615 620

Leu Val Ala Arg Ile Thr Arg Gly Gly Thr Ile Ser Tyr Asp Asp Ser
625 630 635 640

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

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr
660 665 670

Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val
675 680 685

Thr Val Ser Ser His His His His His His Glu Pro Glu Ala
690 695 700

<210> 99

<211> 702

<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 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 His Gly Thr Val Ile Glu Ser

275

280

285

Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu
 290 295 300

Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly
 305 310 315 320

Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu
 325 330 335

Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val
 340 345 350

Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys
 355 360 365

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

Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu
 385 390 395 400

Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly
 405 410 415

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

Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly
 435 440 445

Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp
 450 455 460

Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe
 465 470 475 480

Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn
 485 490 495

Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn
500 505 510

Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val
515 520 525

Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val
530 535 540

Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser
545 550 555 560

Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
565 570 575

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
580 585 590

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

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
610 615 620

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
625 630 635 640

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

Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
660 665 670

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
675 680 685

Thr Val Ser Ser His His His His His Glu Pro Glu Ala
690 695 700

<210> 100

<211> 702
<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly
275 280 285

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

Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile
305 310 315 320

Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln
325 330 335

Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr
340 345 350

Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn
355 360 365

Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser
370 375 380

Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn
385 390 395 400

Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val
405 410 415

His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg
420 425 430

Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
435 440 445

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
450 455 460

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
465 470 475 480

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
485 490 495

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
515 520 525

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
530 535 540

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

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
565 570 575

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

Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser
595 600 605

Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Lys Gln Arg Glu
610 615 620

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

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

Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Val
660 665 670

Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr Gln Val
675 680 685

Thr Val Ser Ser His His His His His Glu Pro Glu Ala
690 695 700

<210> 101

<211> 832

<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly
275 280 285

Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser His Gly Thr Val

290

295

300

Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile
 305 310 315 320

Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln
 325 330 335

Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr
 340 345 350

Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn
 355 360 365

Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser
 370 375 380

Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn
 385 390 395 400

Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val
 405 410 415

His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg
 420 425 430

Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
 435 440 445

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
 450 455 460

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
 465 470 475 480

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 485 490 495

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
515 520 525

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
530 535 540

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

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
565 570 575

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
580 585 590

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
595 600 605

Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
610 615 620

Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
625 630 635 640

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
660 665 670

Tyr Cys Ala Arg Gly Val Gly Ala Phe Arg Pro Tyr Arg Lys His Glu
675 680 685

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Arg Gly Gly Gly Gly Ser
690 695 700

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Leu Thr Gln
705 710 715 720

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

725

730

735

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys
 740 745 750

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro
 755 760 765

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala
 770 775 780

Ser Leu Thr Thr Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
 785 790 795 800

Cys Asn Ser Ser Pro Phe Glu His Asn Leu Val Val Phe Gly Gly Gly
 805 810 815

Thr Lys Leu Thr Val Leu His His His His His His Glu Pro Glu Ala
 820 825 830

<210> 102

<211> 276

<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 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> 103
<211> 573
<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu

165

170

175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
 195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
 210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
 225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
 245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
 260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys 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 Ser
405 410 415

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

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

Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn
450 455 460

Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser
465 470 475 480

Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser
485 490 495

Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser
500 505 510

Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu
515 520 525

Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg
530 535 540

Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg
545 550 555 560

Ser Arg Cys His His His His His His Glu Pro Glu Ala
565 570

<210> 104

<211> 573

<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 His Gly Thr Val Ile Glu Ser Leu Glu Ser
20 25 30

Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser
35 40 45

Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys
50 55 60

Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val
65 70 75 80

Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser
85 90 95

His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala
100 105 110

Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg
115 120 125

Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu
130 135 140

Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys 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 Ser Gly Gly
275 280 285

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

Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile
305 310 315 320

Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln
325 330 335

Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr
340 345 350

Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn
355 360 365

Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser
370 375 380

Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn
385 390 395 400

Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val
405 410 415

His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg
420 425 430

Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
435 440 445

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
450 455 460

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
465 470 475 480

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
485 490 495

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
515 520 525

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
530 535 540

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

Val Ser Ser His His His His His His Glu Pro Glu Ala
565 570

<210> 105

<211> 1511

<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 His Gly Thr Val Ile Glu Ser Leu Glu Ser	20	25	30
Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser	35	40	45
Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys	50	55	60
Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val	65	70	75
Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser	85	90	95
His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala	100	105	110
Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg	115	120	125
Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu	130	135	140
Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro Gly	145	150	155
Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Ala His Lys Ser Glu	165	170	175
Ile Ala His Arg Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu	180	185	190
Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu	195	200	205
His Ala Lys Leu Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val	210	215	220

Ala Asp Glu Ser Ala Ala Asn Cys Asp Lys Ser Leu His Thr Leu Phe
225 230 235 240

Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu
245 250 255

Leu Ala Asp Cys Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe
260 265 270

Leu Gln His Lys Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro
275 280 285

Glu Ala Glu Ala Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe
290 295 300

Met Gly His Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr
305 310 315 320

Ala Pro Glu Leu Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr
325 330 335

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

Asp Gly Val Lys Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met
355 360 365

Lys Cys Ser Ser Met Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp
370 375 380

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

Ile Thr Lys Leu Ala Thr Asp Leu Thr Lys Val Asn Lys Glu Cys Cys
405 410 415

His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys
420 425 430

Tyr Met Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys

435

440

445

Cys Asp Lys Pro Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu
 450 455 460

His Asp Thr Met Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val
 465 470 475 480

Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe
 485 490 495

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

Val Ser Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu Glu
 515 520 525

Lys Cys Cys Ala Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu
 530 535 540

Ala Glu Phe Gln Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr
 545 550 555 560

Asn Cys Asp Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala
 565 570 575

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

Leu Val Glu Ala Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys
 595 600 605

Thr Leu Pro Glu Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser
 610 615 620

Ala Ile Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser
 625 630 635 640

Glu His Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro
 645 650 655

Cys Phe Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe
660 665 670

Lys Ala Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu
675 680 685

Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val Lys
690 695 700

His Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp
705 710 715 720

Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr
725 730 735

Cys Phe Ser Thr Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala
740 745 750

Leu Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
755 760 765

Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe
770 775 780

Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile
785 790 795 800

Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln
805 810 815

Ile Ile Ser Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln
820 825 830

Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr
835 840 845

Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala
850 855 860

Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu

865		870		875		880
Leu Ile Arg Val	Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys					
	885		890			895
Arg Lys Arg Ser	Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys					
	900		905			910
Gly Leu Pro Gly	Ser Glu Ala His Lys Ser Glu Ile Ala His Arg Tyr					
	915		920			925
Asn Asp Leu Gly	Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala Phe					
	930		935			940
Ser Gln Tyr Leu	Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu Val					
945		950		955		960
Gln Glu Val Thr	Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala					
	965		970			975
Ala Asn Cys Asp	Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys					
	980		985			990
Ala Ile Pro Asn	Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys Cys					
	995		1000			1005
Thr Lys Gln Glu	Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys					
	1010		1015			1020
Asp Asp Asn Pro	Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu					
	1025		1030			1035
Ala Met Cys Thr	Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly					
	1040		1045			1050
His Tyr Leu His	Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala					
	1055		1060			1065
Pro Glu Leu Leu	Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr					
	1070		1075			1080

Gln	Cys	Cys	Ala	Glu	Ala	Asp	Lys	Glu	Ser	Cys	Leu	Thr	Pro	Lys
1085						1090					1095			
Leu	Asp	Gly	Val	Lys	Glu	Lys	Ala	Leu	Val	Ser	Ser	Val	Arg	Gln
1100						1105					1110			
Arg	Met	Lys	Cys	Ser	Ser	Met	Gln	Lys	Phe	Gly	Glu	Arg	Ala	Phe
1115						1120					1125			
Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Thr	Phe	Pro	Asn	Ala
1130						1135					1140			
Asp	Phe	Ala	Glu	Ile	Thr	Lys	Leu	Ala	Thr	Asp	Leu	Thr	Lys	Val
1145						1150					1155			
Asn	Lys	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp
1160						1165					1170			
Arg	Ala	Glu	Leu	Ala	Lys	Tyr	Met	Cys	Glu	Asn	Gln	Ala	Thr	Ile
1175						1180					1185			
Ser	Ser	Lys	Leu	Gln	Thr	Cys	Cys	Asp	Lys	Pro	Leu	Leu	Lys	Lys
1190						1195					1200			
Ala	His	Cys	Leu	Ser	Glu	Val	Glu	His	Asp	Thr	Met	Pro	Ala	Asp
1205						1210					1215			
Leu	Pro	Ala	Ile	Ala	Ala	Asp	Phe	Val	Glu	Asp	Gln	Glu	Val	Cys
1220						1225					1230			
Lys	Asn	Tyr	Ala	Glu	Ala	Lys	Asp	Val	Phe	Leu	Gly	Thr	Phe	Leu
1235						1240					1245			
Tyr	Glu	Tyr	Ser	Arg	Arg	His	Pro	Asp	Tyr	Ser	Val	Ser	Leu	Leu
1250						1255					1260			
Leu	Arg	Leu	Ala	Lys	Lys	Tyr	Glu	Ala	Thr	Leu	Glu	Lys	Cys	Cys
1265						1270					1275			
Ala	Glu	Ala	Asn	Pro	Pro	Ala	Cys	Tyr	Gly	Thr	Val	Leu	Ala	Glu

1280							1285								1290
Phe	Gln	Pro	Leu	Val	Glu	Glu	Pro	Lys	Asn	Leu	Val	Lys	Thr	Asn	
1295						1300					1305				
Cys	Asp	Leu	Tyr	Glu	Lys	Leu	Gly	Glu	Tyr	Gly	Phe	Gln	Asn	Ala	
1310						1315					1320				
Ile	Leu	Val	Arg	Tyr	Thr	Gln	Lys	Ala	Pro	Gln	Val	Ser	Thr	Pro	
1325						1330					1335				
Thr	Leu	Val	Glu	Ala	Ala	Arg	Asn	Leu	Gly	Arg	Val	Gly	Thr	Lys	
1340						1345					1350				
Cys	Cys	Thr	Leu	Pro	Glu	Asp	Gln	Arg	Leu	Pro	Cys	Val	Glu	Asp	
1355						1360					1365				
Tyr	Leu	Ser	Ala	Ile	Leu	Asn	Arg	Val	Cys	Leu	Leu	His	Glu	Lys	
1370						1375					1380				
Thr	Pro	Val	Ser	Glu	His	Val	Thr	Lys	Cys	Cys	Ser	Gly	Ser	Leu	
1385						1390					1395				
Val	Glu	Arg	Arg	Pro	Cys	Phe	Ser	Ala	Leu	Thr	Val	Asp	Glu	Thr	
1400						1405					1410				
Tyr	Val	Pro	Lys	Glu	Phe	Lys	Ala	Glu	Thr	Phe	Thr	Phe	His	Ser	
1415						1420					1425				
Asp	Ile	Cys	Thr	Leu	Pro	Glu	Lys	Glu	Lys	Gln	Ile	Lys	Lys	Gln	
1430						1435					1440				
Thr	Ala	Leu	Ala	Glu	Leu	Val	Lys	His	Lys	Pro	Lys	Ala	Thr	Ala	
1445						1450					1455				
Glu	Gln	Leu	Lys	Thr	Val	Met	Asp	Asp	Phe	Ala	Gln	Phe	Leu	Asp	
1460						1465					1470				
Thr	Cys	Cys	Lys	Ala	Ala	Asp	Lys	Asp	Thr	Cys	Phe	Ser	Thr	Glu	
1475						1480					1485				

Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala His His
1490 1495 1500

His His His His Glu Pro Glu Ala
1505 1510

<210> 106

<211> 1511

<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 Glu Ala His Lys Ser Glu Ile Ala His Arg
20 25 30

Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala
35 40 45

Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu
50 55 60

Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

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

Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys
100 105 110

Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
115 120 125

Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
130 135 140

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr
145 150 155 160

Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
165 170 175

Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala
180 185 190

Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys
195 200 205

Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
210 215 220

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

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu
245 250 255

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

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

Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro
290 295 300

Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met
305 310 315 320

Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
325 330 335

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

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

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

Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln
385 390 395 400

Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu
405 410 415

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

Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala
435 440 445

Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu
450 455 460

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

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

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

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

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

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

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

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr
580 585 590

Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala Ser Gly
595 600 605

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser His Gly Thr
610 615 620

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

Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp
645 650 655

Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe
660 665 670

Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn
675 680 685

Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn
690 695 700

Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val
705 710 715 720

Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val
725 730 735

Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser
740 745 750

Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
755 760 765

Ser Glu Ala His Lys Ser Glu Ile Ala His Arg Tyr Asn Asp Leu Gly
770 775 780

Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu
785 790 795 800

Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu Val Gln Glu Val Thr
805 810 815

Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Ala Asn Cys Asp
820 825 830

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn
835 840 845

Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys Cys Thr Lys Gln Glu
850 855 860

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Ser
865 870 875 880

Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala Met Cys Thr Ser Phe
885 890 895

Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr Leu His Glu Val Ala
900 905 910

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala Glu
915 920 925

Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala Glu Ala Asp Lys Glu
930 935 940

Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys Glu Lys Ala Leu Val
945 950 955 960

Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser Met Gln Lys Phe Gly
965 970 975

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Thr Phe
980 985 990

Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu Ala Thr Asp Leu Thr
995 1000 1005

Lys Val Asn Lys Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala
1010 1015 1020

Asp Asp Arg Ala Glu Leu Ala Lys Tyr Met Cys Glu Asn Gln Ala
1025 1030 1035

Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro Leu Leu
1040 1045 1050

Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met Pro
1055 1060 1065

Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
1070 1075 1080

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Thr
1085 1090 1095

Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Ser
1100 1105 1110

Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu Glu Lys
1115 1120 1125

Cys Cys Ala Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu
1130 1135 1140

Ala Glu Phe Gln Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys
1145 1150 1155

Thr Asn Cys Asp Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln
1160 1165 1170

Asn Ala Ile Leu Val Arg Tyr Thr Gln Lys Ala Pro Gln Val Ser
1175 1180 1185

Thr Pro Thr Leu Val Glu Ala Ala Arg Asn Leu Gly Arg Val Gly
1190 1195 1200

Thr Lys Cys Cys Thr Leu Pro Glu Asp Gln Arg Leu Pro Cys Val
1205 1210 1215

Glu Asp Tyr Leu Ser Ala Ile Leu Asn Arg Val Cys Leu Leu His
1220 1225 1230

Glu Lys Thr Pro Val Ser Glu His Val Thr Lys Cys Cys Ser Gly
1235 1240 1245

Ser Leu Val Glu Arg Arg Pro Cys Phe Ser Ala Leu Thr Val Asp
1250 1255 1260

Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala Glu Thr Phe Thr Phe
1265 1270 1275

His Ser Asp Ile Cys Thr Leu Pro Glu Lys Glu Lys Gln Ile Lys
1280 1285 1290

Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His Lys Pro Lys Ala
1295 1300 1305

Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp Phe Ala Gln Phe
1310 1315 1320

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser
1325 1330 1335

Thr Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala
1340 1345 1350

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
1355 1360 1365

His Gly Thr Val Ile Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe
1370 1375 1380

Asn Ser Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp
1385 1390 1395

Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln
1400 1405 1410

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

Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile Glu Ser His
1430 1435 1440

Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala
1445 1450 1455

Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val Gln
1460 1465 1470

Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
1475 1480 1485

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys His His
1490 1495 1500

His His His His Glu Pro Glu Ala
1505 1510

<210> 107

<211> 2110

<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 Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Glu Ala His Lys Ser Glu Ile Ala His Arg
20 25 30

Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala
35 40 45

Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu

50

55

60

Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

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

Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys
100 105 110

Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
115 120 125

Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
130 135 140

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr
145 150 155 160

Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
165 170 175

Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala
180 185 190

Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys
195 200 205

Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
210 215 220

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

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu
245 250 255

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

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

Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro
290 295 300

Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met
305 310 315 320

Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
325 330 335

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

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

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

Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln
385 390 395 400

Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu
405 410 415

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

Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala
435 440 445

Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu
450 455 460

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

Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu His Val Thr

485

490

495

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

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

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

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

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

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr
 580 585 590

Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala Ser Gly
 595 600 605

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser His Gly Thr
 610 615 620

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

Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp
 645 650 655

Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe
 660 665 670

Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn
 675 680 685

Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn
 690 695 700

Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val
705 710 715 720

Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val
725 730 735

Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser
740 745 750

Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
755 760 765

Ser Glu Ala His Lys Ser Glu Ile Ala His Arg Tyr Asn Asp Leu Gly
770 775 780

Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu
785 790 795 800

Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu Val Gln Glu Val Thr
805 810 815

Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Ala Asn Cys Asp
820 825 830

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn
835 840 845

Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys Cys Thr Lys Gln Glu
850 855 860

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Ser
865 870 875 880

Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala Met Cys Thr Ser Phe
885 890 895

Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr Leu His Glu Val Ala
900 905 910

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala Glu

915

920

925

Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala Glu Ala Asp Lys Glu
 930 935 940

Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys Glu Lys Ala Leu Val
 945 950 955 960

Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser Met Gln Lys Phe Gly
 965 970 975

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Thr Phe
 980 985 990

Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu Ala Thr Asp Leu Thr
 995 1000 1005

Lys Val Asn Lys Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala
 1010 1015 1020

Asp Asp Arg Ala Glu Leu Ala Lys Tyr Met Cys Glu Asn Gln Ala
 1025 1030 1035

Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro Leu Leu
 1040 1045 1050

Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met Pro
 1055 1060 1065

Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
 1070 1075 1080

Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Thr
 1085 1090 1095

Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser Val Ser
 1100 1105 1110

Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu Glu Lys
 1115 1120 1125

Cys Cys Ala Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu
1130 1135 1140

Ala Glu Phe Gln Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys
1145 1150 1155

Thr Asn Cys Asp Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln
1160 1165 1170

Asn Ala Ile Leu Val Arg Tyr Thr Gln Lys Ala Pro Gln Val Ser
1175 1180 1185

Thr Pro Thr Leu Val Glu Ala Ala Arg Asn Leu Gly Arg Val Gly
1190 1195 1200

Thr Lys Cys Cys Thr Leu Pro Glu Asp Gln Arg Leu Pro Cys Val
1205 1210 1215

Glu Asp Tyr Leu Ser Ala Ile Leu Asn Arg Val Cys Leu Leu His
1220 1225 1230

Glu Lys Thr Pro Val Ser Glu His Val Thr Lys Cys Cys Ser Gly
1235 1240 1245

Ser Leu Val Glu Arg Arg Pro Cys Phe Ser Ala Leu Thr Val Asp
1250 1255 1260

Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala Glu Thr Phe Thr Phe
1265 1270 1275

His Ser Asp Ile Cys Thr Leu Pro Glu Lys Glu Lys Gln Ile Lys
1280 1285 1290

Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His Lys Pro Lys Ala
1295 1300 1305

Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp Phe Ala Gln Phe
1310 1315 1320

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser

1325						1330						1335			
Thr	Glu	Gly	Pro	Asn	Leu	Val	Thr	Arg	Cys	Lys	Asp	Ala	Leu	Ala	
1340						1345					1350				
Ser	Gly	Gly	Pro	Gly	Pro	Ala	Gly	Met	Lys	Gly	Leu	Pro	Gly	Ser	
1355						1360					1365				
His	Gly	Thr	Val	Ile	Glu	Ser	Leu	Glu	Ser	Leu	Asn	Asn	Tyr	Phe	
1370						1375					1380				
Asn	Ser	Ser	Gly	Ile	Asp	Val	Glu	Glu	Lys	Ser	Leu	Phe	Leu	Asp	
1385						1390					1395				
Ile	Trp	Arg	Asn	Trp	Gln	Lys	Asp	Gly	Asp	Met	Lys	Ile	Leu	Gln	
1400						1405					1410				
Ser	Gln	Ile	Ile	Ser	Phe	Tyr	Leu	Arg	Leu	Phe	Glu	Val	Leu	Lys	
1415						1420					1425				
Asp	Asn	Gln	Ala	Ile	Ser	Asn	Asn	Ile	Ser	Val	Ile	Glu	Ser	His	
1430						1435					1440				
Leu	Ile	Thr	Thr	Phe	Phe	Ser	Asn	Ser	Lys	Ala	Lys	Lys	Asp	Ala	
1445						1450					1455				
Phe	Met	Ser	Ile	Ala	Lys	Phe	Glu	Val	Asn	Asn	Pro	Gln	Val	Gln	
1460						1465					1470				
Arg	Gln	Ala	Phe	Asn	Glu	Leu	Ile	Arg	Val	Val	His	Gln	Leu	Leu	
1475						1480					1485				
Pro	Glu	Ser	Ser	Leu	Arg	Lys	Arg	Lys	Arg	Ser	Arg	Cys	Ser	Gly	
1490						1495					1500				
Gly	Pro	Gly	Pro	Ala	Gly	Met	Lys	Gly	Leu	Pro	Gly	Ser	Glu	Ala	
1505						1510					1515				
His	Lys	Ser	Glu	Ile	Ala	His	Arg	Tyr	Asn	Asp	Leu	Gly	Glu	Gln	
1520						1525					1530				

His Phe Lys Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln
1535 1540 1545

Lys Cys Ser Tyr Asp Glu His Ala Lys Leu Val Gln Glu Val Thr
1550 1555 1560

Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Ala Asn Cys
1565 1570 1575

Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile
1580 1585 1590

Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys Cys Thr
1595 1600 1605

Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp
1610 1615 1620

Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
1625 1630 1635

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His
1640 1645 1650

Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
1655 1660 1665

Glu Leu Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln
1670 1675 1680

Cys Cys Ala Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu
1685 1690 1695

Asp Gly Val Lys Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg
1700 1705 1710

Met Lys Cys Ser Ser Met Gln Lys Phe Gly Glu Arg Ala Phe Lys
1715 1720 1725

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

1730	1735	1740
Phe Ala Glu Ile Thr Lys 1745	Leu Ala Thr Asp Leu Thr 1750	Lys Val Asn 1755
Lys Glu Cys Cys His Gly 1760	Asp Leu Leu Glu Cys 1765	Ala Asp Asp Arg 1770
Ala Glu Leu Ala Lys Tyr 1775	Met Cys Glu Asn Gln 1780	Ala Thr Ile Ser 1785
Ser Lys Leu Gln Thr Cys 1790	Cys Asp Lys Pro Leu 1795	Leu Lys Lys Ala 1800
His Cys Leu Ser Glu Val 1805	Glu His Asp Thr Met 1810	Pro Ala Asp Leu 1815
Pro Ala Ile Ala Ala Asp 1820	Phe Val Glu Asp Gln 1825	Glu Val Cys Lys 1830
Asn Tyr Ala Glu Ala Lys 1835	Asp Val Phe Leu Gly 1840	Thr Phe Leu Tyr 1845
Glu Tyr Ser Arg Arg His 1850	Pro Asp Tyr Ser Val 1855	Ser Leu Leu Leu 1860
Arg Leu Ala Lys Lys Tyr 1865	Glu Ala Thr Leu Glu 1870	Lys Cys Cys Ala 1875
Glu Ala Asn Pro Pro Ala 1880	Cys Tyr Gly Thr Val 1885	Leu Ala Glu Phe 1890
Gln Pro Leu Val Glu Glu 1895	Pro Lys Asn Leu Val 1900	Lys Thr Asn Cys 1905
Asp Leu Tyr Glu Lys Leu 1910	Gly Glu Tyr Gly Phe 1915	Gln Asn Ala Ile 1920
Leu Val Arg Tyr Thr Gln 1925	Lys Ala Pro Gln Val 1930	Ser Thr Pro Thr 1935

Leu Val Glu Ala Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys
1940 1945 1950

Cys Thr Leu Pro Glu Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr
1955 1960 1965

Leu Ser Ala Ile Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr
1970 1975 1980

Pro Val Ser Glu His Val Thr Lys Cys Cys Ser Gly Ser Leu Val
1985 1990 1995

Glu Arg Arg Pro Cys Phe Ser Ala Leu Thr Val Asp Glu Thr Tyr
2000 2005 2010

Val Pro Lys Glu Phe Lys Ala Glu Thr Phe Thr Phe His Ser Asp
2015 2020 2025

Ile Cys Thr Leu Pro Glu Lys Glu Lys Gln Ile Lys Lys Gln Thr
2030 2035 2040

Ala Leu Ala Glu Leu Val Lys His Lys Pro Lys Ala Thr Ala Glu
2045 2050 2055

Gln Leu Lys Thr Val Met Asp Asp Phe Ala Gln Phe Leu Asp Thr
2060 2065 2070

Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr Glu Gly
2075 2080 2085

Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala His His His
2090 2095 2100

His His His Glu Pro Glu Ala
2105 2110

<210> 108

<211> 2120

<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 Glu Ala His Lys Ser Glu Ile Ala His Arg
20 25 30

Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala
35 40 45

Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu
50 55 60

Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

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

Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys
100 105 110

Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
115 120 125

Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
130 135 140

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr
145 150 155 160

Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
165 170 175

Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala
180 185 190

Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys
195 200 205

Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
210 215 220

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

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu
245 250 255

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

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

Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro
290 295 300

Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met
305 310 315 320

Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
325 330 335

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

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

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

Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln
385 390 395 400

Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu
405 410 415

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

Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala
435 440 445

Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu
450 455 460

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

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

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

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

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

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

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

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr
580 585 590

Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala Ser Gly
595 600 605

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser His Gly Thr
610 615 620

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

Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp
645 650 655

Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe
660 665 670

Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn
675 680 685

Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn
690 695 700

Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val
705 710 715 720

Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val
725 730 735

Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser
740 745 750

Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
755 760 765

Ser Gly Gly Gly Gly Ser Glu Ala His Lys Ser Glu Ile Ala His Arg
770 775 780

Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala
785 790 795 800

Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu
805 810 815

Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
820 825 830

Ala Ala Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu
835 840 845

Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys
850 855 860

Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
865 870 875 880

Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
885 890 895

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr
900 905 910

Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
915 920 925

Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala
930 935 940

Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys
945 950 955 960

Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
965 970 975

Met Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg
980 985 990

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu
995 1000 1005

Ala Thr Asp Leu Thr Lys Val Asn Lys Glu Cys Cys His Gly Asp
1010 1015 1020

Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys Tyr Met
1025 1030 1035

Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys
1040 1045 1050

Asp Lys Pro Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu
1055 1060 1065

His Asp Thr Met Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe
1070 1075 1080

Val Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp
1085 1090 1095

Val Phe Leu Gly Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro
1100 1105 1110

Asp Tyr Ser Val Ser Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu
1115 1120 1125

Ala Thr Leu Glu Lys Cys Cys Ala Glu Ala Asn Pro Pro Ala Cys
1130 1135 1140

Tyr Gly Thr Val Leu Ala Glu Phe Gln Pro Leu Val Glu Glu Pro
1145 1150 1155

Lys Asn Leu Val Lys Thr Asn Cys Asp Leu Tyr Glu Lys Leu Gly
1160 1165 1170

Glu Tyr Gly Phe Gln Asn Ala Ile Leu Val Arg Tyr Thr Gln Lys
1175 1180 1185

Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala Ala Arg Asn
1190 1195 1200

Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu Asp Gln
1205 1210 1215

Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala Ile Leu Asn Arg
1220 1225 1230

Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu His Val Thr
1235 1240 1245

Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro Cys Phe Ser
1250 1255 1260

Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala
1265 1270 1275

Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu Lys
1280 1285 1290

Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val Lys
1295 1300 1305

His Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp
1310 1315 1320

Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys
1325 1330 1335

Asp Thr Cys Phe Ser Thr Glu Gly Pro Asn Leu Val Thr Arg Cys
1340 1345 1350

Lys Asp Ala Leu Ala Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly
1355 1360 1365

Pro Ala Gly Met Lys Gly Leu Pro Gly Ser His Gly Thr Val Ile
1370 1375 1380

Glu Ser Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile
1385 1390 1395

Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp
1400 1405 1410

Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser
1415 1420 1425

Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile
1430 1435 1440

Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe
1445 1450 1455

Phe Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala
1460 1465 1470

Lys Phe Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn
1475 1480 1485

Glu Leu Ile Arg Val Val His Gln Leu Leu Pro Glu Ser Ser Leu
1490 1495 1500

Arg Lys Arg Lys Arg Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala
1505 1510 1515

Gly Met Lys Gly Leu Pro Gly Ser Glu Ala His Lys Ser Glu Ile
1520 1525 1530

Ala His Arg Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu
1535 1540 1545

Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp
1550 1555 1560

Glu His Ala Lys Leu Val Gln Glu Val Thr Asp Phe Ala Lys Thr
1565 1570 1575

Cys Val Ala Asp Glu Ser Ala Ala Asn Cys Asp Lys Ser Leu His
1580 1585 1590

Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu Arg Glu
1595 1600 1605

Asn Tyr Gly Glu Leu Ala Asp Cys Cys Thr Lys Gln Glu Pro Glu
1610 1615 1620

Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Ser Leu
1625 1630 1635

Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala Met Cys Thr Ser Phe
1640 1645 1650

Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr Leu His Glu Val
1655 1660 1665

Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Tyr Tyr
1670 1675 1680

Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala Glu Ala
1685 1690 1695

Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys Glu
1700 1705 1710

Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
1715 1720 1725

Met Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala
1730 1735 1740

Arg Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr
1745 1750 1755

Lys Leu Ala Thr Asp Leu Thr Lys Val Asn Lys Glu Cys Cys His
1760 1765 1770

Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys
1775 1780 1785

Tyr Met Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr
1790 1795 1800

Cys Cys Asp Lys Pro Leu Leu Lys Lys Ala His Cys Leu Ser Glu
1805 1810 1815

Val Glu His Asp Thr Met Pro Ala Asp Leu Pro Ala Ile Ala Ala
1820 1825 1830

Asp Phe Val Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala Glu Ala
1835 1840 1845

Lys Asp Val Phe Leu Gly Thr Phe Leu Tyr Glu Tyr Ser Arg Arg
1850 1855 1860

His Pro Asp Tyr Ser Val Ser Leu Leu Leu Arg Leu Ala Lys Lys
1865 1870 1875

Tyr Glu Ala Thr Leu Glu Lys Cys Cys Ala Glu Ala Asn Pro Pro
1880 1885 1890

Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln Pro Leu Val Glu
1895 1900 1905

Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu Tyr Glu Lys
1910 1915 1920

Leu Gly Glu Tyr Gly Phe Gln Asn Ala Ile Leu Val Arg Tyr Thr
1925 1930 1935

Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala Ala
1940 1945 1950

Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu
1955 1960 1965

Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala Ile Leu
1970 1975 1980

Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu His
1985 1990 1995

Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro Cys
2000 2005 2010

Phe Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe
2015 2020 2025

Lys Ala Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro
2030 2035 2040

Glu Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu
2045 2050 2055

Val Lys His Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val
2060 2065 2070

Met Asp Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala
2075 2080 2085

Asp Lys Asp Thr Cys Phe Ser Thr Glu Gly Pro Asn Leu Val Thr
2090 2095 2100

Arg Cys Lys Asp Ala Leu Ala His His His His His His Glu Pro
2105 2110 2115

Glu Ala
2120

<210> 109

<211> 2130

<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 Glu Ala His Lys Ser Glu Ile Ala His Arg
20 25 30

Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala
35 40 45

Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu
50 55 60

Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

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

Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys

100

105

110

Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
 115 120 125

Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
 130 135 140

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr
 145 150 155 160

Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
 165 170 175

Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala
 180 185 190

Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys
 195 200 205

Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
 210 215 220

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

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu
 245 250 255

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

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

Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro
 290 295 300

Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met
 305 310 315 320

Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
325 330 335

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

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

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

Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln
385 390 395 400

Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu
405 410 415

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

Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala
435 440 445

Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu
450 455 460

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

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

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

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

Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu Lys Glu Lys Gln

530

535

540

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

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

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr
 580 585 590

Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala Ser Gly
 595 600 605

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser His Gly Thr
 610 615 620

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

Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp
 645 650 655

Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe
 660 665 670

Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn
 675 680 685

Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn
 690 695 700

Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val
 705 710 715 720

Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val
 725 730 735

Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser
 740 745 750

Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
755 760 765

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ala His Lys Ser
770 775 780

Glu Ile Ala His Arg Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly
785 790 795 800

Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp
805 810 815

Glu His Ala Lys Leu Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys
820 825 830

Val Ala Asp Glu Ser Ala Ala Asn Cys Asp Lys Ser Leu His Thr Leu
835 840 845

Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly
850 855 860

Glu Leu Ala Asp Cys Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys
865 870 875 880

Phe Leu Gln His Lys Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg
885 890 895

Pro Glu Ala Glu Ala Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr
900 905 910

Phe Met Gly His Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe
915 920 925

Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu
930 935 940

Thr Gln Cys Cys Ala Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys
945 950 955 960

Leu Asp Gly Val Lys Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg

965

970

975

Met Lys Cys Ser Ser Met Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala
 980 985 990

Trp Ala Val Ala Arg Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala
 995 1000 1005

Glu Ile Thr Lys Leu Ala Thr Asp Leu Thr Lys Val Asn Lys Glu
 1010 1015 1020

Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu
 1025 1030 1035

Leu Ala Lys Tyr Met Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys
 1040 1045 1050

Leu Gln Thr Cys Cys Asp Lys Pro Leu Leu Lys Lys Ala His Cys
 1055 1060 1065

Leu Ser Glu Val Glu His Asp Thr Met Pro Ala Asp Leu Pro Ala
 1070 1075 1080

Ile Ala Ala Asp Phe Val Glu Asp Gln Glu Val Cys Lys Asn Tyr
 1085 1090 1095

Ala Glu Ala Lys Asp Val Phe Leu Gly Thr Phe Leu Tyr Glu Tyr
 1100 1105 1110

Ser Arg Arg His Pro Asp Tyr Ser Val Ser Leu Leu Leu Arg Leu
 1115 1120 1125

Ala Lys Lys Tyr Glu Ala Thr Leu Glu Lys Cys Cys Ala Glu Ala
 1130 1135 1140

Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln Pro
 1145 1150 1155

Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu
 1160 1165 1170

Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Ile Leu Val
1175 1180 1185

Arg Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val
1190 1195 1200

Glu Ala Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr
1205 1210 1215

Leu Pro Glu Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser
1220 1225 1230

Ala Ile Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val
1235 1240 1245

Ser Glu His Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg
1250 1255 1260

Arg Pro Cys Phe Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro
1265 1270 1275

Lys Glu Phe Lys Ala Glu Thr Phe Thr Phe His Ser Asp Ile Cys
1280 1285 1290

Thr Leu Pro Glu Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu
1295 1300 1305

Ala Glu Leu Val Lys His Lys Pro Lys Ala Thr Ala Glu Gln Leu
1310 1315 1320

Lys Thr Val Met Asp Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys
1325 1330 1335

Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr Glu Gly Pro Asn
1340 1345 1350

Leu Val Thr Arg Cys Lys Asp Ala Leu Ala Gly Gly Gly Gly Ser
1355 1360 1365

Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys

1370

1375

1380

Gly Leu Pro Gly Ser His Gly Thr Val Ile Glu Ser Leu Glu Ser
1385 1390 1395

Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu Lys
1400 1405 1410

Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly Asp
1415 1420 1425

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu
1430 1435 1440

Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser
1445 1450 1455

Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys
1460 1465 1470

Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn
1475 1480 1485

Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val
1490 1495 1500

Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg
1505 1510 1515

Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu
1520 1525 1530

Pro Gly Ser Glu Ala His Lys Ser Glu Ile Ala His Arg Tyr Asn
1535 1540 1545

Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala Phe
1550 1555 1560

Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu
1565 1570 1575

Val	Gln	Glu	Val	Thr	Asp	Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu
1580						1585					1590			
Ser	Ala	Ala	Asn	Cys	Asp	Lys	Ser	Leu	His	Thr	Leu	Phe	Gly	Asp
1595						1600					1605			
Lys	Leu	Cys	Ala	Ile	Pro	Asn	Leu	Arg	Glu	Asn	Tyr	Gly	Glu	Leu
1610						1615					1620			
Ala	Asp	Cys	Cys	Thr	Lys	Gln	Glu	Pro	Glu	Arg	Asn	Glu	Cys	Phe
1625						1630					1635			
Leu	Gln	His	Lys	Asp	Asp	Asn	Pro	Ser	Leu	Pro	Pro	Phe	Glu	Arg
1640						1645					1650			
Pro	Glu	Ala	Glu	Ala	Met	Cys	Thr	Ser	Phe	Lys	Glu	Asn	Pro	Thr
1655						1660					1665			
Thr	Phe	Met	Gly	His	Tyr	Leu	His	Glu	Val	Ala	Arg	Arg	His	Pro
1670						1675					1680			
Tyr	Phe	Tyr	Ala	Pro	Glu	Leu	Leu	Tyr	Tyr	Ala	Glu	Gln	Tyr	Asn
1685						1690					1695			
Glu	Ile	Leu	Thr	Gln	Cys	Cys	Ala	Glu	Ala	Asp	Lys	Glu	Ser	Cys
1700						1705					1710			
Leu	Thr	Pro	Lys	Leu	Asp	Gly	Val	Lys	Glu	Lys	Ala	Leu	Val	Ser
1715						1720					1725			
Ser	Val	Arg	Gln	Arg	Met	Lys	Cys	Ser	Ser	Met	Gln	Lys	Phe	Gly
1730						1735					1740			
Glu	Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Thr
1745						1750					1755			
Phe	Pro	Asn	Ala	Asp	Phe	Ala	Glu	Ile	Thr	Lys	Leu	Ala	Thr	Asp
1760						1765					1770			
Leu	Thr	Lys	Val	Asn	Lys	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu

1775	1780	1785
Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys Tyr Met Cys Glu Asn 1790 1795 1800		
Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro 1805 1810 1815		
Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr 1820 1825 1830		
Met Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp 1835 1840 1845		
Gln Glu Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu 1850 1855 1860		
Gly Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr Ser 1865 1870 1875		
Val Ser Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu 1880 1885 1890		
Glu Lys Cys Cys Ala Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr 1895 1900 1905		
Val Leu Ala Glu Phe Gln Pro Leu Val Glu Glu Pro Lys Asn Leu 1910 1915 1920		
Val Lys Thr Asn Cys Asp Leu Tyr Glu Lys Leu Gly Glu Tyr Gly 1925 1930 1935		
Phe Gln Asn Ala Ile Leu Val Arg Tyr Thr Gln Lys Ala Pro Gln 1940 1945 1950		
Val Ser Thr Pro Thr Leu Val Glu Ala Ala Arg Asn Leu Gly Arg 1955 1960 1965		
Val Gly Thr Lys Cys Cys Thr Leu Pro Glu Asp Gln Arg Leu Pro 1970 1975 1980		

Cys Val Glu Asp Tyr Leu Ser Ala Ile Leu Asn Arg Val Cys Leu
1985 1990 1995

Leu His Glu Lys Thr Pro Val Ser Glu His Val Thr Lys Cys Cys
2000 2005 2010

Ser Gly Ser Leu Val Glu Arg Arg Pro Cys Phe Ser Ala Leu Thr
2015 2020 2025

Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala Glu Thr Phe
2030 2035 2040

Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu Lys Glu Lys Gln
2045 2050 2055

Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His Lys Pro
2060 2065 2070

Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp Phe Ala
2075 2080 2085

Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys
2090 2095 2100

Phe Ser Thr Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala
2105 2110 2115

Leu Ala His His His His His His Glu Pro Glu Ala
2120 2125 2130

<210> 110

<211> 703

<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys Gly Gly Gly
275 280 285

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Gly
420 425 430

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

Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn
450 455 460

Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser
465 470 475 480

Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser
485 490 495

Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser
500 505 510

Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu
515 520 525

Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg
530 535 540

Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg
545 550 555 560

Ser Arg Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
565 570 575

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
580 585 590

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

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
610 615 620

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
660 665 670

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
675 680 685

Val Thr Val Ser Ser His His His His His His Glu Pro Glu Ala
690 695 700

<210> 111

<211> 832

<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 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 His Gly Thr Val Ile Glu Ser Leu
145 150 155 160

Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu Glu
165 170 175

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

Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu Phe
195 200 205

Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val Ile
210 215 220

Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys Lys
225 230 235 240

Asp Ala Phe Met Ser Ile Ala Lys Phe Glu Val Asn Asn Pro Gln Val
245 250 255

Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu Leu
260 265 270

Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys 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 Ser
 405 410 415

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

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

Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn
 450 455 460

Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser
 465 470 475 480

Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser
 485 490 495

Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser
 500 505 510

Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe Glu
 515 520 525

Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg
 530 535 540

Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg
 545 550 555 560

Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
565 570 575

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
580 585 590

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

Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
610 615 620

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

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr
660 665 670

Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu
675 680 685

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
690 695 700

Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala
705 710 715 720

Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr
725 730 735

Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro Gly Lys Gln
740 745 750

Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser Thr Asn Tyr Ala
755 760 765

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn

770

775

780

Thr Val Tyr Leu Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val
 785 790 795 800

Tyr Val Cys Asn Arg Asn Phe Asp Arg Ile Tyr Trp Gly Gln Gly Thr
 805 810 815

Gln Val Thr Val Ser Ser His His His His His Glu Pro Glu Ala
 820 825 830

<210> 112

<211> 832

<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 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 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 His Gly Thr Val Ile Glu Ser
275 280 285

Leu Glu Ser Leu Asn Asn Tyr Phe Asn Ser Ser Gly Ile Asp Val Glu
290 295 300

Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg Asn Trp Gln Lys Asp Gly
305 310 315 320

Asp Met Lys Ile Leu Gln Ser Gln Ile Ile Ser Phe Tyr Leu Arg Leu
325 330 335

Phe Glu Val Leu Lys Asp Asn Gln Ala Ile Ser Asn Asn Ile Ser Val
340 345 350

Ile Glu Ser His Leu Ile Thr Thr Phe Phe Ser Asn Ser Lys Ala Lys
355 360 365

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

Val Gln Arg Gln Ala Phe Asn Glu Leu Ile Arg Val Val His Gln Leu
385 390 395 400

Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys Arg Ser Arg Cys 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

Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser His
545 550 555 560

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

Ser Gly Ile Asp Val Glu Glu Lys Ser Leu Phe Leu Asp Ile Trp Arg
580 585 590

Asn Trp Gln Lys Asp Gly Asp Met Lys Ile Leu Gln Ser Gln Ile Ile
595 600 605

Ser Phe Tyr Leu Arg Leu Phe Glu Val Leu Lys Asp Asn Gln Ala Ile
610 615 620

Ser Asn Asn Ile Ser Val Ile Glu Ser His Leu Ile Thr Thr Phe Phe
625 630 635 640

Ser Asn Ser Lys Ala Lys Lys Asp Ala Phe Met Ser Ile Ala Lys Phe
645 650 655

Glu Val Asn Asn Pro Gln Val Gln Arg Gln Ala Phe Asn Glu Leu Ile
660 665 670

Arg Val Val His Gln Leu Leu Pro Glu Ser Ser Leu Arg Lys Arg Lys
675 680 685

Arg Ser Arg Cys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu
690 695 700

Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
705 710 715 720

Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
725 730 735

Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
740 745 750

Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala
755 760 765

Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
770 775 780

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
785 790 795 800

Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr
805 810 815

Leu Val Thr Val Ser Ser His His His His His His Glu Pro Glu Ala
820 825 830

<210> 113

<211> 549

<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 Arg Val Ile Pro Val Ser Gly Pro Ala Arg
20 25 30

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

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

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

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

Glu Thr Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr

100

105

110

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

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

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

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

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

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

Met Gly Tyr Leu Ser Ser Ala Ser Gly Gly Pro Gly Pro Ala Gly Met
 210 215 220

Lys Gly Leu Pro Gly Ser Met Trp Glu Leu Glu Lys Asp Val Tyr Val
 225 230 235 240

Val Glu Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr Val Asn Leu
 245 250 255

Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 260 265 270

Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr Val Lys
 275 280 285

Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Thr
 290 295 300

Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly Ile Trp
 305 310 315 320

Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu Lys Cys
325 330 335

Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu Val Gln
340 345 350

Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser Pro
355 360 365

Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser Ala Glu Lys
370 375 380

Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser Cys Gln
385 390 395 400

Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu
405 410 415

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

Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln
435 440 445

Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro
450 455 460

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

Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu Gly Cys
485 490 495

Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr Glu Val Gln
500 505 510

Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr Tyr Asn
515 520 525

Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg Ser His

530

535

540

His His His His His
545

<210> 114

<211> 579

<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 Arg Val Ile Pro Val Ser Gly Pro Ala Arg
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Met Gly Tyr Leu Ser Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser Gly Gly Gly Gly Ser Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
225 230 235 240

Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
245 250 255

Gly Gly Gly Ser Met Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu
260 265 270

Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr Val Asn Leu Thr Cys
275 280 285

Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Arg His
290 295 300

Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr Val Lys Glu Phe
305 310 315 320

Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Thr Leu Ser
325 330 335

His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly Ile Trp Ser Thr
340 345 350

Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu Lys Cys Glu Ala
355 360 365

Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu Val Gln Arg Asn
370 375 380

Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser Ser Pro Asp Ser
385 390 395 400

Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser Ala Glu Lys Val Thr
405 410 415

Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser Cys Gln Glu Asp
420 425 430

Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu Ala Leu
435 440 445

Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser Thr Ser Phe Phe
450 455 460

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

Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Ser
485 490 495

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe Phe Val Arg Ile
500 505 510

Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu Gly Cys Asn Gln
515 520 525

Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr Glu Val Gln Cys Lys
530 535 540

Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr Tyr Asn Ser Ser
545 550 555 560

Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg Ser His His His
565 570 575

His His His

<210> 115

<211> 809

<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 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 Met Trp Glu Leu Glu Lys Asp Val
145 150 155 160

Tyr Val Val Glu Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr Val
165 170 175

Asn Leu Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser
180 185 190

Asp Gln Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr
195 200 205

Val Lys Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly
210 215 220

Glu Thr Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly
225 230 235 240

Ile Trp Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu
245 250 255

Lys Cys Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu
260 265 270

Val Gln Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser
275 280 285

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

Glu Lys Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser
305 310 315 320

Cys Gln Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile
325 330 335

Glu Leu Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser
340 345 350

Thr Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
355 360 365

Leu Gln Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu

370

375

380

Tyr Pro Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe
 385 390 395 400

Phe Val Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu
 405 410 415

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

Val Gln Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr
 435 440 445

Tyr Asn Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg
 450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 465 470 475 480

Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu Ser Gln Ser Arg
 485 490 495

Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu Lys
 500 505 510

Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp Ile
 515 520 525

Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu Leu
 530 535 540

His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr Thr
 545 550 555 560

Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr Leu
 565 570 575

Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu Phe
 580 585 590

Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile Ile
595 600 605

Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu Leu Met Gln Ser Leu
610 615 620

Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu Ala
625 630 635 640

Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala Phe
645 650 655

Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser Ser
660 665 670

Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
675 680 685

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
690 695 700

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
705 710 715 720

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
725 730 735

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
740 745 750

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
755 760 765

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
770 775 780

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
785 790 795 800

Val Ser Ser His His His His His His

<210> 116
 <211> 938
 <212> PRT
 <213> Artificial Sequence

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

<400> 116
 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 Met Trp Glu Leu Glu Lys Asp
275 280 285

Val Tyr Val Val Glu Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr
290 295 300

Val Asn Leu Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr
305 310 315 320

Ser Asp Gln Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile
325 330 335

Thr Val Lys Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly
340 345 350

Gly Glu Thr Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn
355 360 365

Gly Ile Trp Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe
370 375 380

Leu Lys Cys Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp
385 390 395 400

Leu Val Gln Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser
405 410 415

Ser Ser Pro Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser
420 425 430

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

Ser Cys Gln Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro
450 455 460

Ile Glu Leu Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr
465 470 475 480

Ser Thr Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
485 490 495

Asn Leu Gln Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp
500 505 510

Glu Tyr Pro Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys
515 520 525

Phe Phe Val Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu
530 535 540

Glu Gly Cys Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr
545 550 555 560

Glu Val Gln Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg
565 570 575

Tyr Tyr Asn Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val
580 585 590

Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
595 600 605

Ser Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu Ser Gln Ser
610 615 620

Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu
625 630 635 640

Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp
645 650 655

Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu
660 665 670

Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr
675 680 685

Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr
690 695 700

Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu
705 710 715 720

Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile
725 730 735

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

Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu
755 760 765

Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala
770 775 780

Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser
785 790 795 800

Ser Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
805 810 815

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
820 825 830

Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys
835 840 845

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
850 855 860

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
865 870 875 880

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
885 890 895

Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr
900 905 910

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
915 920 925

Thr Val Ser Ser His His His His His His
930 935

<210> 117

<211> 938

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 117

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 Met Trp Glu Leu Glu Lys Asp
275 280 285

Val Tyr Val Val Glu Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr
290 295 300

Val Asn Leu Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr
305 310 315 320

Ser Asp Gln Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile
325 330 335

Thr Val Lys Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly
340 345 350

Gly Glu Thr Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn
355 360 365

Gly Ile Trp Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe
370 375 380

Leu Lys Cys Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp
385 390 395 400

Leu Val Gln Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser
405 410 415

Ser Ser Pro Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser
420 425 430

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

Ser Cys Gln Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro
450 455 460

Ile Glu Leu Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr

465		470		475		480
Ser Thr Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys						
		485		490		495
Asn Leu Gln Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp						
		500		505		510
Glu Tyr Pro Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys						
		515		520		525
Phe Phe Val Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu						
		530		535		540
Glu Gly Cys Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr						
545		550		555		560
Glu Val Gln Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg						
		565		570		575
Tyr Tyr Asn Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val						
		580		585		590
Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly						
		595		600		605
Ser Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu Ser Gln Ser						
		610		615		620
Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu						
625		630		635		640
Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp						
		645		650		655
Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu						
		660		665		670
Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr						
		675		680		685

Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr
690 695 700

Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu
705 710 715 720

Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile
725 730 735

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

Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu
755 760 765

Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala
770 775 780

Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser
785 790 795 800

Ser Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly
805 810 815

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
820 825 830

Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys
835 840 845

Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
850 855 860

Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser
865 870 875 880

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu
885 890 895

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

900

905

910

Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val
 915 920 925

Thr Val Ser Ser His His His His His His
 930 935

<210> 118

<211> 938

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 118

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 Met Trp Glu Leu Glu Lys Asp Val
145 150 155 160

Tyr Val Val Glu Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr Val
165 170 175

Asn Leu Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser
180 185 190

Asp Gln Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr
195 200 205

Val Lys Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly
210 215 220

Glu Thr Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly
225 230 235 240

Ile Trp Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu
245 250 255

Lys Cys Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu
260 265 270

Val Gln Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser
275 280 285

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

Glu Lys Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser
305 310 315 320

Cys Gln Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile
325 330 335

Glu Leu Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser
340 345 350

Thr Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
355 360 365

Leu Gln Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu
370 375 380

Tyr Pro Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe
385 390 395 400

Phe Val Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu
405 410 415

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

Val Gln Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr
435 440 445

Tyr Asn Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg
450 455 460

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu Ser Gln Ser Arg
485 490 495

Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr Ala Arg Glu Lys
500 505 510

Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp His Glu Asp Ile
515 520 525

Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu Pro Leu Glu Leu
530 535 540

His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr Ser Ser Thr Thr
545 550 555 560

Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu Met Met Thr Leu
565 570 575

Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Thr Glu Phe
580 585 590

Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His Gln Gln Ile Ile
595 600 605

Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu Leu Met Gln Ser Leu
610 615 620

Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro Val Gly Glu Ala
625 630 635 640

Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu Leu His Ala Phe
645 650 655

Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly Tyr Leu Ser Ser
660 665 670

Ala Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser
675 680 685

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
690 695 700

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
705 710 715 720

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
725 730 735

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val
740 745 750

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
755 760 765

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
770 775 780

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
785 790 795 800

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
805 810 815

Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
820 825 830

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ile Phe Ser
835 840 845

Ile Asp Ile Met Ser Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu
850 855 860

Leu Val Ala Arg Ile Thr Arg Gly Gly Thr Ile Ser Tyr Asp Asp Ser
865 870 875 880

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
885 890 895

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Gly Val Tyr Tyr
900 905 910

Cys Asn Ala Leu Tyr Gly Thr Asp Tyr Trp Gly Lys Gly Thr Gln Val
915 920 925

Thr Val Ser Ser His His His His His His
930 935

<210> 119

<211> 962

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 119

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 Ile Trp Glu Leu Lys Lys Asp Val Tyr Val	20	25	30
Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu	35	40	45
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln	50	55	60
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	65	70	75
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val	85	90	95
Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp	100	105	110
Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe	115	120	125
Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	130	135	140
Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg	145	150	155
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser	165	170	175
Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu	180	185	190
Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile	195	200	205
Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr	210	215	220

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro Ala
340 345 350

Arg Cys Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met
355 360 365

Val Lys Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu
370 375 380

Asp Ile Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys
385 390 395 400

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

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

Thr Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu

435

440

445

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

His Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile
 465 470 475 480

Asp Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln
 485 490 495

Lys Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu
 500 505 510

Cys Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg
 515 520 525

Val Met Gly Tyr Leu Ser Ser Ala Gly Gly Gly Ser Gly Gly Gly
 530 535 540

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 565 570 575

Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser
 580 585 590

Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser
 595 600 605

Asn Ile Gly Ser Asn Thr Val Lys Trp Tyr Gln Gln Leu Pro Gly Thr
 610 615 620

Ala Pro Lys Leu Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val
 625 630 635 640

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

Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
660 665 670

Tyr Asp Arg Tyr Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys
675 680 685

Val Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
690 695 700

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
705 710 715 720

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
725 730 735

Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
740 745 750

Glu Trp Val Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
755 760 765

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
770 775 780

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
785 790 795 800

Tyr Tyr Cys Lys Thr His Gly Ser His Asp Asn Trp Gly Gln Gly Thr
805 810 815

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
820 825 830

Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
835 840 845

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
850 855 860

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys

865 870 875 880

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
 885 890 895

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
 900 905 910

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
 915 920 925

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
 930 935 940

Gly Thr Leu Val Thr Val Ser Ser His His His His His His Glu Pro
945 950 955 960

Glu Ala

<210> 120

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 120

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 Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro Ala
340 345 350

Arg Cys Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met
355 360 365

Val Lys Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu
370 375 380

Asp Ile Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys
385 390 395 400

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

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

Thr Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu
435 440 445

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

His Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile
465 470 475 480

Asp Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln
485 490 495

Lys Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu
500 505 510

Cys Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg
515 520 525

Val Met Gly Tyr Leu Ser Ser Ala Ser Gly Gly Pro Gly Pro Ala Gly
530 535 540

Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
545 550 555 560

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
565 570 575

Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser
580 585 590

Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser
595 600 605

Asn Ile Gly Ser Asn Thr Val Lys Trp Tyr Gln Gln Leu Pro Gly Thr
610 615 620

Ala Pro Lys Leu Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val
625 630 635 640

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

Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
660 665 670

Tyr Asp Arg Tyr Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys
675 680 685

Val Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
690 695 700

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
705 710 715 720

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
725 730 735

Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
740 745 750

Glu Trp Val Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
755 760 765

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
770 775 780

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
785 790 795 800

Tyr Tyr Cys Lys Thr His Gly Ser His Asp Asn Trp Gly Gln Gly Thr
805 810 815

Met Val Thr Val Ser Ser His His His His His Glu Pro Glu Ala
820 825 830

<210> 121
<211> 1091
<212> PRT
<213> Artificial Sequence

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

<400> 121
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 Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
20 25 30

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

Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln

50

55

60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro Ala
340 345 350

Arg Cys Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met
355 360 365

Val Lys Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu
370 375 380

Asp Ile Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys
385 390 395 400

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

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

Thr Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu
435 440 445

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

His Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile
465 470 475 480

Asp Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln

485

490

495

Lys Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu
 500 505 510

Cys Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg
 515 520 525

Val Met Gly Tyr Leu Ser Ser Ala Ser Gly Gly Pro Gly Pro Ala Gly
 530 535 540

Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 545 550 555 560

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 565 570 575

Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser
 580 585 590

Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser
 595 600 605

Asn Ile Gly Ser Asn Thr Val Lys Trp Tyr Gln Gln Leu Pro Gly Thr
 610 615 620

Ala Pro Lys Leu Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val
 625 630 635 640

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

Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
 660 665 670

Tyr Asp Arg Tyr Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys
 675 680 685

Val Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 690 695 700

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
705 710 715 720

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
725 730 735

Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
740 745 750

Glu Trp Val Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
755 760 765

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
770 775 780

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
785 790 795 800

Tyr Tyr Cys Lys Thr His Gly Ser His Asp Asn Trp Gly Gln Gly Thr
805 810 815

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
820 825 830

Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
835 840 845

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
850 855 860

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
865 870 875 880

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
885 890 895

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
900 905 910

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

915

920

925

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
930 935 940

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
945 950 955 960

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Gly
965 970 975

Gly Leu Ala Gln Ala Gly Gly Ser Leu Ser Leu Ser Cys Ala Ala Ser
980 985 990

Gly Phe Thr Val Ser Asn Ser Val Met Ala Trp Tyr Arg Gln Thr Pro
995 1000 1005

Gly Lys Gln Arg Glu Phe Val Ala Ile Ile Asn Ser Val Gly Ser
1010 1015 1020

Thr Asn Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
1025 1030 1035

Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn Asn Leu Lys
1040 1045 1050

Pro Glu Asp Thr Ala Val Tyr Val Cys Asn Arg Asn Phe Asp Arg
1055 1060 1065

Ile Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser His His
1070 1075 1080

His His His His Glu Pro Glu Ala
1085 1090

<210> 122

<211> 1091

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 122

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 Ile Trp Glu Leu Lys Lys Asp Val Tyr
145 150 155 160

Val Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val
165 170 175

Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp
180 185 190

Gln Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val
195 200 205

Lys Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu
210 215 220

Val Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile
225 230 235 240

Trp Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr
245 250 255

Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp
260 265 270

Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser
275 280 285

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

Ser Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val
305 310 315 320

Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
325 330 335

Ile Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr
340 345 350

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
355 360 365

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser
370 375 380

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
385 390 395 400

Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp
405 410 415

Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn
420 425 430

Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp
435 440 445

Ser Glu Trp Ala Ser Val Pro Cys Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Gly Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro
465 470 475 480

Ala Arg Cys Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp
485 490 495

Met Val Lys Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala
500 505 510

Glu Asp Ile Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu
515 520 525

Lys Thr Cys Leu Pro Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala
530 535 540

Thr Arg Glu Thr Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln
545 550 555 560

Lys Thr Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp
565 570 575

Leu Lys Met Tyr Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln
580 585 590

Asn His Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala
595 600 605

Ile Asp Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg
610 615 620

Gln Lys Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys
625 630 635 640

Leu Cys Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn
645 650 655

Arg Val Met Gly Tyr Leu Ser Ser Ala Ser Gly Gly Pro Gly Pro Ala
660 665 670

Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
675 680 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
690 695 700

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
705 710 715 720

Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Arg
725 730 735

Ser Asn Ile Gly Ser Asn Thr Val Lys Trp Tyr Gln Gln Leu Pro Gly
740 745 750

Thr Ala Pro Lys Leu Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly
755 760 765

Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
770 775 780

Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
785 790 795 800

Ser Tyr Asp Arg Tyr Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr
805 810 815

Lys Val Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
820 825 830

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
835 840 845

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
850 855 860

Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
865 870 875 880

Leu Glu Trp Val Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr
885 890 895

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
900 905 910

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
915 920 925

Val Tyr Tyr Cys Lys Thr His Gly Ser His Asp Asn Trp Gly Gln Gly
930 935 940

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
945 950 955 960

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
965 970 975

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
980 985 990

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly
995 1000 1005

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
1010 1015 1020

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
1025 1030 1035

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
1040 1045 1050

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu
1055 1060 1065

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His
1070 1075 1080

His His His His Glu Pro Glu Ala
1085 1090

<210> 123
<211> 1091
<212> PRT
<213> Artificial Sequence

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

<400> 123
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 Ile Trp Glu Leu Lys Lys Asp Val Tyr
 145 150 155 160

Val Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val
 165 170 175

Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp
 180 185 190

Gln Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val
 195 200 205

Lys Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu
 210 215 220

Val Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile
 225 230 235 240

Trp Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr
 245 250 255

Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp
 260 265 270

Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser
 275 280 285

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

Ser Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val
 305 310 315 320

Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 325 330 335

Ile Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr
 340 345 350

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
355 360 365

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser
370 375 380

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
385 390 395 400

Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp
405 410 415

Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn
420 425 430

Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp
435 440 445

Ser Glu Trp Ala Ser Val Pro Cys Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Gly Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro
465 470 475 480

Ala Arg Cys Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp
485 490 495

Met Val Lys Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala
500 505 510

Glu Asp Ile Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu
515 520 525

Lys Thr Cys Leu Pro Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala
530 535 540

Thr Arg Glu Thr Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln
545 550 555 560

Lys Thr Ser Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp

565

570

575

Leu Lys Met Tyr Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln
 580 585 590

Asn His Asn His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala
 595 600 605

Ile Asp Glu Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg
 610 615 620

Gln Lys Pro Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys
 625 630 635 640

Leu Cys Ile Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn
 645 650 655

Arg Val Met Gly Tyr Leu Ser Ser Ala Ser Gly Gly Pro Gly Pro Ala
 660 665 670

Gly Met Lys Gly Leu Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 675 680 685

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 690 695 700

Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
 705 710 715 720

Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Arg
 725 730 735

Ser Asn Ile Gly Ser Asn Thr Val Lys Trp Tyr Gln Gln Leu Pro Gly
 740 745 750

Thr Ala Pro Lys Leu Leu Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly
 755 760 765

Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
 770 775 780

Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
785 790 795 800

Ser Tyr Asp Arg Tyr Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr
805 810 815

Lys Val Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
820 825 830

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
835 840 845

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
850 855 860

Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
865 870 875 880

Leu Glu Trp Val Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr
885 890 895

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
900 905 910

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
915 920 925

Val Tyr Tyr Cys Lys Thr His Gly Ser His Asp Asn Trp Gly Gln Gly
930 935 940

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
945 950 955 960

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
965 970 975

Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
980 985 990

Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly

995

1000

1005

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp
 1010 1015 1020

Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 1025 1030 1035

Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 1040 1045 1050

Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu
 1055 1060 1065

Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His
 1070 1075 1080

His His His His Glu Pro Glu Ala
 1085 1090

<210> 124

<211> 674

<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 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> 125

<211> 674

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 125

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		635		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> 126
 <211> 425
 <212> PRT
 <213> Artificial Sequence

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

<400> 126
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> 127

<211> 425

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 127

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> 128
<211> 555
<212> PRT
<213> Artificial Sequence

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

<400> 128
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> 129

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 129

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> 130

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 130

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> 131

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 131

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> 132

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 132

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> 133

<211> 689

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 133

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 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> 134

<211> 545

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 134

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> 135
<211> 575
<212> PRT
<213> Artificial Sequence

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

<400> 135
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 His His His His His His
565 570 575

<210> 136

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 136

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 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> 137

<211> 806

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 137

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	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
580 585 590

Ile Tyr Ser Ala Ser Phe Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser
595 600 605

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
610 615 620

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Thr Tyr Pro
625 630 635 640

Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Gly Gly Pro
645 650 655

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Ala Pro Thr Ser Ser

660

665

670

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
675 680 685

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

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
705 710 715 720

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
725 730 735

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
740 745 750

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
755 760 765

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
770 775 780

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> 138

<211> 676

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 138

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> 139
<211> 421
<212> PRT
<213> Artificial Sequence

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

<400> 139
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> 140

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 140

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> 141
<211> 550
<212> PRT
<213> Artificial Sequence

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

<400> 141
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 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 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> 142

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 142

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> 143
<211> 290
<212> PRT
<213> Artificial Sequence

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

<400> 143
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 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> 144

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 144

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> 145
<211> 689
<212> PRT
<213> Artificial Sequence

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

<400> 145
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> 146

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 146

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> 147

<211> 674

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 147

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> 148
<211> 704
<212> PRT
<213> Artificial Sequence

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

<400> 148
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
690 695 700

<210> 149

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 149

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> 150

<211> 689
<212> PRT
<213> Artificial Sequence

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

<400> 150
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> 151

<211> 700

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 151

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> 152

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 152

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> 153

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 153

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> 154

<211> 279
<212> PRT
<213> Artificial Sequence

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

<400> 154
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> 155

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 155

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 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

<210> 156

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 156

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> 157
<211> 295
<212> PRT
<213> Artificial Sequence

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

<400> 157
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> 158

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 158

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> 159

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 159

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> 160

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 160

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> 161
<211> 708
<212> PRT
<213> Artificial Sequence

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

<400> 161
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> 162
<211> 708
<212> PRT
<213> Artificial Sequence

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

<400> 162
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> 163
<211> 708
<212> PRT
<213> Artificial Sequence

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

<400> 163
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> 164
<211> 161
<212> PRT
<213> Artificial Sequence

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

<400> 164
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> 165

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 165

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
420 425 430 435

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> 166

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 166

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> 167
<211> 708
<212> PRT
<213> Artificial Sequence

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

<400> 167
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> 168

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 168

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 Cys Asp Leu Pro Gln Thr His Asn
145 150 155 160

Leu Arg Asn Lys Arg Ala Leu Thr Leu Val Gln Met Arg Arg Leu
165 170 175

Ser Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln
180 185 190

Glu Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val
195 200 205

Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp
210 215 220

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp
225 230 235 240

Leu His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val
245 250 255

Gly Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val
260 265 270

Arg Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His
275 280 285

Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu
290 295 300

Ser Ser Ser Ala Asn Val Ser Gly Gly Pro Gly Pro Ala Gly Met Lys
305 310 315 320

Gly Leu Pro Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
325 330 335

Val Gln Pro Gly Asn Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
340 345 350

Thr Phe Ser Lys Phe Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys
355 360 365

Gly Leu Glu Trp Val Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu
370 375 380

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
385 390 395 400

Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr
405 410 415

Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln
420 425 430

Gly Thr Leu Val Thr Val Ser Ser His His His His His His Glu Pro
435 440 445

Glu Ala
450

<210> 169
<211> 198
<212> PRT
<213> Artificial Sequence

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

<400> 169
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 Cys Asp Leu Pro Gln Thr His Asn Leu Arg
20 25 30

Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser Pro
35 40 45

Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu Lys
50 55 60

Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu Ser
65 70 75 80

Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser Ser
85 90 95

Ala Ala Trp Asn Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu His
100 105 110

Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly Val
115 120 125

Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg Lys
130 135 140

Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser Pro
145 150 155 160

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

Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys His His His His
180 185 190

His His Glu Pro Glu Ala
195

<210> 170
<211> 328
<212> PRT
<213> Artificial Sequence

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

<400> 170
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 Cys Asp Leu Pro Gln Thr His Asn
145 150 155 160

Leu Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu
165 170 175

Ser Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln
180 185 190

Glu Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val
195 200 205

Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp
210 215 220

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp
225 230 235 240

Leu His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val
245 250 255

Gly Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val
260 265 270

Arg Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His
275 280 285

Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu
290 295 300

Ser Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys His His
305 310 315 320

His His His His Glu Pro Glu Ala
325

<210> 171
<211> 328
<212> PRT
<213> Artificial Sequence

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

<400> 171
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 Cys Asp Leu Pro Gln Thr His Asn Leu Arg
20 25 30

Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser Pro
35 40 45

Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu Lys
50 55 60

Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu Ser
65 70 75 80

Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser Ser
85 90 95

Ala Ala Trp Asn Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu His
100 105 110

Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly Val
115 120 125

Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg Lys
130 135 140

Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser Pro
145 150 155 160

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

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

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln Leu Val
195 200 205

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg Leu Ser
210 215 220

Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser Trp Val
225 230 235 240

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Gly
245 250 255

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

Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met Asn Ser
275 280 285

Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly Gly Ser
290 295 300

Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr Val Ser Ser His His
305 310 315 320

His His His His Glu Pro Glu Ala
325

<210> 172

<211> 1396

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 172

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 Ala His Lys Ser Glu Ile Ala His Arg
20 25 30

Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala
35 40 45

Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu
50 55 60

Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

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

Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys
100 105 110

Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
115 120 125

Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
130 135 140

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr
145 150 155 160

Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
165 170 175

Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala
180 185 190

Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys
195 200 205

Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
210 215 220

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

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu
245 250 255

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

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

Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro
290 295 300

Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met
305 310 315 320

Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
325 330 335

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

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

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

Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln
385 390 395 400

Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu
405 410 415

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

Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala
435 440 445

Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu
450 455 460

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

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

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

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

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

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

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

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr
580 585 590

Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala Ser Gly
595 600 605

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Cys Asp Leu
610 615 620

Pro Gln Thr His Asn Leu Arg Asn Lys Arg Ala Leu Thr Leu Leu Val
625 630 635 640

Gln Met Arg Arg Leu Ser Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp
645 650 655

Phe Gly Phe Pro Gln Glu Lys Val Asp Ala Gln Gln Ile Lys Lys Ala
660 665 670

Gln Ala Ile Pro Val Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile
675 680 685

Phe Thr Ser Lys Asp Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp
690 695 700

Ser Phe Cys Asn Asp Leu His Gln Gln Leu Asn Asp Leu Gln Gly Cys
705 710 715 720

Leu Met Gln Gln Val Gly Val Gln Glu Phe Pro Leu Thr Gln Glu Asp
725 730 735

Ala Leu Leu Ala Val Arg Lys Tyr Phe His Arg Ile Thr Val Tyr Leu
740 745 750

Arg Glu Lys Lys His Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu
755 760 765

Val Trp Arg Ala Leu Ser Ser Ser Ala Asn Val Leu Gly Arg Leu Arg
770 775 780

Glu Glu Lys Ser Gly Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro
785 790 795 800

Gly Ser Glu Ala His Lys Ser Glu Ile Ala His Arg Tyr Asn Asp Leu
805 810 815

Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala Phe Ser Gln Tyr
820 825 830

Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu Val Gln Glu Val
835 840 845

Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Ala Asn Cys
850 855 860

Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Ala Ile Pro
865 870 875 880

Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys Cys Thr Lys Gln
885 890 895

Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro
900 905 910

Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala Met Cys Thr Ser
915 920 925

Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr Leu His Glu Val
930 935 940

Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala
945 950 955 960

Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala Glu Ala Asp Lys
965 970 975

Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys Glu Lys Ala Leu
980 985 990

Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser Met Gln Lys Phe
995 1000 1005

Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln
1010 1015 1020

Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu Ala Thr
1025 1030 1035

Asp Leu Thr Lys Val Asn Lys Glu Cys Cys His Gly Asp Leu Leu
1040 1045 1050

Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala Lys Tyr Met Cys Glu
1055 1060 1065

Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys
1070 1075 1080

Pro	Leu	Leu	Lys	Lys	Ala	His	Cys	Leu	Ser	Glu	Val	Glu	His	Asp
1085						1090					1095			
Thr	Met	Pro	Ala	Asp	Leu	Pro	Ala	Ile	Ala	Ala	Asp	Phe	Val	Glu
1100						1105					1110			
Asp	Gln	Glu	Val	Cys	Lys	Asn	Tyr	Ala	Glu	Ala	Lys	Asp	Val	Phe
1115						1120					1125			
Leu	Gly	Thr	Phe	Leu	Tyr	Glu	Tyr	Ser	Arg	Arg	His	Pro	Asp	Tyr
1130						1135					1140			
Ser	Val	Ser	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Lys	Tyr	Glu	Ala	Thr
1145						1150					1155			
Leu	Glu	Lys	Cys	Cys	Ala	Glu	Ala	Asn	Pro	Pro	Ala	Cys	Tyr	Gly
1160						1165					1170			
Thr	Val	Leu	Ala	Glu	Phe	Gln	Pro	Leu	Val	Glu	Glu	Pro	Lys	Asn
1175						1180					1185			
Leu	Val	Lys	Thr	Asn	Cys	Asp	Leu	Tyr	Glu	Lys	Leu	Gly	Glu	Tyr
1190						1195					1200			
Gly	Phe	Gln	Asn	Ala	Ile	Leu	Val	Arg	Tyr	Thr	Gln	Lys	Ala	Pro
1205						1210					1215			
Gln	Val	Ser	Thr	Pro	Thr	Leu	Val	Glu	Ala	Ala	Arg	Asn	Leu	Gly
1220						1225					1230			
Arg	Val	Gly	Thr	Lys	Cys	Cys	Thr	Leu	Pro	Glu	Asp	Gln	Arg	Leu
1235						1240					1245			
Pro	Cys	Val	Glu	Asp	Tyr	Leu	Ser	Ala	Ile	Leu	Asn	Arg	Val	Cys
1250						1255					1260			
Leu	Leu	His	Glu	Lys	Thr	Pro	Val	Ser	Glu	His	Val	Thr	Lys	Cys
1265						1270					1275			
Cys	Ser	Gly	Ser	Leu	Val	Glu	Arg	Arg	Pro	Cys	Phe	Ser	Ala	Leu
1280						1285					1290			

Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala Glu Thr
1295 1300 1305

Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu Lys Glu Lys
1310 1315 1320

Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His Lys
1325 1330 1335

Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp Phe
1340 1345 1350

Ala Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr
1355 1360 1365

Cys Phe Ser Thr Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp
1370 1375 1380

Ala Leu Ala His His His His His His Glu Pro Glu Ala
1385 1390 1395

<210> 173
<211> 797
<212> PRT
<213> Artificial Sequence

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

<400> 173
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 Ala His Lys Ser Glu Ile Ala His Arg
20 25 30

Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly Leu Val Leu Ile Ala
35 40 45

Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp Glu His Ala Lys Leu

50

55

60

Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys Val Ala Asp Glu Ser
65 70 75 80

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

Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly Glu Leu Ala Asp Cys
100 105 110

Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys
115 120 125

Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg Pro Glu Ala Glu Ala
130 135 140

Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr Phe Met Gly His Tyr
145 150 155 160

Leu His Glu Val Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu
165 170 175

Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu Thr Gln Cys Cys Ala
180 185 190

Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys Leu Asp Gly Val Lys
195 200 205

Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg Met Lys Cys Ser Ser
210 215 220

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

Leu Ser Gln Thr Phe Pro Asn Ala Asp Phe Ala Glu Ile Thr Lys Leu
245 250 255

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

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

Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr Cys Cys Asp Lys Pro
290 295 300

Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val Glu His Asp Thr Met
305 310 315 320

Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe Val Glu Asp Gln Glu
325 330 335

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

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

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

Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val Leu Ala Glu Phe Gln
385 390 395 400

Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr Asn Cys Asp Leu
405 410 415

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

Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val Glu Ala
435 440 445

Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu Pro Glu
450 455 460

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

Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu His Val Thr

485

490

495

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

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

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

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

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

Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe Ser Thr
 580 585 590

Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala Ser Gly
 595 600 605

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Cys Asp Leu
 610 615 620

Pro Gln Thr His Asn Leu Arg Asn Lys Arg Ala Leu Thr Leu Leu Val
 625 630 635 640

Gln Met Arg Arg Leu Ser Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp
 645 650 655

Phe Gly Phe Pro Gln Glu Lys Val Asp Ala Gln Gln Ile Lys Lys Ala
 660 665 670

Gln Ala Ile Pro Val Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile
 675 680 685

Phe Thr Ser Lys Asp Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp
 690 695 700

Ser Phe Cys Asn Asp Leu His Gln Gln Leu Asn Asp Leu Gln Gly Cys
705 710 715 720

Leu Met Gln Gln Val Gly Val Gln Glu Phe Pro Leu Thr Gln Glu Asp
725 730 735

Ala Leu Leu Ala Val Arg Lys Tyr Phe His Arg Ile Thr Val Tyr Leu
740 745 750

Arg Glu Lys Lys His Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu
755 760 765

Val Trp Arg Ala Leu Ser Ser Ser Ala Asn Val Leu Gly Arg Leu Arg
770 775 780

Glu Glu Lys His His His His His His Glu Pro Glu Ala
785 790 795

<210> 174
<211> 797
<212> PRT
<213> Artificial Sequence

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

<400> 174
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 Cys Asp Leu Pro Gln Thr His Asn Leu Arg
20 25 30

Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser Pro
35 40 45

Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu Lys
50 55 60

Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu Ser
65 70 75 80

Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser Ser
85 90 95

Ala Ala Trp Asn Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu His
100 105 110

Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly Val
115 120 125

Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg Lys
130 135 140

Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser Pro
145 150 155 160

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

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

Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Ala His Lys Ser
195 200 205

Glu Ile Ala His Arg Tyr Asn Asp Leu Gly Glu Gln His Phe Lys Gly
210 215 220

Leu Val Leu Ile Ala Phe Ser Gln Tyr Leu Gln Lys Cys Ser Tyr Asp
225 230 235 240

Glu His Ala Lys Leu Val Gln Glu Val Thr Asp Phe Ala Lys Thr Cys
245 250 255

Val Ala Asp Glu Ser Ala Ala Asn Cys Asp Lys Ser Leu His Thr Leu
260 265 270

Phe Gly Asp Lys Leu Cys Ala Ile Pro Asn Leu Arg Glu Asn Tyr Gly
275 280 285

Glu Leu Ala Asp Cys Cys Thr Lys Gln Glu Pro Glu Arg Asn Glu Cys
290 295 300

Phe Leu Gln His Lys Asp Asp Asn Pro Ser Leu Pro Pro Phe Glu Arg
305 310 315 320

Pro Glu Ala Glu Ala Met Cys Thr Ser Phe Lys Glu Asn Pro Thr Thr
325 330 335

Phe Met Gly His Tyr Leu His Glu Val Ala Arg Arg His Pro Tyr Phe
340 345 350

Tyr Ala Pro Glu Leu Leu Tyr Tyr Ala Glu Gln Tyr Asn Glu Ile Leu
355 360 365

Thr Gln Cys Cys Ala Glu Ala Asp Lys Glu Ser Cys Leu Thr Pro Lys
370 375 380

Leu Asp Gly Val Lys Glu Lys Ala Leu Val Ser Ser Val Arg Gln Arg
385 390 395 400

Met Lys Cys Ser Ser Met Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala
405 410 415

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

Glu Ile Thr Lys Leu Ala Thr Asp Leu Thr Lys Val Asn Lys Glu Cys
435 440 445

Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Glu Leu Ala
450 455 460

Lys Tyr Met Cys Glu Asn Gln Ala Thr Ile Ser Ser Lys Leu Gln Thr
465 470 475 480

Cys Cys Asp Lys Pro Leu Leu Lys Lys Ala His Cys Leu Ser Glu Val
485 490 495

Glu His Asp Thr Met Pro Ala Asp Leu Pro Ala Ile Ala Ala Asp Phe
500 505 510

Val Glu Asp Gln Glu Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val
515 520 525

Phe Leu Gly Thr Phe Leu Tyr Glu Tyr Ser Arg Arg His Pro Asp Tyr
530 535 540

Ser Val Ser Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala Thr Leu
545 550 555 560

Glu Lys Cys Cys Ala Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr Val
565 570 575

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

Thr Asn Cys Asp Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn
595 600 605

Ala Ile Leu Val Arg Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro
610 615 620

Thr Leu Val Glu Ala Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys
625 630 635 640

Cys Thr Leu Pro Glu Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu
645 650 655

Ser Ala Ile Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val
660 665 670

Ser Glu His Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg
675 680 685

Pro Cys Phe Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu
690 695 700

Phe Lys Ala Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro
705 710 715 720

Glu Lys Glu Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val
725 730 735

Lys His Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp
740 745 750

Asp Phe Ala Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp
755 760 765

Thr Cys Phe Ser Thr Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp
770 775 780

Ala Leu Ala His His His His His His Glu Pro Glu Ala
785 790 795

<210> 175
<211> 587
<212> PRT
<213> Artificial Sequence

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

<400> 175
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 Cys Asp Leu Pro Gln Thr His
275 280 285

Asn Leu Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg
290 295 300

Leu Ser Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro

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

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln
530 535 540

Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile
545 550 555 560

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

Ser His His His His His His Glu Pro Glu Ala
580 585

<210> 176

<211> 587

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 176

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 Cys Asp Leu Pro Gln Thr His Asn
145 150 155 160

Leu Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu
165 170 175

Ser Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln
180 185 190

Glu Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val
195 200 205

Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp
210 215 220

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp
225 230 235 240

Leu His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val
245 250 255

Gly Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val
260 265 270

Arg Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His
275 280 285

Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu
290 295 300

Ser Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys Ser Gly
305 310 315 320

Gly Pro Gly Pro Ala Gly Met Lys Gly Leu Pro Gly Ser Glu Val Gln
325 330 335

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
340 345 350

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
355 360 365

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

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
385 390 395 400

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
405 410 415

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
420 425 430

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
450 455 460

Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Ala Gln Ala Gly Gly Ser
465 470 475 480

Leu Ser Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Asn Ser Val
485 490 495

Met Ala Trp Tyr Arg Gln Thr Pro Gly Lys Gln Arg Glu Phe Val Ala
500 505 510

Ile Ile Asn Ser Val Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys Gly
515 520 525

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln
530 535 540

Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Val Tyr Val Cys Asn Arg
545 550 555 560

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

Ser His His His His His His Glu Pro Glu Ala
580 585

<210> 177

<211> 458

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 177

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 Cys Asp Leu Pro Gln Thr His Asn
 145 150 155 160

Leu Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu
 165 170 175

Ser Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln
 180 185 190

Glu Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val
 195 200 205

Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp
 210 215 220

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Ser Phe Cys Asn Asp
 225 230 235 240

Leu His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val
 245 250 255

Gly Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val
 260 265 270

Arg Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His
 275 280 285

Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu
 290 295 300

Ser Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys Gly Gly
 305 310 315 320

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 325 330 335

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn Ser Leu Arg
340 345 350

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe Gly Met Ser
355 360 365

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

Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Glu Ser Val Lys Gly Arg
385 390 395 400

Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr Leu Gln Met
405 410 415

Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ile Gly
420 425 430

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

His His His His His His Glu Pro Glu Ala
450 455

<210> 178

<211> 579

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 178

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> 179

<211> 579

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 179

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 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

495

Pro Glu Ala

$\langle 400 \rangle$ 180

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> 181

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 181

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> 182
<211> 613
<212> PRT
<213> Artificial Sequence

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

<400> 182
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> 183

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 183

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> 184

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 184

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> 185

<211> 398

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 185

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> 186

<211> 518
<212> PRT
<213> Artificial Sequence

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

<400> 186
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> 187

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 187

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 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> 188
<211> 382
<212> PRT
<213> Artificial Sequence

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

<400> 188
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> 189

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 189

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 Gly Ser Gly 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> 190

<211> 509

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 190

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 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> 191

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 191

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> 192

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 192

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 Ser Val Leu Thr Gln Pro Pro Ser Val
20 25 30

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

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

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

Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
85 90 95

Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
100 105 110

Ser Tyr Asp Arg Tyr Thr His Pro Ala Leu Leu Phe Gly Thr Gly Thr
115 120 125

Lys Val Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

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

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

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

Leu Glu Trp Val Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr
195 200 205

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

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

Val Tyr Tyr Cys Lys Thr His Gly Ser His Asp Asn Trp Gly Gln Gly
245 250 255

Thr Met Val Thr Val Ser Ser His His His His His His
260 265

<210> 193
<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> 193
Leu Pro Xaa Thr Gly
1 5

<210> 194
<211> 124
<212> PRT
<213> Artificial Sequence

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

<400> 194
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

<210> 195

<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> 195

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> 196
<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> 196
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> 197
<211> 7
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown: protease-cleavable sequence"

<400> 197
Gly Pro Leu Gly Val Arg Gly
1 5

<210> 198
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown: protease-cleavable sequence"

<400> 198
Ile Pro Val Ser Leu Arg Ser Gly
1 5

<210> 199
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
protease-cleavable sequence"

<400> 199
Val Pro Leu Ser Leu Tyr Ser Gly
1 5

<210> 200
<211> 10
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
protease-cleavable sequence"

<400> 200
Ser Gly Glu Ser Pro Ala Tyr Tyr Thr Ala
1 5 10

<210> 201
<211> 5
<212> PRT
<213> Artificial Sequence

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

<400> 201
Gly Gly Gly Gly Ser
1 5

<210> 202
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source

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

<400> 202

Gly Ser Gly Ser Gly Ser
1 5

<210> 203

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 203

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

<210> 204

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 204

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

<210> 205

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic 6xHis tag"

<400> 205

His His His His His His
1 5