

SEQUENCE LISTING

<110> NANJING LEGEND BIOTECH CO., LTD.

<120> NEF-CONTAINING T CELLS AND METHODS OF PRODUCING THEREOF

<130> 76142-20020.42

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> PCT/CN2019/125681

<151> 2019-12-16

<150> PCT/CN2019/103041

<151> 2019-08-28

<160> 247

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 29

<212> PRT

<213> Homo sapiens

<400> 1

Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg
1				5				10						15	
Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn			
		20						25							

<210> 2

<211> 28

<212> PRT

<213> Homo sapiens

<400> 2

Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys
1			5					10						15	
Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg				
			20					25							

<210> 3

<211> 29

<212> PRT

<213> Homo sapiens

<400> 3

Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys
1				5				10						15	

Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly Asn
20 25

<210> 4

<211> 29

<212> PRT

<213> Homo sapiens

<400> 4

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
1 5 10 15
Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
20 25

<210> 5

<211> 29

<212> PRT

<213> Homo sapiens

<400> 5

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
1 5 10 15
Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
20 25

<210> 6

<211> 29

<212> PRT

<213> Homo sapiens

<400> 6

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
1 5 10 15
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
20 25

<210> 7

<211> 112

<212> PRT

<213> Homo sapiens

<400> 7

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30
Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45
Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg
65					70					75					80
Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala
			85						90					95	
Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg
			100					105					110		

<210> 8
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 <212> PRT
 <213> Homo sapiens

Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln
1				5				10						15	
Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln			
			20					25							

<210> 9
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 <212> PRT
 <213> Homo sapiens

Asp	Ala	Gly	Asp	Glu	Tyr	Glu	Asp	Glu	Asn	Leu	Tyr	Glu	Gly	Leu	Asn
1				5				10						15	
Leu	Asp	Asp	Cys	Ser	Met	Tyr	Glu	Asp	Ile	Ser	Arg	Gly			
			20					25							

<210> 10
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 <212> PRT
 <213> Homo sapiens

Asp	Ser	Lys	Ala	Gly	Met	Glu	Glu	Asp	His	Thr	Tyr	Glu	Gly	Leu	Asp
1				5				10						15	
Ile	Asp	Gln	Thr	Ala	Thr	Tyr	Glu	Asp	Ile	Val	Thr	Leu			
			20					25							

<210> 11
 <211> 29
 <212> PRT
 <213> Homo sapiens

Ala	Ile	Thr	Ser	Tyr	Glu	Lys	Ser	Asp	Gly	Val	Tyr	Thr	Gly	Leu	Ser
1				5				10						15	
Thr	Arg	Asn	Gln	Glu	Thr	Tyr	Glu	Thr	Leu	Lys	His	Glu			
			20					25							

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12
Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly
1 5 10

<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 13
Gly Gly Ser Gly
1

<210> 14
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Gly Ser
1

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15
Gly Ser Gly Ser Gly Ser
1 5

<210> 16
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
Pro Pro Pro Tyr Gln Pro Leu Gly Gly Gly Gly Ser
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 18
<211> 1
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Gly
1

<210> 19
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15
Lys Gly

<210> 20

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

<220>
<223> Synthetic Construct

<400> 20
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 21
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 22
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly
1 5 10 15
Ser Gly Ser Gly Gly Gly Gly Ser
20

<210> 23
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 23
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly
1 5 10 15
Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
20 25 30
Gly Ser

<210> 24
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 25
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 25
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser
20

<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26
Gly Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 27
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val

1	5	10	15
Glu	Glu Asn Pro Gly Pro		
	20		

<210> 28
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 28
Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15
Glu Asn Pro Gly Pro
20

<210> 29
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 29
Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15
Val Glu Ser Asn Pro Gly Pro
20

<210> 30
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15
Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 31
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 31

ggaagcggag ctactaactt cagcctgctg aagcaggctg gagacgtgga ggagaaccct 60
ggacct 66

<210> 32

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 32

ggcagtggag agggcagagg aagtctgcta acatgcggtg acgtcgagga gaatcctggc 60
cca 63

<210> 33

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 33

ggaagcggac agtgtactaa ttatgctctc ttgaaattgg ctggagatgt tgagagcaac 60
cctggacct 69

<210> 34

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

ggaagcggag tgaaacagac tttgaatttt gaccttctca agttggcggg agacgtggag 60
tccaaccctg gacct 75

<210> 35

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 35

gcccctctcc ctcccccccc cctaacgtta ctggccgaag ccgcttgga taaggccggt 60

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gtgcgtttgt ctatatgtta ttttccacca tattgccgtc ttttggcaat gtgagggccc 120
ggaaacctgg ccctgtcttc ttgacgagca ttcctagggg tctttcccct ctcgccaaag 180
gaatgcaagg tctgttgaat gtcgtgaagg aagcagttcc tctggaagct tcttgaagac 240
aaacaacgtc tgtagcgacc ctttgcaggc agcggaaacc cccacctggc gacaggtgcc 300
tctgcggcca aaagccacgt gtataagata cacctgcaaa ggcggcacaa ccccagtgcc 360
acgttgtgag ttggatagtt gtggaaagag tcaaatggct ctcctcaagc gtattcaaca 420
aggggctgaa ggatgcccag aaggtacccc attgtatggg atctgatctg gggcctcggg 480
gcacatgctt tacatgtgtt tagtcgaggt taaaaaacg tctaggcccc ccgaaccacg 540
gggacgtggg tttcctttga aaaacacgat gataatatgg ccaca 585

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<210> 36

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 36

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Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 1           5           10           15
Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
          20           25           30
Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
      35           40

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<210> 37

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 37

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Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 1           5           10           15
Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
          20           25           30
Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Gly Gly Ser Gly Lys Arg
      35           40           45
Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
      50           55           60
Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
      65           70           75           80
Glu Glu Glu Gly Gly Cys Glu Leu Gly Gly Ser Gly Lys Arg Gly Arg
          85           90           95
Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
          100          105          110
Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
          115          120          125
Glu Gly Gly Cys Glu Leu
      130

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<210> 38
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38
Arg Val Lys Phe Ser Arg Ser Ala Asp Arg Gly Arg Asp Pro Glu Met
1 5 10 15
Gly Gly Lys Gly Ala Leu Pro Pro Arg Gly Gly Ser Gly Arg Val Lys
20 25 30
Phe Ser Arg Ser Ala Asp Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45
Gly Ala Leu Pro Pro Arg
50

<210> 39
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala Tyr Gln Gln
1 5 10 15
Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
20 25 30
Tyr Asp Val Leu Asp Lys Arg Gly Glu Asn Leu Tyr Phe Gln Ser Gly
35 40 45
Gly Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
50 55 60
Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65 70 75 80
Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
85 90 95
Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Gly Gly Ser Gly
100 105 110

<210> 40
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ala	Pro	Ala	Tyr	Gln	Gln
1				5					10					15	
Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu
			20					25					30		
Tyr	Asp	Val	Leu	Asp	Lys	Arg	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly
		35					40					45			
Gly	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu
	50					55					60				
Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Gly	Ala
65					70				75					80	
Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu
			85						90					95	
Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Gly	Gly	Ser	Gly
			100					105					110		

<210> 41

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 41

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Pro	Arg	Arg	Lys	Asn	Pro
1				5					10					15	
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala
			20					25					30		
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly
		35					40					45			
Gly	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln
	50					55					60				
Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Pro
65					70					75				80	
Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp
			85						90					95	
Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Gly	Ser	Gly
			100					105					110		

<210> 42

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 42

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Arg	Arg	Arg	Gly	Lys
1				5					10					15	
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr

			20					25					30				
Tyr	Asp	Ala	Leu	His	Met	Gln	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly		
		35					40					45					
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu		
	50					55					60						
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Gly	Glu		
65					70					75					80		
Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr		
				85					90					95			
Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Gly	Gly	Ser	Gly		
			100					105					110				

<210> 43
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Arg	Pro	Pro	Pro	Val		
1				5					10					15			
Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr		
			20					25					30				
Ser	Gly	Leu	Asn	Gln	Arg	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly		
	35						40					45					
Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys		
	50					55					60						
Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Glu	Arg	Pro		
65				70					75					80			
Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg		
				85				90						95			
Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly					
			100					105									

<210> 44
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg	Lys	Gln	Arg	Ile	Thr		
1				5					10					15			
Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val		
			20					25					30				
Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly		
	35					40						45					
Gly	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu		

50		55		60	
Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Gly Arg					
65		70		75	80
Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly					
	85		90		95
Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Gly Gly Ser Gly					
	100		105		110

<210> 45
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 45	
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Asp Glu Tyr	
1	5
Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn Leu Asp Asp Cys Ser Met	
	20
Tyr Glu Asp Ile Ser Arg Gly Gly Glu Asn Leu Tyr Phe Gln Ser Gly	
	35
Gly Asp Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu	
	50
Asn Leu Asp Asp Cys Ser Met Tyr Glu Asp Ile Ser Arg Gly Gly Asp	
65	70
Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn Leu	
	85
Asp Asp Cys Ser Met Tyr Glu Asp Ile Ser Arg Gly Gly Gly Ser Gly	
	100
	105
	110

<210> 46
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 46	
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ser Lys Ala Gly Met	
1	5
Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr	
	20
Tyr Glu Asp Ile Val Thr Leu Gly Glu Asn Leu Tyr Phe Gln Ser Gly	
	35
Gly Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly Leu	
	50
Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Gly Asp	
65	70
Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile	
	75
	80

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<210> 47
<211> 112
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

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<210> 48
<211> 117
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

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<210> 49
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 49
 Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly Ala Pro Ala Tyr Gln Gln
 1 5 10 15
 Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 20 25 30
 Tyr Asp Val Leu Asp Lys Arg Gly Gly Ser Gly Ala Pro Ala Tyr Gln
 35 40 45
 Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
 50 55 60
 Glu Tyr Asp Val Leu Asp Lys Arg Gly Gly Ser Gly Ala Pro Ala Tyr
 65 70 75 80
 Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 85 90 95
 Glu Glu Tyr Asp Val Leu Asp Lys Arg Gly Gly Ser Gly
 100 105

<210> 50
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 50
 Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly Glu Arg Pro Pro Pro Val
 1 5 10 15
 Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr
 20 25 30
 Ser Gly Leu Asn Gln Arg Gly Gly Ser Gly Glu Arg Pro Pro Pro Val
 35 40 45
 Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr
 50 55 60
 Ser Gly Leu Asn Gln Arg Gly Gly Ser Gly Glu Arg Pro Pro Pro Val
 65 70 75 80
 Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr
 85 90 95
 Ser Gly Leu Asn Gln Arg Gly Gly Ser Gly
 100 105

<210> 51

<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51
Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly Asp Thr Gln Ala Leu Leu
1 5 10 15
Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln
20 25 30
Tyr Ser His Leu Gly Gly Asn Gly Gly Ser Gly Glu Arg Pro Pro Pro
35 40 45
Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu
50 55 60
Tyr Ser Gly Leu Asn Gln Arg Gly Gly Ser Gly Asp Lys Gln Thr Leu
65 70 75 80
Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu Asp Asp
85 90 95
Gln Tyr Ser His Leu Gln Gly Asn Gly Gly Ser Gly Arg Lys Gln Arg
100 105 110
Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser
115 120 125
Asp Val Tyr Ser Asp Leu Asn Thr Gln Gly Gly Ser Gly
130 135 140

<210> 52
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 60
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120
gaactgggtg gttctggtaa acggggcaga aagaaactcc tgtatatatt caaacaacca 180
tttatgagac cagtacaaac tactcaagag gaagatggct gtagctgccg atttccagaa 240
gaagaagaag gaggatgtga actgggtggt tctggtaaac ggggcagaaa gaaactcctg 300
tatatatcca aacaaccatt tatgagacca gtacaaacta ctcaagagga agatggctgt 360
agctgccgat ttccagaaga agaagaagga ggatgtgaac tg 402

<210> 53
<211> 162
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53

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agagtgaagt tcagcaggag cgcagaccgt ggccgggacc ctgagatggg gggaaagggc 60
gccctgcccc ctcgcggtgg ttctggtaga gtgaagttca gcaggagcgc agaccgtggc 120
cgggaccctg agatgggggg aaagggcgcc ctgccccctc gc 162
```

<210> 54

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 54

```
ggcggcggag gctctggcgg cggaggaagc gccccgcgt accagcaggg ccagaaccag 60
ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagaggt 120
gaaaatttgt attttcaatc tgggtggtccg agaaggaaga accctcagga aggcctgtac 180
aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 240
cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 300
acctacgacg cccttcacat gcagggtggt tctggt 336
```

<210> 55

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 55

```
ggcggcggag gctctggcgg cggaggaagc gccccgcgt accagcaggg ccagaaccag 60
ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagaggt 120
gaaaatttgt attttcaatc tgggtggtgcc cccgcgtacc agcagggccca gaaccagctc 180
tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagaggcgcc 240
cccgcgtacc agcagggccca gaaccagctc tataacgagc tcaatctagg acgaagagag 300
gagtacgatg ttttggacaa gagaggtggt tctggt 336
```

<210> 56

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 56

```
ggcggcggag gctctggcgg cggaggaagc ccgagaagga agaaccctca ggaaggcctg 60
tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggt 120
gaaaatttgt attttcaatc tgggtggtccg agaaggaaga accctcagga aggcctgtac 180
aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcccg 240
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag 300
gcctacagtg agattgggat gaaaggtggt tctggt 336
```

<210> 57

<211> 336

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57
ggcggcggag gctctggcgg cggaggaagc gagcgccgga ggggcaaggg gcacgatggc 60
ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcagggt 120
gaaaatttgt attttcaatc tgggtggtgag cgccggagggg gcaaggggca cgatggcctt 180
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcagggcgag 240
cgccggagggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 300
acctacgacg cccttcacat gcagggtggt tctggt 336

<210> 58
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 58
ggcggcggag gctctggcgg cggaggaagc gagaggccac cacctgttcc caaccagac 60
tatgagccca tccggaaggg ccagcgggac ctgtattctg gcctgaatca gagagggtgaa 120
aatttgtatt ttcaatctgg tggtagagagg ccaccacctg ttcccaaccc agactatgag 180
cccatccgga aaggccagcg ggacctgtat tctggcctga atcagagagg cgagaggcca 240
ccacctgttc ccaaccaga ctatgagccc atccggaaag gccagcggga cctgtattct 300
ggcctgaatc agagaggtgg ttctggt 327

<210> 59
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59
ggcggcggag gctctggcgg cggaggaagc cggaaacagc gtatcactga gaccgagtcg 60
ccttatcagg agctccaggg tcagagggtcg gatgtctaca gcgacctcaa cacacagggt 120
gaaaatttgt attttcaatc tgggtggtcgg aaacagcgta tctactgagac cgagtcgcct 180
tatcaggagc tccagggtca gaggtcggat gtctacagcg acctcaacac acagggccgg 240
aaacagcgta tctactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300
gtctacagcg acctcaacac acaggggtggt tctggt 336

<210> 60
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 60

```
ggcggcggag gctctggcgg cggaggaagc gatgccgggg atgaatatga agatgaaaac 60
ctttatgaag gcctgaacct ggacgactgc tccatgtatg aggacatctc ccggggcggt 120
gaaaatttgt attttcaatc tgggtggtgat gccggggatg aatatgaaga tgaaaacctt 180
tatgaaggcc tgaacctgga cgactgctcc atgtatgagg acatctcccg gggcggcgat 240
gccggggatg aatatgaaga tgaaaacctt tatgaaggcc tgaacctgga cgactgctcc 300
atgtatgagg acatctcccg gggcgggtggt tctggt 336
```

<210> 61

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 61

```
ggcggcggag gctctggcgg cggaggaagc gacagcaagg ctggcatgga ggaagatcac 60
acctacgagg gcctggacat tgaccagaca gccacctatg aggacatagt gacgctgggt 120
gaaaatttgt attttcaatc tgggtggtgac agcaaggctg gcatggagga agatcacacc 180
tacgagggcc tggacattga ccagacagcc acctatgagg acatagtgac gctgggcgac 240
agcaaggctg gcatggagga agatcacacc tacgagggcc tggacattga ccagacagcc 300
acctatgagg acatagtgac gctgggtggt tctggt 336
```

<210> 62

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

```
ggcggcggag gctctggcgg cggaggaagc gctataacca gctatgagaa atcagatggt 60
gtttacacgg gcctgagcac caggaaccag gagacttacg agactctgaa gcatgagggt 120
gaaaatttgt attttcaatc tgggtggtgct ataaccagct atgagaaatc agatggtggt 180
tacacgggcc tgagcaccag gaaccaggag acttacgaga ctctgaagca tgagggcgct 240
ataaccagct atgagaaatc agatggtggt tacacgggcc tgagcaccag gaaccaggag 300
acttacgaga ctctgaagca tgagggtggt tctggt 336
```

<210> 63

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 63

```
cctcctccat accagcctct cggcggcgcc ggcagcgccc ccgcgtacca gcagggccag 60
aaccagctct ataaccagct caatctagga cgaagagagg agtacgatgt tttggacaag 120
agaggtgaaa atttgtatct tcaatctggt ggtccgagaa ggaagaacct tcagggaaggc 180
ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa 240
ggcagcgagc gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc 300
```

accaaggaca cctacgacgc ccttcacatg cagggtagcg gcagcggtag ctaa 354

<210> 64

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 64

```
ggtgaaaatt tgtatatttca atctggtggt gccccgcgt accagcaggg ccagaaccag 60
ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagaggt 120
ggttctggtg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta 180
ggacgaagag aggagtacga tgttttggaac aagagaggtg gttctggtgc cccccgcgtac 240
cagcagggcc agaaccagct ctataacgag ctcaatctag gacgaagaga ggagtacgat 300
gttttggaac agagaggtgg ttctggttaa 330
```

<210> 65

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 65

```
ggtgaaaatt tgtatatttca atctggtggt gagaggccac cacctgttcc caaccagac 60
tatgagccca tccggaaagg ccagcgggac ctgtattctg gcctgaatca gagaggtggt 120
tctggtgaga ggccaccacc tggtcccaac ccagactatg agcccatccg gaaaggccag 180
cgggacctgt attctggcct gaatcagaga ggtggttctg gtgagaggcc accacctgtt 240
cccaaccag actatgagcc catccgaaa ggccagcggg acctgtattc tggcctgaat 300
cagagaggtg gttctggtta a 321
```

<210> 66

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 66

```
ggtgaaaatt tgtatatttca atctggtggt gacacacaag ctctgttgag gaatgaccag 60
gtctatcagc ccctccgaga tcgagatgat gctcagtaca gccaccttgaggaggaaacgggt 120
ggttctggtg agaggccacc acctgttccc aaccagact atgagcccat ccggaaaggc 180
cagcgggacc tgtattctgg cctgaatcag agaggtggtt ctggtgacaa gcagactctg 240
ttgccaatg accagctcta ccagcccctc aaggatcgag aagatgacca gtacagccac 300
cttcaaggaa acggtggttc tggtcggaaa cagcgatatca ctgagaccga gtcgccttat 360
caggagctcc agggtcagag gtcggatgtc tacagcgacc tcaacacaca ggtggttct 420
ggttaa 426
```

<210> 67

<211> 21

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 67
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro
20

<210> 68
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 68
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15
Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30
Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 69
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 69
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15
Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 70
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	
1				5					10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu	
			20					25					30			
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	
		35					40					45				
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys	
	50					55					60					
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln	
65					70					75					80	
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe	
				85					90					95		
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr	
			100					105					110			
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
	115						120					125				
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	
	130					135					140					
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	
145					150					155					160	
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
				165					170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly	
			180					185					190			
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro	
	195					200						205				
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	
	210					215					220					
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp	
225					230					235					240	
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr	
				245					250					255		
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe	
			260					265					270			
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	
		275					280						285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	
	290					295					300					
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	
305					310					315					320	
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	
				325					330					335		
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	
			340					345					350			
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	
		355					360					365				
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	
	370					375					380					
Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	
385					390					395					400	
Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	
				405					410					415		
Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Gly	Arg	Asp	Pro	Glu	Met		
			420					425				430				

Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	
		435					440					445				
Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	
	450					455					460					
Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	
465					470					475					480	
Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	
				485					490					495		
Pro	Pro	Arg														

<210> 71
 <211> 528
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 71

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	
1				5					10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu	
			20					25					30			
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	
		35				40						45				
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys	
	50					55					60					
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln	
65					70					75				80		
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe	
				85					90					95		
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr	
			100					105					110			
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
		115					120					125				
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	
	130					135					140					
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	
145					150					155					160	
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
				165					170					175		
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly	
			180					185					190			
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro	
		195					200						205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	
	210					215					220					
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp	
225					230					235					240	
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr	
				245					250					255		
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe	

Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser
				85					90					95	
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser
			100					105					110		
Ala	Asp	Tyr	Tyr	Cys	Ala	Arg	Ser	Asn	Tyr	Tyr	Gly	Ser	Ser	Tyr	Trp
		115					120					125			
Phe	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	Ile	Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys
				165					170					175	
Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	Asp	Trp
			180					185					190		
Tyr	Gln	Lys	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr
		195					200					205			
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser
	210					215					220				
Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala
225					230					235					240
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly
				245					250					255	
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro
			260					265					270		
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu
		275					280					285			
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg
	290					295					300				
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly
305					310					315					320
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys
				325					330					335	
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg
			340					345					350		
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro
		355					360					365			
Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser
	370					375					380				
Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu
385					390					395					400
Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg
				405					410					415	
Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln
			420					425					430		
Glu	Gly	Leu	Tyr	Asn	Glu										

<210> 73
 <211> 518
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 73

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu
			20					25					30		
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
		35					40					45			
Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Gln
	50				55						60				
Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser
65				70						75					80
Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser
				85					90					95	
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser
			100					105					110		
Ala	Asp	Tyr	Tyr	Cys	Ala	Arg	Ser	Asn	Tyr	Tyr	Gly	Ser	Ser	Tyr	Trp
		115					120					125			
Phe	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	Ile	Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys
				165					170					175	
Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	Asp	Trp
			180					185					190		
Tyr	Gln	Lys	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr
		195					200					205			
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser
	210					215					220				
Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala
225				230					235						240
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly
				245					250					255	
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro
			260					265					270		
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu
		275					280					285			
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg
	290					295					300				
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly
305					310					315					320
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys
				325					330					335	
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg
			340				345						350		
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro

cctcaggaag	gcctgtacaa	tgaactgcag	aaagataaga	tggcggaggc	ctacagtgag	1380
attgggatga	aaggcgagcg	ccggaggggc	aaggggcacg	atggccttta	ccagggtctc	1440
agtacagcca	ccaaggacac	ctacgacgcc	cttcacatgc	aggccctgcc	ccctcgctaa	1500

<210> 75

<211> 1587

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 75

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cccgacatcg	tgctgaccca	gagccccccc	agcctggcca	tgtctctggg	caagagagcc	120
accatcagct	gccgggccag	cgagagcgtg	accatcctgg	gcagccacct	gatccactgg	180
tatcagcaga	agcccggcca	gccccccacc	ctgtctgatcc	agctcgccag	caatgtgcag	240
accggcgtgc	ccgccagatt	cagcggcagc	ggcagcagaa	ccgacttcac	cctgaccatc	300
gaccccgtgg	aagaggacga	cgtggccgtg	tactactgcc	tgacagaccg	gaccatcccc	360
cggacctttg	gcggaggcac	caaaactggaa	atcaagggca	gcaccagcgg	ctccggcaag	420
cctggctctg	gcgagggcag	cacaaaggga	cagattcagc	tggtgcagag	cggccctgag	480
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gactacagca	tcaactgggt	gaaaagagcc	cctggcaagg	gcctgaagtg	gatgggctgg	600
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gcgccgcgac	caccaacacc	ggcgcccacc	atcgcgctgc	agcccctgtc	cctgcgcccc	900
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gatatctaca	tctgggcgcc	cttggccggg	acttgtgggg	tccttctcct	gtcactgggt	1020
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gaagaaggag	gatgtgaact	gggtgaaaat	ttgtattttc	aatctggtgg	tgacacacaa	1200
gctctgttga	ggaatgacca	ggtctatcag	cccctccgag	atcgagatga	tgctcagtac	1260
agccaccttg	gaggaaacgg	tggttctggt	gagaggccac	cacctgttcc	caaccagac	1320
tatgagccca	tccggaaagg	ccagcgggac	ctgtattctg	gcctgaatca	gagaggtgg	1380
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actgagaccg	agtcgcctta	tcaggagctc	cagggtcaga	ggtcggatgt	ctacagcgac	1560
ctcaacacac	agggtggttc	tggttaa				1587

<210> 76

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 76

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atgagctgca	aggccagcgg	ctacaccttc	accagctata	acatgcactg	ggtgaagcag	180

acccttgga	agggactgga	gtggatcgga	gctatctacc	ctggaaacgg	agacacctca	240
tacaaccaga	agttcaaggg	aaaggctacc	ctgaccgctg	acaagagcag	cagcaccgct	300
tacatgcagc	tgagctcact	gaccagcgag	gactccgccg	actactactg	cgccagaagc	360
aactactacg	gaagcagcta	ctggttcttc	gacgtgtggg	gagctggaac	caccgtgacc	420
gtgtcaagcg	gcggcggagg	ctccggaggc	ggaggatctg	gcggcggcgg	cagcgacatc	480
gtgctgaccc	agagccctgc	tatcctgtct	gccagccctg	gagagaaggt	gacatgacc	540
tgacagagcta	gcagcagcgt	gaactacatg	gactggtatc	agaaaaagcc	cggcagctca	600
cctaagcctt	ggatctacgc	taccagcaac	ttagccagcg	gcgtgcctgc	tagattctcc	660
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aaactcctgt	atatattcaa	acaaccattt	atgagaccag	tacaaactac	tcaagaggaa	1080
gatggctgta	gctgccgatt	tccagaagaa	gaagaaggag	gatgtgaact	gagagtgaag	1140
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gagatggggg	gaaagccgag	aaggaagaac	cctcaggaag	gcctgtacaa	tgaactgcag	1320
aaagataaga	tggcggaggc	ctacagttag	attgggatga	aaggcgagcg	ccggaggggc	1380
aaggggcacg	atggccttta	ccagggtctc	agtacagcca	ccaaggacac	ctacgacgcc	1440
cttcacatgc	aggccctgcc	ccctcgctaa				1470

<210> 77

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 77

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cctgaggtgc	agctgcagca	gagcggagct	gagctggtga	agcctggcgc	tagcgtgaag	120
atgagctgca	aggccagcgg	ctacaccttc	accagctata	acatgcactg	ggtgaagcag	180
acccttgga	agggactgga	gtggatcgga	gctatctacc	ctggaaacgg	agacacctca	240
tacaaccaga	agttcaaggg	aaaggctacc	ctgaccgctg	acaagagcag	cagcaccgct	300
tacatgcagc	tgagctcact	gaccagcgag	gactccgccg	actactactg	cgccagaagc	360
aactactacg	gaagcagcta	ctggttcttc	gacgtgtggg	gagctggaac	caccgtgacc	420
gtgtcaagcg	gcggcggagg	ctccggaggc	ggaggatctg	gcggcggcgg	cagcgacatc	480
gtgctgaccc	agagccctgc	tatcctgtct	gccagccctg	gagagaaggt	gacatgacc	540
tgacagagcta	gcagcagcgt	gaactacatg	gactggtatc	agaaaaagcc	cggcagctca	600
cctaagcctt	ggatctacgc	taccagcaac	ttagccagcg	gcgtgcctgc	tagattctcc	660
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aacggtggtt	ctggtcggaa	acagcgtatc	actgagaccg	agtcgcctta	tcaggagctc	1500
cagggtcaga	ggtcggatgt	ctacagcgac	ctcaacacac	agggtgggtc	tggttaa	1557

<210> 78

<211> 2835

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 78

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acagtccaag	aagagtgcgg	caaggccttg	aaaaagtcct	ggggtaaagg	taaaatgact	180
ccagacggcc	gccgcctgca	agaaggagac	acctttgatg	agtgggatga	tgatgaagaa	240
gaagtaggct	tccctgtgca	acctcgagtc	cccttaagac	agatgacctt	taaattagca	300
gtggactttt	cccacttttt	aaaatcaaag	gggggactgg	atgggatata	ttactctgaa	360
agaagagaaa	agatcctgaa	tttgtatgcc	ttgaacgagt	ggggaataat	agatgattgg	420
caagcttact	caccaggccc	ggggataagg	tacccgagag	tctttggctt	ctgctttaag	480
ctagtcccag	tggacctgca	tgaggaggca	cgcaactgtg	agagacactg	tgctgcacat	540
ccagcacaga	tgggggaaga	tcctgatgga	atagatcatg	gagaagtctt	ggtctggaag	600
tttgacccga	agttggcggg	ggagtaccgc	ccggacatgt	ttaaggacat	gcacgaacat	660
gcaaagcgct	gaacgcgtgc	ccctctccct	ccccccccc	taacgttact	ggccgaagcc	720
gcttggaaata	aggccgggtg	gcgtttgtct	atatgttatt	ttccaccata	ttgccgtctt	780
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gagaaggtga	ccatgacctg	cagagctagc	agcagcgtga	actacatgga	ctggtatcag	1860
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gtgcctgcta	gattctccgg	aagcggctct	ggaaccagct	actcccttac	catcagcaga	1980
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tgcaaacggg	gcagaaagaa	actcctgtat	atattcaaac	aaccatttat	gagaccagta	2340
caaactactc	aagaggaaga	tggctgtagc	tgccgatttc	cagaagaaga	agaaggagga	2400

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tgtgaactgg gtgaaaattt gtattttcaa tctggtggtg acacacaagc tctgttgagg 2460
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ggtggttctg gttaa                                     2835

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<210> 79

<211> 206

<212> PRT

<213> Human immunodeficiency virus

<400> 79

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Met Gly Gly Lys Trp Ser Lys Ser Ser Val Ile Gly Trp Pro Thr Val
 1           5           10           15
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Arg Val Gly Ala
      20           25           30
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
      35           40           45
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
      50           55           60
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
      65           70           75           80
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
      85           90           95
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
      100          105          110
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
      115          120          125
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
      130          135          140
Leu Val Pro Val Glu Pro Asp Lys Ile Glu Glu Ala Asn Lys Gly Glu
      145          150          155          160
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
      165          170          175
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
      180          185          190
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys
      195          200          205

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<210> 80

<211> 257

<212> PRT

<213> Human immunodeficiency virus

<400> 80

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Met Gly Ala Ser Gly Ser Lys Lys Leu Ser Lys His Ser Arg Gly Leu
 1           5           10           15
Arg Glu Arg Leu Leu Arg Ala Arg Gly Asp Gly Tyr Gly Lys Gln Arg
      20           25           30
Asp Ala Ser Gly Gly Glu Tyr Ser Gln Phe Gln Glu Glu Ser Gly Arg

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130		135		140
Trp Cys Phe Lys Leu Val	Pro Val Asp Pro Lys Ala Val Glu Glu Ala			
145	150	155	160	
Asn Glu Gly Glu Asp Asn Cys Leu Leu His Pro Val Cys Gln His Gly				
	165	170	175	
Met Glu Asp Glu His Arg Glu Val Leu Met Trp Lys Phe Asp Ser Gln				
	180	185	190	
Leu Ala Arg Arg His Met Ala Arg Glu Leu His Pro Glu Phe Tyr Lys				
	195	200	205	
Asp Cys				
210				

<210> 82
 <211> 129
 <212> PRT
 <213> Human immunodeficiency virus

<400> 82
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Arg Glu Arg Met Arg Arg Thr Glu Pro Ala Val Glu Pro Ala Ala Glu
20 25 30
Pro Ala Ala Glu Gly Val Gly Ala Ala Trp Leu Leu Pro Asp Trp Gln
35 40 45
Asn Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp
50 55 60
Cys Phe Lys Leu Val Pro Val Asp Pro Gly Ala Val Glu Glu Ala Asn
65 70 75 80
Glu Gly Glu Asn Asn Cys Leu Leu His Pro Val Cys Gln His Gly Met
85 90 95
Glu Asp Glu Gln Arg Glu Val Leu Val Cys Lys Phe Asp Ser Leu Leu
100 105 110
Ala Arg Arg His Met Ala Arg Glu Leu His Pro Glu Phe Tyr Lys Asp
115 120 125
Cys

<210> 83
 <211> 180
 <212> PRT
 <213> Human immunodeficiency virus

<400> 83
Met Gly Ala Ser Gly Ser Lys Lys Arg Ser Lys Pro Leu Gln Gly Leu
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Gln Glu Arg Leu Leu Gln Ala Arg Gly Glu Thr Cys Gly Gly Arg Cys
20 25 30
Asn Glu Ser Gly Gly Gly Tyr Leu Gln Ser His Glu Gly Ser Gly Arg
35 40 45
Glu Gln Asn Ser Pro Ser Cys Glu Gly Gln Arg Tyr Gln Gln Gly Asp
50 55 60
Phe Val Asn Thr Pro Trp Arg Thr Pro Ala Ala Glu Arg Glu Lys Glu

65					70					75				80
Leu	Tyr	Lys	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Leu	Asp	Asp	Asp
				85					90				95	
Gln	Val	Gly	Phe	Pro	Val	Thr	Pro	Arg	Val	Pro	Leu	Arg	Pro	Met
			100					105					110	Thr
Phe	Lys	Leu	Ala	Val	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly
		115					120					125		Gly
Leu	Glu	Gly	Leu	Phe	Tyr	Ser	Gln	Arg	Arg	His	Arg	Ile	Leu	Asp
	130					135					140			Leu
Tyr	Leu	Asp	Lys	Ala	Phe	Thr	Leu	Tyr	Pro	Glu	Glu	Phe	Gly	His
145					150					155				Asn
Ser	Gly	Leu	Pro	Glu	Lys	Glu	Trp	Lys	Ala	Arg	Leu	Lys	Ala	Arg
				165					170					175
Ile	Pro	Phe	Ser											
			180											

<210> 84

<211> 223

<212> PRT

<213> Simian immunodeficiency virus

<400> 84

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Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Thr	Val	Gln	Glu	Glu	Cys	Gly	Lys
		35				40						45			
Ala	Leu	Lys	Lys	Ser	Trp	Gly	Lys	Gly	Lys	Met	Thr	Pro	Asp	Gly	Arg
	50					55				60					
Arg	Leu	Gln	Glu	Gly	Asp	Thr	Phe	Asp	Glu	Trp	Asp	Asp	Asp	Glu	Glu
65					70				75						80
Glu	Val	Gly	Phe	Pro	Val	Gln	Pro	Arg	Val	Pro	Leu	Arg	Gln	Met	Thr
				85					90					95	
Tyr	Lys	Leu	Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly
			100					105					110		
Leu	Asp	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Glu	Lys	Ile	Leu	Asn	Leu
		115				120						125			
Tyr	Ala	Leu	Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser
	130					135					140				
Pro	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys
145					150					155					160
Leu	Val	Pro	Val	Asp	Leu	His	Glu	Glu	Ala	Arg	Asn	Cys	Glu	Arg	His
				165					170					175	
Cys	Leu	Met	His	Pro	Ala	Gln	Met	Gly	Glu	Asp	Pro	Asp	Gly	Ile	Asp
			180					185					190		
His	Gly	Glu	Val	Leu	Val	Trp	Lys	Phe	Asp	Pro	Lys	Leu	Ala	Val	Glu
	195						200					205			
Tyr	Arg	Pro	Asp	Met	Phe	Lys	Asp	Met	His	Glu	His	Ala	Lys	Arg	
	210					215					220				

<210> 85

<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 85
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Trp Arg Gly Leu Arg Gly Lys Pro Gly Ala Asp Trp Val Leu Leu Ser
20 25 30
Asp Pro Leu Ile Gly Gln Ser Ser Thr Val Gln Glu Glu Cys Gly Lys
35 40 45
Ala Leu Lys Lys Ser Trp Gly Lys Gly Lys Met Thr Pro Asp Gly Arg
50 55 60
Arg Leu Gln Glu Gly Asp Thr Phe Asp Glu Trp Asp Asp Asp Glu Glu
65 70 75 80
Glu Val Gly Phe Pro Val Gln Pro Arg Val Pro Leu Arg Gln Met Thr
85 90 95
Tyr Lys Leu Ala Val Asp Phe Ser His Phe Leu Lys Ser Lys Gly Gly
100 105 110
Leu Asp Gly Ile Tyr Tyr Ser Glu Arg Arg Glu Lys Ile Leu Asn Leu
115 120 125
Tyr Ala Leu Asn Glu Trp Gly Ile Ile Asp Asp Trp Gln Ala Tyr Ser
130 135 140
Pro Gly Pro Gly Ile Arg Tyr Pro Arg Val Phe Gly Phe Cys Phe Lys
145 150 155 160
Leu Val Pro Val Asp Leu His Glu Glu Ala Arg Asn Cys Glu Arg His
165 170 175
Cys Ala Ala His Pro Ala Gln Met Gly Glu Asp Pro Asp Gly Ile Asp
180 185 190
His Gly Glu Val Leu Val Trp Lys Phe Asp Pro Lys Leu Ala Val Glu
195 200 205
Tyr Arg Pro Asp Met Phe Lys Asp Met His Glu His Ala Lys Arg
210 215 220

<210> 86
<211> 223
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 86
Met Gly Ser Ser Asn Ser Lys Arg Gln Gln Gln Gly Leu Leu Lys Leu
1 5 10 15
Trp Arg Gly Leu Arg Gly Lys Pro Gly Ala Asp Trp Val Leu Leu Ser
20 25 30
Asp Pro Leu Ile Gly Gln Ser Ser Thr Val Gln Glu Glu Cys Gly Lys
35 40 45
Ala Leu Lys Lys Ser Trp Gly Lys Gly Lys Met Thr Pro Asp Gly Arg

50		55		60											
Arg	Leu	Gln	Glu	Gly	Asp	Thr	Phe	Asp	Glu	Trp	Asp	Asp	Asp	Glu	Glu
65					70					75				80	
Glu	Val	Gly	Phe	Pro	Val	Gln	Pro	Arg	Val	Pro	Leu	Arg	Gln	Met	Thr
				85					90					95	
Tyr	Lys	Leu	Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly
			100					105					110		
Leu	Asp	Gly	Ile	Tyr	Tyr	Ser	Glu	Ala	Ala	Glu	Lys	Ile	Leu	Asn	Leu
		115					120					125			
Tyr	Ala	Leu	Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser
	130					135					140				
Pro	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys
145					150					155					160
Leu	Val	Pro	Val	Asp	Leu	His	Glu	Glu	Ala	Arg	Asn	Cys	Glu	Arg	His
				165					170					175	
Cys	Ala	Ala	His	Pro	Ala	Gln	Met	Gly	Glu	Asp	Pro	Asp	Gly	Ile	Asp
			180					185					190		
His	Gly	Glu	Val	Leu	Val	Trp	Lys	Phe	Asp	Pro	Lys	Leu	Ala	Val	Glu
	195						200					205			
Tyr	Arg	Pro	Asp	Met	Phe	Lys	Asp	Met	His	Glu	His	Ala	Lys	Arg	
	210					215					220				

<210> 87

<211> 223

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 87

Met	Gly	Ser	Ser	Asn	Ser	Lys	Arg	Gln	Gln	Gln	Gly	Leu	Leu	Lys	Leu
1				5				10						15	
Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Thr	Val	Gln	Glu	Glu	Cys	Gly	Lys
	35					40					45				
Ala	Leu	Lys	Lys	Ser	Trp	Gly	Lys	Gly	Lys	Met	Thr	Pro	Asp	Gly	Arg
	50					55				60					
Arg	Leu	Gln	Glu	Gly	Asp	Thr	Phe	Asp	Glu	Trp	Asp	Asp	Asp	Glu	Glu
65				70					75					80	
Glu	Val	Gly	Phe	Pro	Val	Gln	Pro	Arg	Val	Pro	Leu	Arg	Gln	Met	Thr
				85					90					95	
Tyr	Lys	Leu	Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly
			100					105					110		
Leu	Asp	Gly	Ile	Tyr	Tyr	Ser	Glu	Ala	Ala	Glu	Lys	Ile	Leu	Asn	Leu
	115						120					125			
Tyr	Ala	Leu	Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser
	130					135					140				
Pro	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys
145					150					155					160
Leu	Val	Pro	Val	Asp	Leu	His	Glu	Glu	His	Asn	Cys	Glu	Arg	His	
				165				170					175		

Cys	Ala	Ala	His	Pro	Ala	Gln	Met	Gly	Ala	Ala	Pro	Asp	Gly	Ile	Asp
			180					185					190		
His	Gly	Glu	Val	Leu	Val	Trp	Lys	Phe	Asp	Pro	Lys	Leu	Ala	Val	Glu
		195					200					205			
Tyr	Arg	Pro	Asp	Met	Phe	Lys	Asp	Met	His	Glu	His	Ala	Lys	Arg	
	210					215					220				

<210> 88

<211> 223

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 88

Met	Gly	Ser	Ser	Asn	Ser	Lys	Arg	Gln	Gln	Gln	Gly	Leu	Leu	Lys	Leu
1				5				10						15	
Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Thr	Val	Gln	Glu	Glu	Cys	Gly	Lys
		35				40					45				
Ala	Leu	Lys	Lys	Ser	Trp	Gly	Lys	Gly	Lys	Met	Thr	Pro	Asp	Gly	Arg
	50					55				60					
Arg	Leu	Gln	Glu	Gly	Asp	Thr	Phe	Asp	Glu	Trp	Asp	Asp	Asp	Glu	Glu
65					70				75						80
Glu	Val	Gly	Phe	Pro	Val	Gln	Pro	Arg	Val	Pro	Leu	Arg	Gln	Met	Thr
				85				90						95	
Tyr	Lys	Leu	Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly
			100					105					110		
Leu	Asp	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Glu	Lys	Ile	Leu	Asn	Leu
	115						120					125			
Tyr	Ala	Leu	Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser
	130					135					140				
Pro	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys
145					150					155					160
Leu	Val	Pro	Val	Asp	Leu	His	Glu	Glu	His	Asn	Cys	Glu	Arg	His	
				165				170					175		
Cys	Ala	Ala	His	Pro	Ala	Gln	Met	Gly	Ala	Ala	Pro	Asp	Gly	Ile	Asp
			180					185					190		
His	Gly	Glu	Val	Leu	Val	Trp	Lys	Phe	Asp	Pro	Lys	Leu	Ala	Val	Glu
		195					200					205			
Tyr	Arg	Pro	Asp	Met	Phe	Lys	Asp	Met	His	Glu	His	Ala	Lys	Arg	
	210					215					220				

<210> 89

<211> 223

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 89

Met	Gly	Ser	Ser	Asn	Ser	Lys	Arg	Gln	Gln	Gln	Gly	Leu	Leu	Lys	Leu
1				5				10						15	
Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Thr	Val	Gln	Glu	Glu	Cys	Gly	Lys
		35				40						45			
Ala	Leu	Lys	Lys	Ser	Trp	Gly	Lys	Gly	Lys	Met	Thr	Pro	Asp	Gly	Arg
	50				55					60					
Arg	Leu	Gln	Glu	Gly	Asp	Thr	Phe	Asp	Glu	Trp	Asp	Asp	Asp	Glu	Glu
65				70				75						80	
Glu	Val	Gly	Phe	Pro	Val	Gln	Pro	Arg	Val	Pro	Leu	Arg	Gln	Met	Thr
			85					90						95	
Tyr	Lys	Leu	Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly
			100					105					110		
Leu	Asp	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Glu	Lys	Ile	Leu	Asn	Leu
	115					120						125			
Tyr	Ala	Leu	Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser
	130					135					140				
Pro	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys
145				150						155					160
Leu	Val	Pro	Val	Asp	Leu	His	Glu	Glu	Ala	Arg	Asn	Cys	Glu	Arg	His
			165					170						175	
Cys	Ala	Ala	His	Pro	Ala	Gln	Met	Gly	Ala	Ala	Pro	Asp	Gly	Ile	Asp
		180				185							190		
His	Gly	Glu	Val	Leu	Val	Trp	Lys	Phe	Asp	Pro	Lys	Leu	Ala	Val	Glu
	195					200						205			
Tyr	Arg	Pro	Asp	Met	Phe	Lys	Asp	Met	His	Glu	His	Ala	Lys	Arg	
	210					215					220				

<210> 90

<211> 618

<212> DNA

<213> Human immunodeficiency virus

<400> 90

atgggtggca	agtggtcaaa	aagtagtggtg	attggatggc	ctactgtaag	ggaaagaatg	60
agacgagctg	agccagcagc	agataggggtg	ggagcagcat	ctcgagacct	ggaaaaacat	120
ggagcaatca	caagtagcaa	tacagcagct	accaatgctg	cttgtgcctg	gctagaagca	180
caagaggagg	aggaggtggg	ttttccagtc	acacctcagg	tacctttaag	accaatgact	240
tacaaggcag	ctgtagatct	tagccacttt	ttaaaagaaa	agggggggact	ggaagggcta	300
attcactccc	aaagaagaca	agatatacctt	gatctgtgga	tctaccacac	acaaggctac	360
ttccctgatt	ggcagaacta	cacaccaggg	ccaggggtca	gatataccact	gacctttgga	420
tggtgctaca	agctagtacc	agttgagcca	gataagatag	aagaggccaa	taaaggagag	480
aacaccagct	tgttacaccc	tgtgagcctg	catgggatgg	atgaccgga	gagagaagtg	540
ttagagtgga	ggtttgacag	ccgcctagca	tttcatcacg	tggcccgaga	gctgcatccg	600
gagtacttca	agaactgc					618

<210> 91

<211> 771

<212> DNA

<213> Human immunodeficiency virus

<400> 91

```
atgggtgcga gtggatccaa gaagctttcc aagcattcgc gaggactacg agagagactc 60
ttgcgggcgc gtggggatgg ttatgggaag cagcgcgacg catcgggagg ggaatactcg 120
cagttccaag aagaatcagg cagggagcag aactcgcctt cctgtgaggg acagcagtat 180
cagcagggag agtacatgaa cagcccatgg agaaaccag caacagaaag acagaaagat 240
ttgtataggc agcaaaatat ggatgatgta gattctgatg atgatgacct aataggagtt 300
cctgttacac caagagtacc acggagagaa atgacctata aattggcaat agatatgtca 360
cattttataa aagaaaaagg gggactgcaa gggatgtttt acagtaggag gagacataga 420
atcctagaca tatacctaga aaaagaggaa gggataatac cagattggca gaattatact 480
catgggccag gagtaaggta cccaatgtac ttcgggtggc tgtggaagct agtatcagta 540
gaactctcac aagaggcaga ggaagatgag gccaaactgt tagtacaccc agcacaaaca 600
agcagacatg atgatgagca tggggagaca ttagtggtggc agtttgactc catgctggcc 660
tataactaca aggccttcac tctgtacca gaagagtttg ggcacaagtc aggattgcca 720
gagaaagaat ggaaggcaaa actgaaagca agagggatac catatagtga a 771
```

<210> 92

<211> 630

<212> DNA

<213> Human immunodeficiency virus

<400> 92

```
atgggtggca agtgggtcaaa atgcagcata gttggatggc ctgatataag agagagaatg 60
agacgaactg agccagcagc agagccagca gcagaaggag taggagcagc gtctcaagac 120
ttagataaac atggagcact tacaagtagc aacacaaaca ccactaatgc tgattgtgct 180
tggccggaag cgcaagagga tgaaggagaa gtaggctttg cagtcagacc tcagagtcct 240
ttaagaccaa tgacttataa gggagcattt gatctcggct tctttttaaa agaaggggga 300
ctggaagggt taatttactc taagaaaagg caagagatcc ttgatttgtg ggtctatcat 360
acacaaggct acttcctga ttggcaaaac tacacaccgg gaccaggggt cagataccca 420
ctgacttttg ggtggtgctt caagctggtt ccagttgacc caaaggcagt agaagaggcc 480
aacgaaggag aagacaactg tctgctacac ccagtgtgcc agcatggaat ggaggatgaa 540
cacagagaag tattaatgtg gaagtttgac agtcaactag cacgcagaca catggcccga 600
gagctacatc cggagttcta caaagactgc 630
```

<210> 93

<211> 387

<212> DNA

<213> Human immunodeficiency virus

<400> 93

```
atgggtggca agtgggtcaaa atgcagcata ggtggatggc ctcagataag agagagaatg 60
agacgaactg agccagcagt agagccagca gcagagccag cagcagaagg agtaggagca 120
gcgtgggtac ttcctgattg gcaaaactac acaccgggac caggagtcag ataccactg 180
acttttgggt ggtgcttcaa gctggtacca gtagaccag gggcagtaga agaggccaac 240
gaaggagaaa acaactgttt gctacaccgg gtgtgccagc atggaatgga ggatgagcaa 300
agagaagtat tagtgtgcaa gtttgacagt ctactagcac gcagacacat ggcccgcgag 360
ctacatccgg agttctacaa agactgc 387
```

<210> 94

<211> 540

<212> DNA

<213> Human immunodeficiency virus

<400> 94

atgggtgcga	gtggatccaa	gaagcgttcc	aagcccttgc	aaggactaca	agagagactc	60
ttgcaggcgc	ggggagagac	ttgtggaggg	cgctgcaacg	aatcgggagg	gggatacttg	120
cagtcccacg	aaggatcagg	cagggagcag	aactcgccct	cctgtgaggg	acagcgatat	180
cagcagggag	atthttgtaa	taccccatgg	agaacccag	cagcagaaaag	ggagaaaagaa	240
ttgtacaaac	agcaaaatat	ggatgatgta	gatctagatg	atgatgacca	agtaggattc	300
cctgtcacac	caagagtacc	attaagacca	atgacattca	aattggcagt	agatatgtct	360
cattttataa	aagaaaaagg	gggactggaa	gggctgtttt	atagtcagag	aagacataga	420
atcctagact	tatacttaga	caaggctttt	actctgtacc	cagaggaatt	tgggcataat	480
tcaggactgc	cagagaaaaga	gtggaaggcg	agactgaaag	caaggggaat	accatttagt	540

<210> 95

<211> 669

<212> DNA

<213> Simian immunodeficiency virus

<400> 95

atgggctcca	gcaactccaa	gaggcagcaa	cagggcttgc	tcaagctctg	gcgagggctg	60
cgaggggaagc	ctggggcaga	ctgggtgcta	ttgtccgatac	cgcttatcgg	gcagtcatca	120
acagtccaag	aagagtgcgg	caaggccttg	aaaaagtcct	ggggtaaagg	taaaatgact	180
ccagacggcc	gccgcctgca	agaaggagac	acctttgatg	agtgggatga	tgatgaagaa	240
gaagtaggct	tccctgtgca	acctcgagtc	cccttaagac	agatgaccta	taaattagca	300
gtggactttt	cccacttttt	aaaatcaaag	gggggactgg	atgggatata	ttactctgaa	360
agaagagaaa	agatcctgaa	tttgtatgcc	ttgaacgagt	ggggaataat	agatgattgg	420
caagcttact	caccaggccc	ggggataagg	taccgagag	tctttggctt	ctgctttaag	480
ctagtcccag	tggacctgca	tgaggaggca	cgcaactgtg	agagacactg	tctgatgcat	540
ccagcacaga	tgggggaaga	tcctgatgga	atagatcatg	gagaagtctt	ggtctggaag	600
tttgacccga	agttggcggt	ggagtaccgc	ccggacatgt	ttaaggacat	gcacgaacat	660
gcaaagcgc						669

<210> 96

<211> 669

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 96

atgggctcca	gcaactccaa	gaggcagcaa	cagggcttgc	tcaagctctg	gcgagggctg	60
cgaggggaagc	ctggggcaga	ctgggtgcta	ttgtccgatac	cgcttatcgg	gcagtcatca	120
acagtccaag	aagagtgcgg	caaggccttg	aaaaagtcct	ggggtaaagg	taaaatgact	180
ccagacggcc	gccgcctgca	agaaggagac	acctttgatg	agtgggatga	tgatgaagaa	240
gaagtaggct	tccctgtgca	acctcgagtc	cccttaagac	agatgaccta	taaattagca	300
gtggactttt	cccacttttt	aaaatcaaag	gggggactgg	atgggatata	ttactctgaa	360
agaagagaaa	agatcctgaa	tttgtatgcc	ttgaacgagt	ggggaataat	agatgattgg	420
caagcttact	caccaggccc	ggggataagg	taccgagag	tctttggctt	ctgctttaag	480
ctagtcccag	tggacctgca	tgaggaggca	cgcaactgtg	agagacactg	tgctgcacat	540
ccagcacaga	tgggggaaga	tcctgatgga	atagatcatg	gagaagtctt	ggtctggaag	600
tttgacccga	agttggcggt	ggagtaccgc	ccggacatgt	ttaaggacat	gcacgaacat	660
gcaaagcgc						669

<210> 97

<211> 669

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 97

```
atgggctcca gcaactccaa gaggcagcaa cagggcttgc tcaagctctg gcgagggctg 60
cgaggggaagc ctggggcaga ctgggtgcta ttgtccgatc cgcttatcgg gcagtcatca 120
acagtccaag aagagtgcgg caaggccttg aaaaagtcct ggggtaaagg taaaatgact 180
ccagacggcc gccgcctgca agaaggagac acctttgatg agtgggatga tgatgaagaa 240
gaagtaggct tccctgtgca acctcgagtc cccttaagac agatgacctt taaattagca 300
gtggactttt cccacttttt aaaatcaaag gggggactgg atgggatata ttactctgaa 360
gctgcagaaa agatcctgaa tttgtatgcc ttgaacgagt ggggaataat agatgattgg 420
caagcttact caccaggccc ggggataagg tacccgagag tctttggctt ctgctttaag 480
ctagtcccag tggacctgca tgaggaggca cgcaactgtg agagacactg tgctgcacat 540
ccagcacaga tgggggaaga tcctgatgga atagatcatg gagaagtctt ggtctggaag 600
tttgaccgca agttggcggt ggagtaccgc ccggacatgt ttaaggacat gcacgaacat 660
gcaaagcgc
```

<210> 98
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 98

```
atgggctcca gcaactccaa gaggcagcaa cagggcttgc tcaagctctg gcgagggctg 60
cgaggggaagc ctggggcaga ctgggtgcta ttgtccgatc cgcttatcgg gcagtcatca 120
acagtccaag aagagtgcgg caaggccttg aaaaagtcct ggggtaaagg taaaatgact 180
ccagacggcc gccgcctgca agaaggagac acctttgatg agtgggatga tgatgaagaa 240
gaagtaggct tccctgtgca acctcgagtc cccttaagac agatgacctt taaattagca 300
gtggactttt cccacttttt aaaatcaaag gggggactgg atgggatata ttactctgaa 360
gctgcagaaa agatcctgaa tttgtatgcc ttgaacgagt ggggaataat agatgattgg 420
caagcttact caccaggccc ggggataagg tacccgagag tctttggctt ctgctttaag 480
ctagtcccag tggacctgca tgaggagcat cacaactgtg agagacactg tgctgcacat 540
ccagcacaga tgggggaggc acctgatgga atagatcatg gagaagtctt ggtctggaag 600
tttgaccgca agttggcggt ggagtaccgc ccggacatgt ttaaggacat gcacgaacat 660
gcaaagcgc
```

<210> 99
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 99

```
atgggctcca gcaactccaa gaggcagcaa cagggcttgc tcaagctctg gcgagggctg 60
cgaggggaagc ctggggcaga ctgggtgcta ttgtccgatc cgcttatcgg gcagtcatca 120
acagtccaag aagagtgcgg caaggccttg aaaaagtcct ggggtaaagg taaaatgact 180
```

```

ccagacggcc gccgcctgca agaaggagac acctttgatg agtgggatga tgatgaagaa 240
gaagtaggct tccctgtgca acctcgagtc cccttaagac agatgaccta taaattagca 300
gtggactttt cccacttttt aaaatcaaag gggggactgg atgggatata ttactctgaa 360
agaagagaaa agatcctgaa tttgtatgcc ttgaacgagt ggggaataat agatgattgg 420
caagcttact caccaggccc ggggataagg tacccgagag tctttggctt ctgctttaag 480
ctagtcccag tggacctgca tgaggagcat cacaactgtg agagacactg tgctgcacat 540
ccagcacaga tgggggcggc acctgatgga atagatcatg gagaagtctt ggtctggaag 600
tttgacccga agttggcggg ggagtaccgc ccggacatgt ttaaggacat gcacgaacat 660
gcaaagcgc

```

<210> 100

<211> 669

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 100

```

atgggctcca gcaactccaa gaggcagcaa cagggcttgc tcaagctctg gcgagggctg 60
cgagggaagc ctggggcaga ctgggtgcta ttgtccgata cgcttatcgg gcagtcacat 120
acagtccaag aagagtgcgg caaggccttg aaaaagtcct ggggtaaagg taaaatgact 180
ccagacggcc gccgcctgca agaaggagac acctttgatg agtgggatga tgatgaagaa 240
gaagtaggct tccctgtgca acctcgagtc cccttaagac agatgaccta taaattagca 300
gtggactttt cccacttttt aaaatcaaag gggggactgg atgggatata ttactctgaa 360
agaagagaaa agatcctgaa tttgtatgcc ttgaacgagt ggggaataat agatgattgg 420
caagcttact caccaggccc ggggataagg tacccgagag tctttggctt ctgctttaag 480
ctagtcccag tggacctgca tgaggaggca cgcaactgtg agagacactg tgctgcacat 540
ccagcacaga tgggggcggc acctgatgga atagatcatg gagaagtctt ggtctggaag 600
tttgacccga agttggcggg ggagtaccgc ccggacatgt ttaaggacat gcacgaacat 660
gcaaagcgc

```

<210> 101

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 2, 3, 14, 15

<223> Xaa = Any Amino Acid

<220>

<221> VARIANT

<222> 5, 6, 7, 8, 9, 10, 11, 12

<223> Xaa = Any Amino Acid, and up to two can be present or absent

<220>

<221> VARIANT

<222> 4, 16

<223> Xaa = Leu or Ile

<400> 101

Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5 10 15

<210> 102

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 1

<223> Xaa = Asp or Glu

<220>

<221> VARIANT

<222> 2, 3

<223> Xaa = Any Amino Acid, and up to two can be present or absent

<220>

<221> VARIANT

<222> 5, 6, 17, 18

<223> Xaa = Any Amino Acid

<220>

<221> VARIANT

<222> 8, 9, 10, 11, 12, 13, 14, 15

<223> Xaa = Any Amino Acid, and up to two can be present or absent

<220>

<221> VARIANT

<222> 7, 19

<223> Xaa = Leu or Ile

<400> 102

Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
1 5 10 15
Xaa Xaa Xaa

<210> 103

<211> 1

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>
<221> VARIANT
<222> 1
<223> Can be present in repeats of any integer

<400> 103
Gly
1

<210> 104
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(2)
<223> Can be present in repeats of any integer

<400> 104
Gly Ser
1

<210> 105
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(4)
<223> Can be present in repeats of any integer

<400> 105
Gly Gly Gly Ser
1

<210> 106
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)..(5)
<223> Can be present in repeats of any integer

<400> 106
Gly Gly Gly Gly Ser
1 5

<210> 107
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> 1
<223> Can be present in repeats of any integer of at least 3 and up to 12

<220>
<221> VARIANT
<222> (1)..(2)
<223> Can be present in repeats of any integer of at least 3 and up to 12

<400> 107
Gly Ser
1

<210> 108
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 108
gagaatcaaa atcggatgaat

20

<210> 109
<211> 516
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 109

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
			20				25					30			
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg
		35					40					45			
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
	50					55				60					
Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala
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	Ser	Leu	Lys	Ser	Glu	Asp	Thr
			100					105					110		
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly
		115					120					125			
Ala	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly
	130					135					140				
Ser	Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly
145					150					155					160
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Tyr	Thr	Tyr	Ser	Thr	Tyr	Ser	Asn
				165					170					175	
Tyr	Tyr	Met	Gly	Trp	Phe	Arg	Glu	Ala	Pro	Gly	Lys	Ala	Arg	Thr	Ser
		180						185					190		
Val	Ala	Ile	Ile	Ser	Ser	Asp	Thr	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val
		195					200					205			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
	210					215					220				
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys
225					230					235					240
Ala	Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr
				245					250					255	
Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
			260					265					270		
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
		275					280					285			
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
	290					295					300				
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys
305					310					315					320
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly
				325					330					335	
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val
			340					345					350		
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu
		355					360					365			
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly
	370					375					380				
Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu
385					390					395					400
Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly
				405					410					415	
Ser	Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile

Ala	Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr		
				245					250					255			
Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro		
			260					265					270				
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro		
		275					280					285					
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu		
	290					295					300						
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys		
305					310					315					320		
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly		
				325					330					335			
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val		
			340					345					350				
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu		
		355					360					365					
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp		
	370					375					380						
Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn		
385					390					395					400		
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg		
				405					410					415			
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly		
			420					425				430					
Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu		
		435					440					445					
Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu		
	450					455					460						
Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His		
465					470					475					480		
Met	Gln	Ala	Leu	Pro	Pro	Arg											
				485													

<210> 111

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 111

Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Asp		
1				5				10					15				
Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg	Ala	Phe	Ser	Thr	Tyr		
		20						25				30					
Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val		
		35					40					45					
Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala	Tyr	Ala	Asp	Ser	Val		
	50					55					60						
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr		
65					70					75					80		
Leu	Gln	Met	Asn	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		

				85					90				95		
Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly	Ala	Trp	Gly	Gln	Gly
			100					105					110		
Thr	Gln	Val	Thr	Val	Ser	Ser									
			115												

<210> 112
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 112															
Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly	Gly
1				5				10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Tyr	Thr	Tyr	Ser	Thr	Tyr	Ser	Asn	Tyr
			20					25					30		
Tyr	Met	Gly	Trp	Phe	Arg	Glu	Ala	Pro	Gly	Lys	Ala	Arg	Thr	Ser	Val
		35					40					45			
Ala	Ile	Ile	Ser	Ser	Asp	Thr	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu
65					70				75					80	
Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys	Ala
				85					90					95	
Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Gln
			100					105					110		
Val	Thr	Val	Ser	Ser											
			115												

<210> 113
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 113					
Ser	Thr	Tyr	Phe	Met	Ala
1				5	

<210> 114
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 114

Gly Ile Ala Trp Ser Gly Gly Ser Thr Ala Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 115

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 115

Ser Arg Gly Ile Glu Val Glu Glu Phe Gly Ala
1 5 10

<210> 116

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 116

Ser Asn Tyr Tyr Met Gly
1 5

<210> 117

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 117

Ile Ile Ser Ser Asp Thr Thr Ile Thr Tyr Lys Asp Ala Val Lys Gly
1 5 10 15

<210> 118

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 118

Ala Trp Thr Ser Asp Trp Ser Val Ala Tyr
1 5 10

<210> 119

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 119

Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10

<210> 120

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 120

Cys Pro Pro Cys Pro
1 5

<210> 121

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 121

Cys Pro Arg Cys Pro
1 5

<210> 122

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 122

Cys Pro Ser Cys Pro
1 5

<210> 123
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 123
Thr Val Ala Ala Pro
1 5

<210> 124
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 124
Gly Gly Gly Gly Ser
1 5

<210> 125
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 125
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> 126
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 126
Ser Ala Cys Tyr Cys Glu Leu Ser
1 5

<210> 127
<211> 17
<212> PRT
<213> Homo sapiens

<400> 127
Asp Arg Val Tyr Glu Glu Leu Asn Ile Tyr Ser Ala Thr Tyr Ser Glu
1 5 10 15
Leu

<210> 128
<211> 29
<212> PRT
<213> Homo sapiens

<400> 128
Ser Ser Pro Lys Gln His Pro Ser Glu Ser Val Tyr Thr Ala Leu Gln
1 5 10 15
Arg Arg Glu Thr Glu Val Tyr Ala Cys Ile Glu Asn Glu
20 25

<210> 129
<211> 18
<212> PRT
<213> Homo sapiens

<400> 129
Leu Tyr Thr Lys Leu Met Asn Glu Asp Pro Met Tyr Ser Met Tyr Ala
1 5 10 15
Lys Leu

<210> 130
<211> 18
<212> PRT
<213> Homo sapiens

<400> 130
Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser
1 5 10 15
Lys Leu

<210> 131
<211> 21
<212> PRT
<213> Homo sapiens

<400> 131

Val Leu Glu Tyr Leu Lys Ile Ala Gln Asn Leu Glu Met Tyr Gly Val
1 5 10 15
Asn Tyr Phe Ser Ile
20

<210> 132

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 132

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Thr Gln Ala Leu Leu
1 5 10 15
Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln
20 25 30
Tyr Ser His Leu Gly Gly Asn Gly Glu Asn Leu Tyr Phe Gln Ser Gly
35 40 45
Gly Asp Thr Gln Ala Leu Leu Arg Asn Asp Gln Val Tyr Gln Pro Leu
50 55 60
Arg Asp Arg Asp Asp Ala Gln Tyr Ser His Leu Gly Gly Asn Gly Asp
65 70 75 80
Thr Gln Ala Leu Leu Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp
85 90 95
Arg Asp Asp Ala Gln Tyr Ser His Leu Gly Gly Asn Gly Gly Ser Gly
100 105 110

<210> 133

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 133

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Gln Thr Leu Leu
1 5 10 15
Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln
20 25 30
Tyr Ser His Leu Gln Gly Asn Gly Glu Asn Leu Tyr Phe Gln Ser Gly
35 40 45
Gly Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu
50 55 60
Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly Asn Gly Asp
65 70 75 80
Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp
85 90 95

Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly
			100					105					110		

<210> 134
 <211> 76
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 134															
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Arg	Val	Tyr	Glu	Glu
1				5					10					15	
Leu	Asn	Ile	Tyr	Ser	Ala	Thr	Tyr	Ser	Glu	Leu	Gly	Glu	Asn	Leu	Tyr
			20					25					30		
Phe	Gln	Ser	Gly	Gly	Asp	Arg	Val	Tyr	Glu	Glu	Leu	Asn	Ile	Tyr	Ser
		35				40						45			
Ala	Thr	Tyr	Ser	Glu	Leu	Gly	Asp	Arg	Val	Tyr	Glu	Glu	Leu	Asn	Ile
	50					55					60				
Tyr	Ser	Ala	Thr	Tyr	Ser	Glu	Leu	Gly	Gly	Ser	Gly				
65					70					75					

<210> 135
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 135															
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Pro	Lys	Gln	His
1				5					10					15	
Pro	Ser	Glu	Ser	Val	Tyr	Thr	Ala	Leu	Gln	Arg	Arg	Glu	Thr	Glu	Val
			20					25					30		
Tyr	Ala	Cys	Ile	Glu	Asn	Glu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly
		35				40						45			
Gly	Ser	Ser	Pro	Lys	Gln	His	Pro	Ser	Glu	Ser	Val	Tyr	Thr	Ala	Leu
	50					55					60				
Gln	Arg	Arg	Glu	Thr	Glu	Val	Tyr	Ala	Cys	Ile	Glu	Asn	Glu	Gly	Ser
65					70					75				80	
Ser	Pro	Lys	Gln	His	Pro	Ser	Glu	Ser	Val	Tyr	Thr	Ala	Leu	Gln	Arg
			85						90					95	
Arg	Glu	Thr	Glu	Val	Tyr	Ala	Cys	Ile	Glu	Asn	Glu	Gly	Gly	Ser	Gly
			100					105					110		

<210> 136
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<223> Synthetic Construct

[illegible]

<213> Artificial Sequence

<223> Synthetic Construct

[illegible]

<210> 138
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 138
Ser Ala Cys Tyr Cys Glu Leu Ser Asp Thr Gln Ala Leu Leu Arg Asn
1 5 10 15
Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr Ser
20 25 30
His Leu Gly Gly Asn Cys Pro Ser Cys Pro Glu Arg Pro Pro Pro Val
35 40 45
Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr
50 55 60
Ser Gly Leu Asn Gln Arg Cys Pro Ser Cys Pro Asp Lys Gln Thr Leu
65 70 75 80
Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu Asp Asp
85 90 95
Gln Tyr Ser His Leu Gln Gly Asn Cys Pro Ser Cys Pro Arg Lys Gln
100 105 110
Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
115 120 125
Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Cys Pro Ser Cys Pro
130 135 140

<210> 139
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 139
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Asp Thr Gln Ala Leu Leu
1 5 10 15
Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln
20 25 30
Tyr Ser His Leu Gly Gly Asn Cys Pro Pro Cys Pro Glu Arg Pro Pro
35 40 45
Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp
50 55 60
Leu Tyr Ser Gly Leu Asn Gln Arg Cys Pro Pro Cys Pro Asp Lys Gln
65 70 75 80
Thr Leu Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu
85 90 95
Asp Asp Gln Tyr Ser His Leu Gln Gly Asn Cys Pro Pro Cys Pro Arg
100 105 110
Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly
115 120 125

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Cys Pro Pro Cys
130 135 140
Pro
145

<210> 140
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 140
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Thr Gln Ala Leu Leu
1 5 10 15
Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln
20 25 30
Tyr Ser His Leu Gly Gly Asn Cys Pro Arg Cys Pro Glu Arg Pro Pro
35 40 45
Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp
50 55 60
Leu Tyr Ser Gly Leu Asn Gln Arg Thr Val Ala Ala Pro Asp Lys Gln
65 70 75 80
Thr Leu Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu
85 90 95
Asp Asp Gln Tyr Ser His Leu Gln Gly Asn Cys Pro Ser Cys Pro Arg
100 105 110
Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly
115 120 125
Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Cys Pro Pro Cys
130 135 140
Pro
145

<210> 141
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 141
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Asp Thr Gln Ala Leu Leu
1 5 10 15
Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln
20 25 30
Tyr Ser His Leu Gly Gly Asn Cys Pro Pro Cys Pro Glu Arg Pro Pro
35 40 45
Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp
50 55 60

Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Cys	Pro	Ser	Cys	Pro	Asp	Lys	Gln
65					70				75					80	
Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	Glu
				85					90					95	
Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Cys	Pro	Arg	Cys	Pro	Arg
			100					105					110		
Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly
		115					120					125			
Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Thr	Val	Ala	Ala
	130					135					140				
Pro															
145															

<210> 142
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Glu	Arg	Pro	Pro	Pro	Val
1			5					10					15		
Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr
		20						25				30			
Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly	Asp	Thr	Gln	Ala	Leu	Leu
		35				40					45				
Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln
	50					55				60					
Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Arg	Lys	Gln	Arg	Ile
65				70						75				80	
Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp
			85					90					95		
Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Gly	Ser	Gly	Asp	Lys	Gln	Thr
			100					105				110			
Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	Glu	Asp
		115					120					125			
Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly			
	130					135					140				

<210> 143
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Lys	Gln	Thr	Leu	Leu
1			5					10					15		

Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp	Gln
			20					25					30		
Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly	Arg	Lys	Gln	Arg	Ile
		35					40					45			
Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp
		50				55					60				
Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Gly	Ser	Gly	Asp	Thr	Gln	Ala
65					70					75					80
Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp
			85						90					95	
Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Glu	Arg	Pro
			100					105					110		
Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg
		115					120					125			
Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly			
		130				135						140			

<210> 144

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 144

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Arg	Lys	Gln	Arg	Ile	Thr
1				5					10					15	
Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val
			20					25				30			
Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Gly	Ser	Gly	Asp	Lys	Gln	Thr	Leu
		35				40					45				
Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp
		50				55					60				
Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly	Glu	Arg	Pro	Pro
65				70						75					80
Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp
			85					90					95		
Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly	Asp	Thr	Gln	Ala
			100					105				110			
Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp
		115				120						125			
Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly			
		130				135						140			

<210> 145

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 145

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Glu	Arg	Pro	Pro	Pro	Val
1				5				10					15		
Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr
			20					25					30		
Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly						
		35					40								

<210> 146

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 146

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln	Ala	Leu	Leu
1				5				10						15	
Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln
			20					25					30		
Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly					
		35					40								

<210> 147

<211> 75

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 147

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln	Ala	Leu	Leu
1				5				10						15	
Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln
			20					25					30		
Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Glu	Arg	Pro	Pro	Pro
		35					40				45				
Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu
	50					55					60				
Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly					
65					70				75						

<210> 148

<211> 76

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 148

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Lys	Gln	Thr	Leu	Leu
1				5				10						15	
Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp	Gln
			20					25					30		
Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly	Arg	Lys	Gln	Arg	Ile
		35				40						45			
Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp
	50					55					60				
Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Gly	Ser	Gly				
65					70					75					

<210> 149

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 149

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln	Ala	Leu	Leu
1				5				10						15	
Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln
			20					25					30		
Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Glu	Arg	Pro	Pro	Pro
		35				40						45			
Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu
	50					55					60				
Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly	Glu	Arg	Pro	Pro	Pro
65					70				75						80
Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu
				85					90					95	
Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly					
			100					105							

<210> 150

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 150

Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln	Ala	Leu	Leu
1				5				10						15	
Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln
			20					25					30		
Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Glu	Arg	Pro	Pro	Pro

65					70					75				80
Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys
				85					90					95
Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly
			100					105					110	

<210> 153
 <211> 502
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 153

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35					40					45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70				75						80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85				90						95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100				105					110			
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
	115						120				125				
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150					155					160
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165				170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
	195					200						205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
	210					215					220				
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230					235					240
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
			260					265					270		
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275					280					285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
	290					295					300				

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 305 310 315 320
 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
 325 330 335
 Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
 340 345 350
 Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 355 360 365
 Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly
 370 375 380
 Cys Glu Leu Asp Thr Gln Ala Leu Leu Arg Asn Asp Gln Val Tyr Gln
 385 390 395 400
 Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr Ser His Leu Gly Gly Asn
 405 410 415
 Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys
 420 425 430
 Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Asp Lys Gln Thr
 435 440 445
 Leu Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu Asp
 450 455 460
 Asp Gln Tyr Ser His Leu Gln Gly Asn Arg Lys Gln Arg Ile Thr Glu
 465 470 475 480
 Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr
 485 490 495
 Ser Asp Leu Asn Thr Gln
 500

<210> 154

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 154

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15
 His Ala Ala Arg Pro Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu
 20 25 30
 Ala Met Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu
 35 40 45
 Ser Val Thr Ile Leu Gly Ser His Leu Ile His Trp Tyr Gln Gln Lys
 50 55 60
 Pro Gly Gln Pro Pro Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln
 65 70 75 80
 Thr Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe
 85 90 95
 Thr Leu Thr Ile Asp Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr
 100 105 110
 Cys Leu Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys
 115 120 125
 Leu Glu Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly

130		135		140	
Glu Gly Ser Thr Lys	Gly Gln Ile Gln Leu Val	Gln Ser Gly Pro Glu			
145	150	155	160		
Leu Lys Lys Pro Gly	Glu Thr Val Lys Ile Ser	Cys Lys Ala Ser Gly			
	165	170	175		
Tyr Thr Phe Thr Asp	Tyr Ser Ile Asn Trp Val	Lys Arg Ala Pro Gly			
	180	185	190		
Lys Gly Leu Lys Trp Met	Gly Trp Ile Asn Thr Glu	Thr Arg Glu Pro			
	195	200	205		
Ala Tyr Ala Tyr Asp Phe	Arg Gly Arg Phe Ala Phe	Ser Leu Glu Thr			
	210	215	220		
Ser Ala Ser Thr Ala Tyr	Leu Gln Ile Asn Asn	Leu Lys Tyr Glu Asp			
225	230	235	240		
Thr Ala Thr Tyr Phe Cys	Ala Leu Asp Tyr Ser	Tyr Ala Met Asp Tyr			
	245	250	255		
Trp Gly Gln Gly Thr Ser	Val Thr Val Ser Ser	Phe Val Pro Val Phe			
	260	265	270		
Leu Pro Thr Ser Thr Thr	Thr Pro Ala Pro Arg	Pro Pro Thr Pro Ala			
	275	280	285		
Pro Thr Ile Ala Ser Gln	Pro Leu Ser Leu Arg	Pro Glu Ala Cys Arg			
	290	295	300		
Pro Ala Ala Gly Gly Ala	Val His Thr Arg Gly	Leu Asp Phe Ala Cys			
305	310	315	320		
Asp Ile Tyr Ile Trp Ala	Pro Leu Ala Gly Thr	Cys Gly Val Leu Leu			
	325	330	335		
Leu Ser Leu Val Ile Thr	Leu Tyr Cys Lys Arg	Gly Arg Lys Lys Leu			
	340	345	350		
Leu Tyr Ile Phe Lys Gln	Pro Phe Met Arg Pro	Val Gln Thr Thr Gln			
	355	360	365		
Glu Glu Asp Gly Cys Ser	Cys Arg Phe Pro Glu	Glu Glu Glu Gly Gly			
	370	375	380		
Cys Glu Leu Gly Ser Gly	Ser Gly Ser Gly Ser	Asp Thr Gln			
385	390	395	400		
Ala Leu Leu Arg Asn Asp	Gln Val Tyr Gln Pro	Leu Arg Asp Arg Asp			
	405	410	415		
Asp Ala Gln Tyr Ser His	Leu Gly Gly Asn Gly	Gly Gly Gly Ser Glu			
	420	425	430		
Arg Pro Pro Pro Val Pro	Asn Pro Asp Tyr Glu	Pro Ile Arg Lys Gly			
	435	440	445		
Gln Arg Asp Leu Tyr Ser	Gly Leu Asn Gln Arg	Gly Gly Gly Gly Ser			
	450	455	460		
Asp Lys Gln Thr Leu Leu	Pro Asn Asp Gln Leu	Tyr Gln Pro Leu Lys			
465	470	475	480		
Asp Arg Glu Asp Asp Gln	Tyr Ser His Leu Gln	Gly Asn Gly Gly Gly			
	485	490	495		
Gly Ser Arg Lys Gln Arg	Ile Thr Glu Thr Glu	Ser Pro Tyr Gln Glu			
	500	505	510		
Leu Gln Gly Gln Arg Ser	Asp Val Tyr Ser Asp	Leu Asn Thr Gln Gly			
	515	520	525		
Gly Gly Gly Ser					
530					

<211> 530
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 155

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25				30			
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35				40					45				
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55				60					
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70				75					80	
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85				90						95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115				120					125				
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135				140					
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150				155					160	
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165				170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
		195				200					205				
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
	210					215				220					
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230				235					240	
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245				250						255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
			260					265					270		
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275					280					285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
	290				295					300					
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
305					310				315					320	
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu
				325					330					335	
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu
			340					345					350		
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
		355					360					365			

Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
370						375				380					
Cys	Glu	Leu	Ser	Ala	Cys	Tyr	Cys	Glu	Leu	Ser	Asp	Thr	Gln	Ala	Leu
385					390					395					400
Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala
				405					410					415	
Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Cys	Pro	Ser	Cys	Pro	Glu	Arg	Pro
			420				425						430		
Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg
		435				440						445			
Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Cys	Pro	Ser	Cys	Pro	Asp	Lys
450						455						460			
Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg
465					470					475					480
Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Cys	Pro	Ser	Cys	Pro
				485					490					495	
Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln
			500					505					510		
Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Cys	Pro	Ser
		515					520					525			
Cys	Pro														
530															

<210> 156

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 156

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35				40						45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
50					55					60					
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70					75					80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85				90						95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115				120						125			
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
130						135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150					155					160
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly

				165				170					175			
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly	
			180					185					190			
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro	
		195					200					205				
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	
		210				215					220					
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp	
225				230					235					240		
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr	
			245					250					255			
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe	
			260					265					270			
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	
		275					280					285				
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	
		290			295						300					
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	
305					310					315					320	
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	
			325						330					335		
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	
		340						345					350			
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	
		355				360						365				
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	
		370				375					380					
Cys	Glu	Leu	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Asp	Thr	Gln	
385				390						395				400		
Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	
			405						410					415		
Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Cys	Pro	Pro	Cys	Pro	Glu	
			420					425					430			
Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	
		435					440					445				
Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Cys	Pro	Pro	Cys	Pro	
		450				455					460					
Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	
465				470						475				480		
Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Cys	Pro	Pro	
			485					490					495			
Cys	Pro	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	
			500					505					510			
Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Cys	
		515					520					525				
Pro	Pro	Cys	Pro													
		530														

<210> 157

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 157

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35					40					45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70					75					80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120					125			
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150					155					160
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165					170					175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
		195				200						205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
	210					215					220				
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230					235					240
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
		260						265					270		
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275					280					285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
	290					295					300				
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
305					310					315					320
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu
				325					330					335	
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu
			340					345					350		
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
		355					360					365			
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
	370					375					380				
Cys	Glu	Leu	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Thr	Gln
385					390				395						400

Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	
				405					410					415		
Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Cys	Pro	Arg	Cys	Pro	Glu	
			420					425					430			
Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	
		435					440					445				
Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Thr	Val	Ala	Ala	Pro	
	450					455					460					
Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	
465				470					475					480		
Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Cys	Pro	Ser	
			485					490					495			
Cys	Pro	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	
		500					505					510				
Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Cys	
	515					520					525					
Pro	Pro	Cys	Pro													
	530															

<210> 158

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 158

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	
1				5				10					15			
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu	
			20				25					30				
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	
		35				40					45					
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys	
	50				55				60							
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln	
65				70				75						80		
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe	
			85				90					95				
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr	
		100					105					110				
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
	115					120					125					
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	
	130					135				140						
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	
145				150				155						160		
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
			165				170					175				
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly	
		180					185				190					
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro	

Met 1	Ala	Leu	Pro	Val 5	Thr	Ala	Leu	Leu	Leu 10	Pro	Leu	Ala	Leu	Leu 15	
His	Ala	Ala	Arg 20	Pro	Asp	Ile	Val	Leu 25	Thr	Gln	Ser	Pro	Pro 30	Ser	Leu
Ala	Met	Ser 35	Leu	Gly	Lys	Arg	Ala 40	Thr	Ile	Ser	Cys 45	Arg	Ala	Ser	Glu
Ser 50	Val	Thr	Ile	Leu	Gly 55	Ser	His	Leu	Ile	His 60	Trp	Tyr	Gln	Gln	Lys
Pro 65	Gly	Gln	Pro	Pro	Thr 70	Leu	Leu	Ile	Gln	Leu 75	Ala	Ser	Asn	Val	Gln
Thr	Gly	Val	Pro	Ala 85	Arg	Phe	Ser	Gly	Ser 90	Gly	Ser	Arg	Thr	Asp 95	Phe
Thr	Leu	Thr	Ile 100	Asp	Pro	Val	Glu	Glu 105	Asp	Asp	Val	Ala	Val	Tyr	Tyr
Cys	Leu	Gln 115	Ser	Arg	Thr	Ile	Pro 120	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
Leu	Glu 130	Ile	Lys	Gly	Ser	Thr 135	Ser	Gly	Ser	Gly 140	Lys	Pro	Gly	Ser	Gly
Glu 145	Gly	Ser	Thr	Lys 150	Gly	Gln	Ile	Gln	Leu 155	Val	Gln	Ser	Gly	Pro	Glu
Leu	Lys	Lys	Pro	Gly 165	Glu	Thr	Val	Lys	Ile 170	Ser	Cys	Lys	Ala	Ser	Gly
Tyr	Thr	Phe	Thr 180	Asp	Tyr	Ser	Ile	Asn 185	Trp	Val	Lys	Arg	Ala	Pro	Gly
Lys	Gly	Leu 195	Lys	Trp	Met	Gly 200	Trp	Ile	Asn 205	Thr	Glu	Thr	Arg	Glu	Pro
Ala	Tyr 210	Ala	Tyr	Asp	Phe	Arg 215	Gly	Arg	Phe 220	Ala	Phe	Ser	Leu	Glu	Thr
Ser 225	Ala	Ser	Thr	Ala 230	Tyr	Leu	Gln	Ile	Asn 235	Asn	Leu	Lys	Tyr	Glu	Asp
Thr	Ala	Thr	Tyr	Phe 245	Cys	Ala	Leu	Asp	Tyr 250	Ser	Tyr	Ala	Met	Asp	Tyr
Trp	Gly	Gln	Gly 260	Thr	Ser	Val	Thr	Val 265	Ser	Ser	Phe	Val	Pro	Val	Phe
Leu	Pro	Thr 275	Ser	Thr	Thr	Thr 280	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
Pro	Thr 290	Ile	Ala	Ser	Gln	Pro 295	Leu	Ser	Leu	Arg	Pro 300	Glu	Ala	Cys	Arg
Pro 305	Ala	Ala	Gly	Gly	Ala 310	Val	His	Thr	Arg	Gly 315	Leu	Asp	Phe	Ala	Cys
Asp	Ile	Tyr	Ile	Trp 325	Ala	Pro	Leu	Ala	Gly 330	Thr	Cys	Gly	Val	Leu	Leu
Leu	Ser	Leu	Val 340	Ile	Thr	Leu	Tyr	Cys 345	Lys	Arg	Gly	Arg	Lys	Lys	Leu
Leu	Tyr	Ile 355	Phe	Lys	Gln	Pro	Phe 360	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
Glu	Glu 370	Asp	Gly	Cys	Ser	Cys 375	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
Cys 385	Glu	Leu	Gly	Glu	Asn 390	Leu	Tyr	Phe	Gln	Ser 395	Gly	Gly	Glu	Arg	Pro
Pro	Pro	Val	Pro	Asn 405	Pro	Asp	Tyr	Glu	Pro 410	Ile	Arg	Lys	Gly	Gln	Arg
Asp	Leu	Tyr	Ser 420	Gly	Leu	Asn	Gln	Arg 425	Gly	Gly	Ser	Gly	Asp	Thr	Gln

Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp
		435					440					445			
Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Arg	Lys
	450					455					460				
Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln
465					470					475					480
Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Gly	Ser	Gly	Asp
			485						490					495	
Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp
		500					505						510		
Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly
		515					520					525			

<210> 160

<211> 528

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 160

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35				40						45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70				75						80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85				90						95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
	115						120					125			
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150					155					160
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165				170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
		195					200					205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
	210					215					220				
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230					235					240
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr

				245					250					255			
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe		
			260					265					270				
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala		
		275					280					285					
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg		
	290				295					300							
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys		
305					310				315						320		
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu		
			325					330					335				
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu		
		340					345					350					
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln		
		355					360				365						
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly		
	370					375				380							
Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Lys	Gln		
385					390				395					400			
Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	Glu		
			405					410					415				
Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly	Arg	Lys		
		420					425					430					
Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln		
	435					440				445							
Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Gly	Ser	Gly	Asp		
	450				455				460								
Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp		
465					470				475					480			
Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly		
			485				490					495					
Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys		
		500					505					510					
Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly		
	515						520					525					

<210> 161

<211> 528

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 161

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu		
1				5				10					15				
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu		
		20					25					30					
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu		
	35				40						45						
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys		
	50					55					60						

Pro 65	Gly	Gln	Pro	Pro	Thr 70	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln 80
Thr	Gly	Val	Pro	Ala 85	Arg	Phe	Ser	Gly	Ser 90	Gly	Ser	Arg	Thr	Asp 95	Phe
Thr	Leu	Thr	Ile 100	Asp	Pro	Val	Glu	Glu 105	Asp	Asp	Val	Ala	Val 110	Tyr	Tyr
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly 125	Gly	Thr	Lys
Leu	Glu 130	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys 140	Pro	Gly	Ser	Gly
Glu 145	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val 155	Gln	Ser	Gly	Pro	Glu 160
Leu	Lys	Lys	Pro	Gly 165	Glu	Thr	Val	Lys	Ile 170	Ser	Cys	Lys	Ala	Ser	Gly 175
Tyr	Thr	Phe	Thr 180	Asp	Tyr	Ser	Ile	Asn 185	Trp	Val	Lys	Arg	Ala 190	Pro	Gly
Lys	Gly	Leu 195	Lys	Trp	Met	Gly	Trp 200	Ile	Asn	Thr	Glu	Thr 205	Arg	Glu	Pro
Ala	Tyr 210	Ala	Tyr	Asp	Phe	Arg	Gly 215	Arg	Phe	Ala	Phe 220	Ser	Leu	Glu	Thr
Ser 225	Ala	Ser	Thr	Ala	Tyr 230	Leu	Gln	Ile	Asn 235	Asn	Leu	Lys	Tyr	Glu	Asp 240
Thr	Ala	Thr	Tyr	Phe 245	Cys	Ala	Leu	Asp	Tyr 250	Ser	Tyr	Ala	Met	Asp 255	Tyr
Trp	Gly	Gln	Gly 260	Thr	Ser	Val	Thr 265	Val	Ser	Ser	Phe	Val 270	Pro	Val	Phe
Leu	Pro	Thr 275	Ser	Thr	Thr	Thr	Pro 280	Ala	Pro	Arg	Pro 285	Pro	Thr	Pro	Ala
Pro	Thr 290	Ile	Ala	Ser	Gln	Pro	Leu 295	Ser	Leu	Arg	Pro 300	Glu	Ala	Cys	Arg
Pro 305	Ala	Ala	Gly	Gly	Ala	Val	His 310	Thr	Arg	Gly	Leu 315	Asp	Phe	Ala	Cys 320
Asp	Ile	Tyr	Ile	Trp 325	Ala	Pro	Leu	Ala	Gly 330	Thr	Cys	Gly	Val	Leu	Leu 335
Leu	Ser	Leu	Val 340	Ile	Thr	Leu	Tyr 345	Cys	Lys	Arg	Gly	Arg 350	Lys	Lys	Leu
Leu	Tyr	Ile 355	Phe	Lys	Gln	Pro	Phe 360	Met	Arg	Pro	Val 365	Gln	Thr	Thr	Gln
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg 375	Phe	Pro	Glu	Glu 380	Glu	Glu	Gly	Gly
Cys 385	Glu	Leu	Gly	Glu	Asn 390	Leu	Tyr	Phe	Gln	Ser 395	Gly	Gly	Arg	Lys	Gln 400
Arg	Ile	Thr	Glu	Thr 405	Glu	Ser	Pro	Tyr	Gln 410	Glu	Leu	Gln	Gly	Gln	Arg 415
Ser	Asp	Val	Tyr 420	Ser	Asp	Leu	Asn 425	Thr	Gln	Gly	Gly	Ser 430	Gly	Asp	Lys
Gln	Thr	Leu	Leu 435	Pro	Asn	Asp	Gln 440	Leu	Tyr	Gln	Pro 445	Leu	Lys	Asp	Arg
Glu	Asp 450	Asp	Gln	Tyr	Ser	His 455	Leu	Gln	Gly	Asn 460	Gly	Gly	Ser	Gly	Glu
Arg 465	Pro	Pro	Pro	Val	Pro	Asn 470	Pro	Asp	Tyr	Glu 475	Pro	Ile	Arg	Lys	Gly 480
Gln	Arg	Asp	Leu	Tyr 485	Ser	Gly	Leu	Asn 490	Gln	Arg	Gly	Gly	Ser	Gly	Asp 495

Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp
			500					505					510		
Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly
		515					520					525			

<210> 162
 <211> 429
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 162

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35				40						45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70					75					80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
	115						120					125			
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150					155					160
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165					170					175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
	195					200						205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
	210					215					220				
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230					235					240
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
			260					265					270		
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275					280					285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
	290					295					300				
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys

305					310					315				320
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu
				325					330					335
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys
			340					345					350	
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr
		355					360					365		
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Gly	Gly
	370					375				380				
Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Glu	Arg
385					390				395					400
Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln
			405					410					415	
Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly		
			420					425						

<210> 163

<211> 430

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 163

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35				40					45				
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55				60					
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70				75					80	
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
			85					90						95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100				105					110			
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
	115					120					125				
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135				140					
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145				150					155					160	
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
			165					170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180				185						190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
	195					200						205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
	210					215					220				

Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230					235					240
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
			260					265						270	
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275					280					285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
	290				295					300					
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
305					310					315					320
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu
				325					330					335	
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu
			340					345					350		
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
	355						360					365			
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
	370					375					380				
Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln
385					390					395					400
Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp
				405					410					415	
Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly		
			420					425					430		

<210> 164

<211> 462

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 164

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35					40					45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70					75					80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120					125			
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly

130		135		140	
Glu Gly Ser Thr Lys	Gly Gln Ile Gln Leu Val	Gln Ser Gly Pro Glu			
145	150	155	160		
Leu Lys Lys Pro Gly	Glu Thr Val Lys Ile Ser	Cys Lys Ala Ser Gly			
165	170	175			
Tyr Thr Phe Thr Asp	Tyr Ser Ile Asn Trp Val	Lys Arg Ala Pro Gly			
180	185	190			
Lys Gly Leu Lys Trp Met	Gly Trp Ile Asn Thr Glu	Thr Arg Glu Pro			
195	200	205			
Ala Tyr Ala Tyr Asp Phe	Arg Gly Arg Phe Ala Phe	Ser Leu Glu Thr			
210	215	220			
Ser Ala Ser Thr Ala Tyr	Leu Gln Ile Asn Asn	Leu Lys Tyr Glu Asp			
225	230	235			
Thr Ala Thr Tyr Phe Cys	Ala Leu Asp Tyr Ser	Tyr Ala Met Asp Tyr			
245	250	255			
Trp Gly Gln Gly Thr Ser	Val Thr Val Ser Ser	Phe Val Pro Val Phe			
260	265	270			
Leu Pro Thr Ser Thr Thr	Thr Pro Ala Pro Arg	Pro Pro Thr Pro Ala			
275	280	285			
Pro Thr Ile Ala Ser Gln	Pro Leu Ser Leu Arg	Pro Glu Ala Cys Arg			
290	295	300			
Pro Ala Ala Gly Gly Ala	Val His Thr Arg Gly	Leu Asp Phe Ala Cys			
305	310	315			
Asp Ile Tyr Ile Trp Ala	Pro Leu Ala Gly Thr	Cys Gly Val Leu Leu			
325	330	335			
Leu Ser Leu Val Ile Thr	Leu Tyr Cys Lys Arg	Gly Arg Lys Lys Leu			
340	345	350			
Leu Tyr Ile Phe Lys Gln	Pro Phe Met Arg Pro	Val Gln Thr Thr Gln			
355	360	365			
Glu Glu Asp Gly Cys Ser	Cys Arg Phe Pro Glu	Glu Glu Glu Gly Gly			
370	375	380			
Cys Glu Leu Gly Glu Asn	Leu Tyr Phe Gln Ser	Gly Gly Asp Thr Gln			
385	390	395			
Ala Leu Leu Arg Asn Asp	Gln Val Tyr Gln Pro	Leu Arg Asp Arg Asp			
405	410	415			
Asp Ala Gln Tyr Ser His	Leu Gly Gly Asn Gly	Gly Ser Gly Glu Arg			
420	425	430			
Pro Pro Pro Val Pro Asn	Pro Asp Tyr Glu Pro	Ile Arg Lys Gly Gln			
435	440	445			
Arg Asp Leu Tyr Ser Gly	Leu Asn Gln Arg Gly	Gly Ser Gly			
450	455	460			

<210> 165
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 165
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu	
			20					25					30			
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	
		35					40					45				
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys	
	50					55					60					
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln	
65					70					75					80	
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe	
				85					90					95		
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr	
			100					105					110			
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
		115					120					125				
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	
	130					135					140					
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	
145					150					155					160	
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
				165					170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly	
			180					185					190			
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro	
		195				200						205				
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	
	210					215				220						
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp	
225					230					235					240	
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr	
				245					250					255		
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe	
			260					265					270			
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	
		275					280					285				
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	
	290					295					300					
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	
305					310					315					320	
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	
				325					330					335		
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	
			340					345					350			
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	
		355					360					365				
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	
	370					375					380					
Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Lys	Gln	
385					390					395					400	
Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	Glu	
				405					410					415		
Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly	Arg	Lys	
		420						425					430			
Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	
		435					440					445				

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

<210> 166

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 166

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25				30			
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35					40					45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50					55					60				
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70					75					80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120					125			
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150					155					160
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165					170					175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
		195				200						205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
					215					220					
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230					235					240
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
			260					265					270		
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275						280				285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
	290					295					300				
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
305					310					315					320
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu

				325					330					335			
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu		
			340					345					350				
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln		
		355					360					365					
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly		
	370					375					380						
Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln		
385					390					395					400		
Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp		
			405					410						415			
Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Glu	Arg		
		420					425						430				
Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln		
		435				440						445					
Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly	Glu	Arg		
	450				455					460							
Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln		
465					470				475						480		
Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly				
				485				490									

<210> 167

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 167

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu		
1				5				10					15				
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu		
			20				25					30					
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu		
	35				40						45						
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys		
	50				55				60								
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln		
65					70				75						80		
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe		
			85				90						95				
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr		
		100					105					110					
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys		
	115				120						125						
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly		
	130				135					140							
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu		
145					150				155						160		
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly		
				165				170						175			

Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly	
			180					185					190			
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro	
		195					200					205				
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	
	210					215					220					
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp	
225					230					235					240	
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr	
				245				250						255		
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe	
			260					265					270			
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	
		275					280					285				
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	
	290					295					300					
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	
305					310					315					320	
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	
				325					330					335		
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	
			340					345					350			
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	
		355					360					365				
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	
	370					375				380						
Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln	
385					390					395					400	
Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	
				405					410					415		
Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Glu	Arg	
			420					425					430			
Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	
		435					440					445				
Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly	Asp	Lys	
	450					455					460					
Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro	Leu	Lys	Asp	Arg	
465					470					475					480	
Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly	Gly	Ser	Gly		
				485					490					495		

<210> 168

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 168

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	
1				5					10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu	

20						25						30			
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35					40					45			
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
		50				55					60				
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65					70					75					80
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85					90					95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115					120					125			
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
		130				135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145					150					155					160
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165				170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
		195					200					205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
		210				215					220				
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225					230					235					240
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
			260					265					270		
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275					280					285			
Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg
		290				295					300				
Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys
				310						315					320
Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu
				325					330					335	
Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu
			340					345					350		
Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln
		355					360					365			
Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly
		370				375					380				
Cys	Glu	Leu	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg	Lys	Gln

450		455		460											
Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu
465				470					475						480
Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly
			485						490					495	
Ser	Gly														

<210> 169
 <211> 498
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 169

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Pro	Ser	Leu
			20					25					30		
Ala	Met	Ser	Leu	Gly	Lys	Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu
		35				40					45				
Ser	Val	Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys
	50				55					60					
Pro	Gly	Gln	Pro	Pro	Thr	Leu	Leu	Ile	Gln	Leu	Ala	Ser	Asn	Val	Gln
65				70					75					80	
Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe
				85				90						95	
Thr	Leu	Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr
			100					105					110		
Cys	Leu	Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		115				120					125				
Leu	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly
	130					135					140				
Glu	Gly	Ser	Thr	Lys	Gly	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu
145				150					155					160	
Leu	Lys	Lys	Pro	Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
				165				170						175	
Tyr	Thr	Phe	Thr	Asp	Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly
			180					185					190		
Lys	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro
		195				200						205			
Ala	Tyr	Ala	Tyr	Asp	Phe	Arg	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr
	210					215					220				
Ser	Ala	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Tyr	Glu	Asp
225				230					235					240	
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Leu	Asp	Tyr	Ser	Tyr	Ala	Met	Asp	Tyr
				245				250						255	
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Phe	Val	Pro	Val	Phe
		260					265						270		
Leu	Pro	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala
		275					280					285			

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
 290 295 300
 Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 305 310 315 320
 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
 325 330 335
 Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu
 340 345 350
 Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
 355 360 365
 Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly
 370 375 380
 Cys Glu Leu Gly Gly Gly Gly Ser Gly Gly Gly Ser Arg Lys Gln
 385 390 395 400
 Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
 405 410 415
 Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Gly Glu Asn Leu Tyr Phe
 420 425 430
 Gln Ser Gly Gly Asp Thr Gln Ala Leu Leu Arg Asn Asp Gln Val Tyr
 435 440 445
 Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr Ser His Leu Gly Gly
 450 455 460
 Asn Gly Glu Arg Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile
 465 470 475 480
 Arg Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Gly Gly
 485 490 495
 Ser Gly

<210> 170

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 170

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15
 His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu
 20 25 30
 Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
 35 40 45
 Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln
 50 55 60
 Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser
 65 70 75 80
 Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
 85 90 95
 Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
 100 105 110
 Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	
1				5					10					15		
His	Ala	Ala	Arg	Pro	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	
			20					25					30			
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	
		35					40					45				
Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Gln	
	50					55					60					
Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	
65				70					75						80	
Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	
			85						90					95		
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	
			100					105					110			
Ala	Asp	Tyr	Tyr	Cys	Ala	Arg	Ser	Asn	Tyr	Tyr	Gly	Ser	Ser	Tyr	Trp	
		115					120					125				
Phe	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	Ile	Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	
			165						170					175		
Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Val	Asn	Tyr	Met	Asp	Trp		
			180					185					190			
Tyr	Gln	Lys	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	
		195					200					205				
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	
	210					215					220					
Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	
225				230						235					240	
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	
				245					250					255		
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	
			260					265					270			
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	
		275					280					285				
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	
	290					295					300					
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	
305				310						315					320	
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	
			325						330					335		
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	
			340					345					350			
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	
		355					360					365				
Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	
	370					375					380					
Ser	Gly	Gly	Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	
385				390						395					400	
Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	
			405						410					415		
Gly	Gly	Ser	Gly	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	
			420					425					430			

Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr
435 440 445
Gln Gly Gly Ser Gly
450

<210> 172
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 172
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu
20 25 30
Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
35 40 45
Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln
50 55 60
Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser
65 70 75 80
Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser
85 90 95
Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
100 105 110
Ala Asp Tyr Tyr Cys Ala Arg Ser Asn Tyr Tyr Gly Ser Ser Tyr Trp
115 120 125
Phe 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 Ile Leu Ser Ala Ser Pro Gly Glu Lys
165 170 175
Val Thr Met Thr Cys Arg Ala Ser Ser Val Asn Tyr Met Asp Trp
180 185 190
Tyr Gln Lys Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr
195 200 205
Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
210 215 220
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala
225 230 235 240
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr Phe Gly
245 250 255
Gly Gly Thr Lys Leu Glu Ile Lys Thr Ser Thr Thr Thr Pro Ala Pro
260 265 270
Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
275 280 285
Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
290 295 300
Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly

305					310					315				320
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys
				325					330					335
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met
			340					345					350	
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe
		355					360					365		
Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Gly	Gly	Gly	Ser	Gly
	370					375					380			
Gly	Gly	Ser	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr
385				390					395					400
Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr
			405					410						415
Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Glu	Arg	Pro	Pro	Pro
		420					425					430		
Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu
	435					440						445		
Ser	Gly	Leu	Asn	Gln	Arg	Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn
	450					455					460			
Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser
465				470					475					480
Leu	Gly	Gly	Asn	Gly	Gly	Ser	Gly							
			485											

<210> 173

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 173

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu
			20				25					30			
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
	35					40					45				
Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Gln
	50				55				60						
Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser
65				70				75						80	
Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser
			85				90						95		
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser
		100					105					110			
Ala	Asp	Tyr	Tyr	Cys	Ala	Arg	Ser	Asn	Tyr	Tyr	Gly	Ser	Ser	Tyr	Trp
	115					120					125				
Phe	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	Ile	Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	
				165					170					175		
Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	Asp	Trp	
			180					185					190			
Tyr	Gln	Lys	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	
		195					200					205				
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	
	210					215					220					
Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	
225					230					235					240	
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	
				245					250					255		
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	
			260					265					270			
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	
		275					280					285				
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	
	290					295					300					
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	
305					310					315					320	
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	
				325					330					335		
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	
			340					345					350			
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	
		355					360					365				
Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
	370					375					380					
Gly	Gly	Ser	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	
385					390					395					400	
Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	
				405					410					415		
Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln	Ala	Leu	Leu	
			420					425					430			
Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	
		435					440					445				
Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	
	450					455					460					
Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	
465					470					475					480	
Leu	Asn	Gln	Arg	Gly	Gly	Ser	Gly									
				485												

<210> 174

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 174

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1				5					10					15			
His	Ala	Ala	Arg	Pro	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu		
			20					25					30				
Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr		
		35					40					45					
Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Gln		
	50				55						60						
Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser		
65				70					75						80		
Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser		
			85					90					95				
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser		
			100					105					110				
Ala	Asp	Tyr	Tyr	Cys	Ala	Arg	Ser	Asn	Tyr	Tyr	Gly	Ser	Ser	Tyr	Trp		
		115					120					125					
Phe	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	Ile	Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys		
			165					170						175			
Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	Asp	Trp		
			180					185					190				
Tyr	Gln	Lys	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr		
	195					200						205					
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser		
	210					215				220							
Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala		
225				230					235						240		
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly		
			245					250						255			
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro		
		260					265						270				
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu		
		275					280					285					
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg		
	290					295					300						
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly		
305				310					315						320		
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys		
			325					330						335			
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg		
		340					345						350				
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro		
		355				360						365					
Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln		
	370				375						380						
Ser	Gly	Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro		
385				390						395					400		
Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly		
			405					410						415			
Gly	Ser	Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln		
		420					425					430					
Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn		

Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	
			260					265					270			
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	
		275					280					285				
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	
	290					295					300					
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	
305					310					315					320	
Thr	Cys	Gly	Val	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys		
			325					330					335			
Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	
			340					345					350			
Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	
		355					360					365				
Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	
	370					375					380					
Ser	Gly	Gly	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	
385					390					395					400	
Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	
				405					410						415	
Gly	Gly	Ser	Gly	Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	
			420					425					430			
Gln	Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	
		435					440					445				
Asn	Gly	Gly	Ser	Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	
	450					455					460					
Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	
465					470					475					480	
Arg	Gly	Gly	Ser	Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	
				485					490					495		
Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	
			500					505					510			
Gly	Asn	Gly	Gly	Ser	Gly											
		515														

<210> 176

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 176

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu	
1				5				10					15			
His	Ala	Ala	Arg	Pro	Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	
			20					25					30			
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg	
		35					40					45				
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	
	50					55				60						
Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala	

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	Ser	Leu	Lys	Ser	Glu	Asp	Thr	
				100					105					110		
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly	
				115					120					125		
Ala	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	
				130					135					140		
Ser	Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly	
145					150					155					160	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Tyr	Thr	Tyr	Ser	Thr	Tyr	Ser	Asn	
				165					170					175		
Tyr	Tyr	Met	Gly	Trp	Phe	Arg	Glu	Ala	Pro	Gly	Lys	Ala	Arg	Thr	Ser	
				180					185					190		
Val	Ala	Ile	Ile	Ser	Ser	Asp	Thr	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val	
				195					200					205		
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	
				210					215					220		
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys	
225					230					235					240	
Ala	Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	
				245					250					255		
Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	
				260					265					270		
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	
				275					280					285		
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	
				290					295					300		
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	
305					310					315					320	
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	
				325					330					335		
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	
				340					345					350		
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	
				355					360					365		
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	
				370					375					380		
Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	
385					390					395					400	
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	
				405					410					415		
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	
				420					425					430		
Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	
				435					440					445		
Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	
				450					455					460		
Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	
465					470					475					480	
Met	Gln	Ala														

<210> 177
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 177

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
			20				25					30			
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg
		35					40					45			
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
	50					55				60					
Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala
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	Ser	Leu	Lys	Ser	Glu	Asp	Thr
		100					105					110			
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly
		115				120					125				
Ala	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly
	130					135				140					
Ser	Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly
145				150					155					160	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Tyr	Thr	Tyr	Ser	Thr	Tyr	Ser	Asn
			165					170					175		
Tyr	Tyr	Met	Gly	Trp	Phe	Arg	Glu	Ala	Pro	Gly	Lys	Ala	Arg	Thr	Ser
		180					185					190			
Val	Ala	Ile	Ile	Ser	Ser	Asp	Thr	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val
		195				200						205			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
	210				215					220					
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys
225				230					235					240	
Ala	Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr
			245					250					255		
Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
		260					265					270			
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
		275				280						285			
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
	290				295					300					
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys
305				310					315					320	
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly
			325					330					335		
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val
			340				345					350			

Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu		
		355					360					365					
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly		
	370					375					380						
Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu		
385					390					395					400		
Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly		
			405						410					415			
Ser	Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile		
		420						425					430				
Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly		
	435						440					445					
Ser	Gly																
	450																

<210> 178

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 178

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu		
1				5					10					15			
His	Ala	Ala	Arg	Pro	Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu		
			20					25					30				
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg		
	35						40					45					
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys		
	50					55				60							
Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala		
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	Ser	Leu	Lys	Ser	Glu	Asp	Thr		
	100						105					110					
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly		
	115					120				125							
Ala	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly		
	130					135				140							
Ser	Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly		
145				150					155					160			
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Tyr	Thr	Tyr	Ser	Thr	Tyr	Ser	Asn		
			165					170					175				
Tyr	Tyr	Met	Gly	Trp	Phe	Arg	Glu	Ala	Pro	Gly	Lys	Ala	Arg	Thr	Ser		
		180					185					190					
Val	Ala	Ile	Ile	Ser	Ser	Asp	Thr	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val		
	195					200						205					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr		
	210					215				220							
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys		

225					230					235				240
Ala	Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly
				245					250				255	
Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg
			260					265					270	
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg
		275					280					285		
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly
	290				295					300				
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr
305				310					315					320
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg
			325					330					335	
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro
			340				345					350		Val
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu
	355						360					365		
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser
	370				375				380					
Gly	Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln	Pro
385					390				395					400
Lys	Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly
			405					410					415	
Ser	Gly	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln
		420					425					430		Glu
Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln
	435					440					445			Gly
Gly	Ser	Gly												
	450													

<210> 179

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 179

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu
1				5					10				15	
His	Ala	Ala	Arg	Pro	Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Leu
			20				25					30		
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Arg
	35					40					45			
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly
	50				55				60					Lys
Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr
65				70				75						80
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn
			85				90					95		Ala
Lys	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Ser	Glu	Asp
			100				105						110	Thr

<210> 180
<211> 486
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 180

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	
His	Ala	Ala	Arg	Pro	Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
			20					25					30		
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg
		35					40					45			
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
	50					55					60				
Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala
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	Ser	Leu	Lys	Ser	Glu	Asp	Thr
			100					105					110		
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly
		115					120					125			
Ala	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly
	130					135						140			
Ser	Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly
145					150					155					160
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Tyr	Thr	Tyr	Ser	Thr	Tyr	Ser	Asn
				165					170					175	
Tyr	Tyr	Met	Gly	Trp	Phe	Arg	Glu	Ala	Pro	Gly	Lys	Ala	Arg	Thr	Ser
			180					185					190		
Val	Ala	Ile	Ile	Ser	Ser	Asp	Thr	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val
		195					200						205		
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
	210					215						220			
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys
225					230					235					240
Ala	Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr
				245					250					255	
Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
			260					265					270		
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
		275					280						285		
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
	290					295					300				
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys
305					310				315						320
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly
				325					330					335	
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val
			340					345					350		
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu
		355					360					365			
Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
	370					375					380				
Ser	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu

385					390					395				400	
Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly	Glu
				405					410					415	
Asn	Leu	Tyr	Phe	Gln	Ser	Gly	Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn
			420					425					430		
Asp	Gln	Val	Tyr	Gln	Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser
		435					440					445			
His	Leu	Gly	Gly	Asn	Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp
	450					455					460				
Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn
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Gln	Arg	Gly	Gly	Ser	Gly										
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<210> 181

<211> 516

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 181

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His	Ala	Ala	Arg	Pro	Ala	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
			20					25					30		
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg
		35					40					45			
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
	50					55				60					
Glu	Arg	Glu	Phe	Val	Ala	Gly	Ile	Ala	Trp	Ser	Gly	Gly	Ser	Thr	Ala
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	Ser	Leu	Lys	Ser	Glu	Asp	Thr
			100					105					110		
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Arg	Gly	Ile	Glu	Val	Glu	Glu	Phe	Gly
		115					120					125			
Ala	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly
	130					135					140				
Ser	Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly
145					150					155					160
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Tyr	Thr	Tyr	Ser	Thr	Tyr	Ser	Asn
				165					170					175	
Tyr	Tyr	Met	Gly	Trp	Phe	Arg	Glu	Ala	Pro	Gly	Lys	Ala	Arg	Thr	Ser
			180					185					190		
Val	Ala	Ile	Ile	Ser	Ser	Asp	Thr	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val
		195					200					205			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
	210					215					220				
Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys
225					230					235					240

Ala	Ala	Trp	Thr	Ser	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr		
				245					250					255			
Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro		
			260					265					270				
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro		
		275					280					285					
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu		
	290					295				300							
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys		
305					310				315						320		
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly		
			325					330						335			
Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val		
			340					345					350				
Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu		
		355					360					365					
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	370					375					380						
Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg		
385					390				395						400		
Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly	Gly	Ser		
			405					410						415			
Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro	Leu		
		420						425					430				
Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly	Gly		
	435				440							445					
Ser	Gly	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu		
	450				455					460							
Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr	Gln	Gly		
465					470				475					480			
Gly	Ser	Gly	Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln		
			485					490						495			
Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn		
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Gly	Gly	Ser	Gly														
		515															

<210> 182

<211> 516

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 182

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu		
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		20					25					30					
Val	Gln	Ala	Gly	Asp	Ser	Leu	Arg	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Arg		
	35					40				45							
Ala	Phe	Ser	Thr	Tyr	Phe	Met	Ala	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys		

	50					55					60				
Glu 65	Arg	Glu	Phe	Val	Ala 70	Gly	Ile	Ala	Trp	Ser 75	Gly	Gly	Ser	Thr	Ala 80
Tyr	Ala	Asp	Ser	Val 85	Lys	Gly	Arg	Phe	Thr 90	Ile	Ser	Arg	Asp	Asn 95	Ala
Lys	Asn	Thr	Val 100	Tyr	Leu	Gln	Met	Asn 105	Ser	Leu	Lys	Ser	Glu	Asp 110	Thr
Ala	Val	Tyr	Tyr 115	Cys	Ala	Ser	Arg	Gly 120	Ile	Glu	Val	Glu	Glu	Phe	Gly
Ala	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr 130	Val	Ser	Ser	Gly	Gly	Gly	Gly
Ser 145	Gln	Val	Gln	Leu	Glu 150	Glu	Ser	Gly	Gly	Gly	Ser	Val	Gln	Ala	Gly 160
Gly	Ser	Leu	Arg	Leu 165	Ser	Cys	Ala	Tyr	Thr 170	Tyr	Ser	Thr	Tyr	Ser	Asn 175
Tyr	Tyr	Met	Gly 180	Trp	Phe	Arg	Glu	Ala 185	Pro	Gly	Lys	Ala	Arg	Thr	Ser
Val	Ala	Ile 195	Ile	Ser	Ser	Asp	Thr 200	Thr	Ile	Thr	Tyr	Lys	Asp	Ala	Val
Lys	Gly	Arg	Phe	Thr	Ile	Ser 215	Lys	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
Leu 225	Gln	Met	Asn	Ser	Leu 230	Lys	Pro	Glu	Asp	Ser	Ala	Met	Tyr	Arg	Cys 240
Ala	Ala	Trp	Thr	Ser 245	Asp	Trp	Ser	Val	Ala	Tyr	Trp	Gly	Gln	Gly	Thr
Gln	Val	Thr	Val 260	Ser	Ser	Thr	Ser	Thr 265	Thr	Thr	Pro	Ala	Pro	Arg	Pro
Pro	Thr	Pro 275	Ala	Pro	Thr	Ile	Ala 280	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
Glu	Ala	Cys	Arg	Pro	Ala	Ala 295	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
Asp 305	Phe	Ala	Cys	Asp	Ile 310	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys 320
Gly	Val	Leu	Leu	Leu 325	Ser	Leu	Val	Ile	Thr 330	Leu	Tyr	Cys	Lys	Arg	Gly
Arg	Lys	Lys	Leu 340	Leu	Tyr	Ile	Phe	Lys 345	Gln	Pro	Phe	Met	Arg	Pro	Val
Gln	Thr	Thr 355	Gln	Glu	Glu	Asp	Gly 360	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu
Glu	Glu	Gly 370	Gly	Cys	Glu	Leu	Gly 375	Glu	Asn	Leu	Tyr	Phe	Gln	Ser	Gly
Gly 385	Arg	Lys	Gln	Arg	Ile 390	Thr	Glu	Thr	Glu	Ser	Pro	Tyr	Gln	Glu	Leu 400
Gln	Gly	Gln	Arg	Ser 405	Asp	Val	Tyr	Ser	Asp 410	Leu	Asn	Thr	Gln	Gly	Gly
Ser	Gly	Asp	Lys 420	Gln	Thr	Leu	Leu	Pro 425	Asn	Asp	Gln	Leu	Tyr	Gln	Pro
Leu	Lys	Asp	Arg 435	Glu	Asp	Asp	Gln 440	Tyr	Ser	His	Leu	Gln	Gly	Asn	Gly
Gly	Ser	Gly 450	Glu	Arg	Pro	Pro	Pro 455	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro
Ile 465	Arg	Lys	Gly	Gln	Arg 470	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly 480
Gly	Ser	Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln

				485					490					495
Pro	Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly
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			515											

<210> 183
 <211> 2748
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 183

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<210> 184

<211> 2637

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 184

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<210> 185

<211> 2640

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 185

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2829

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<210> 198

<211> 181

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 198

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Met Gly Ser Ser Asn Ser Lys Arg Gln Gln Gln Gly Leu Leu Lys Leu
1           5           10           15
Trp Arg Gly Leu Arg Gly Lys Pro Gly Ala Asp Trp Val Leu Leu Ser
           20           25           30
Asp Pro Leu Ile Gly Gln Ser Ser Thr Val Gln Glu Glu Cys Gly Lys

```


<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 200

Met	Gly	Ser	Ser	Asn	Ser	Lys	Arg	Gln	Gln	Gln	Gly	Leu	Leu	Lys	Leu
1				5				10						15	
Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Leu	Arg	Gln	Met	Thr	Tyr	Lys	Leu
		35					40					45			
Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly	Leu	Asp	Gly
	50					55					60				
Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Glu	Lys	Ile	Leu	Asn	Leu	Tyr	Ala	Leu
65				70					75						80
Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser	Pro	Gly	Pro
				85				90						95	
Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys	Leu	Val	Pro
			100					105					110		
Val	Asp	Leu	Gly	Glu	Val	Leu	Val	Trp	Lys	Phe	Asp	Pro	Lys	Leu	Ala
		115					120					125			
Val	Glu	Tyr	Arg	Pro	Asp	Met	Phe	Lys	Asp	Met	His	Glu	His	Ala	Lys
	130					135					140				
Arg															
145															

<210> 201
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 201

Met	Gly	Ser	Ser	Asn	Ser	Lys	Arg	Gln	Gln	Gln	Gly	Leu	Leu	Lys	Leu
1				5				10						15	
Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Leu	Arg	Gln	Met	Thr	Tyr	Lys	Leu
		35					40					45			
Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly	Leu	Asp	Gly
	50					55					60				
Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Glu	Lys	Ile	Leu	Asn	Leu	Tyr	Ala	Leu
65				70					75						80
Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser	Pro	Gly	Pro
				85				90						95	
Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys	Leu	Val	Pro
			100					105					110		
Val	Asp	Leu	His	Glu	Glu	Ala	Arg	Asn	Cys	Glu	Arg	His	Cys	Leu	Met
		115					120					125			

His	Pro	Ala	Gln	Met	Gly	Glu	Asp	Pro	Asp	Gly	Ile	Asp	His
130						135					140		

<210> 202

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 202

Met	Gly	Ser	Ser	Asn	Ser	Lys	Arg	Gln	Gln	Gln	Gly	Leu	Leu	Lys	Leu
1				5				10						15	
Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Lys	Gly	Gly	Leu	Asp	Gly	Ile	Tyr
		35					40					45			
Tyr	Ser	Glu	Arg	Arg	Glu	Lys	Ile	Leu	Asn	Leu	Tyr	Ala	Leu	Asn	Glu
	50					55					60				
Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser	Pro	Gly	Pro	Gly	Ile
65				70						75					80
Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys	Leu	Val	Pro	Val	Asp
			85					90						95	
Leu	Gly	Glu	Val	Leu	Val	Trp	Lys	Phe	Asp	Pro	Lys	Leu	Ala	Val	Glu
			100					105					110		
Tyr	Arg	Pro	Asp	Met	Phe	Lys	Asp	Met	His	Glu	His	Ala	Lys	Arg	
		115					120					125			

<210> 203

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 203

Met	Gly	Ser	Ser	Asn	Ser	Lys	Arg	Gln	Gln	Gln	Gly	Leu	Leu	Lys	Leu
1				5				10						15	
Trp	Arg	Gly	Leu	Arg	Gly	Lys	Pro	Gly	Ala	Asp	Trp	Val	Leu	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Leu	Arg	Gln	Met	Thr	Tyr	Lys	Leu
		35					40					45			
Ala	Val	Asp	Phe	Ser	His	Phe	Leu	Lys	Ser	Lys	Gly	Gly	Leu	Asp	Gly
	50					55					60				
Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Glu	Lys	Ile	Leu	Asn	Leu	Tyr	Ala	Leu
65				70						75					80
Asn	Glu	Trp	Gly	Ile	Ile	Asp	Asp	Trp	Gln	Ala	Tyr	Ser	Pro	Gly	Pro
			85					90						95	
Gly	Ile	Arg	Tyr	Pro	Arg	Val	Phe	Gly	Phe	Cys	Phe	Lys	Leu	Val	Pro
			100					105					110		

Val Asp Leu
115

<210> 204
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 204
Met Leu Arg Gly Lys Pro Gly Ala Asp Trp Val Leu Leu Ser Asp Pro
1 5 10 15
Leu Ile Gly Gln Ser Ser Leu Asp Gly Ile Tyr Tyr Ser Glu Arg Arg
20 25 30
Glu Lys Ile Leu Asn Leu Tyr Ala Leu Asn Glu Trp Gly Ile Ile Asp
35 40 45
Asp Trp Gln Ala Tyr Ser Pro Gly Pro Gly Ile Arg Tyr Pro Arg Val
50 55 60
Phe Gly Phe Cys Phe Lys Leu Val Pro
65 70

<210> 205
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 205
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Lys Leu Glu Glu Ser Gly Gly Leu
20 25 30
Val Gln Ala Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu His
35 40 45
Thr Phe Ser Ser His Val Met Gly Trp Phe Arg Gln Ala Pro Gly Lys
50 55 60
Glu Arg Glu Ser Val Ala Val Ile Gly Trp Arg Asp Ile Ser Thr Ser
65 70 75 80
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95
Lys Lys Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr
100 105 110
Ala Val Tyr Tyr Cys Ala Ala Arg Arg Ile Asp Ala Ala Asp Phe Asp
115 120 125
Ser Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140
Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
145 150 155 160

Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Phe	Thr	Met
				165					170					175	
Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Phe	Val	Ala	Ala
			180					185					190		
Ile	Ser	Leu	Ser	Pro	Thr	Leu	Ala	Tyr	Tyr	Ala	Glu	Ser	Val	Lys	Gly
		195					200					205			
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Val	Leu	Gln
	210				215						220				
Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Ala
225					230					235					240
Asp	Arg	Lys	Ser	Val	Met	Ser	Ile	Arg	Pro	Asp	Tyr	Trp	Gly	Gln	Gly
			245						250					255	
Thr	Gln	Val	Thr	Val	Ser	Ser	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg
			260					265					270		
Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg
		275					280					285			
Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly
	290					295					300				
Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr
305					310					315					320
Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg
			325					330						335	
Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro
			340					345					350		
Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu
		355					360					365			
Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Gly	Glu	Asn	Leu	Tyr	Phe	Gln	Ser
	370					375					380				
Gly	Gly	Asp	Thr	Gln	Ala	Leu	Leu	Arg	Asn	Asp	Gln	Val	Tyr	Gln	Pro
385					390					395					400
Leu	Arg	Asp	Arg	Asp	Asp	Ala	Gln	Tyr	Ser	His	Leu	Gly	Gly	Asn	Gly
			405						410					415	
Gly	Ser	Gly	Glu	Arg	Pro	Pro	Pro	Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro
			420					425					430		
Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu	Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Gly
	435					440						445			
Gly	Ser	Gly	Asp	Lys	Gln	Thr	Leu	Leu	Pro	Asn	Asp	Gln	Leu	Tyr	Gln
	450				455						460				
Pro	Leu	Lys	Asp	Arg	Glu	Asp	Asp	Gln	Tyr	Ser	His	Leu	Gln	Gly	Asn
465					470					475					480
Gly	Gly	Ser	Gly	Arg	Lys	Gln	Arg	Ile	Thr	Glu	Thr	Glu	Ser	Pro	Tyr
			485						490					495	
Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser	Asp	Leu	Asn	Thr
			500					505					510		
Gln	Gly	Gly	Ser	Gly											
		515													

<210> 206

<211> 2706

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 206

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acagtccaag aagagtgcgg caaggcctta agacagatga cctataaatt agcagtggac 180
ttttcccact ttttaaaatc aaagggggga ctggatggga tatattactc tgaaagaaga 240
gaaaagatcc tgaatttgta tgccttgaac gagtggggaa taatagatga ttggcaagct 300
tactcaccag gcccggggat aaggtacccg agagtctttg gcttctgctt taagctagtc 360
ccagtggacc tgcatgagga ggcacgcaac tgtgagagac actgtgctgc acatccagca 420
cagatggggg aagatcctga tggaatagat catggagaag tcttggctct gaagtttgac 480
ccgaagttag cggtggagta ccgcccggac atgtttaagg acatgcacga acatgcaaag 540
cgtgaacgc gtgcccctct ccctccccc cccctaactg tactggccga agccgcttgg 600
aataaggccg gtgtgcgttt gtctatatgt tattttccac catattgccg tcttttggca 660
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gcgtattcaa caaggggctg aaggatgcc agaaggtacc ccattgtatg ggatctgata 1020
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aagaagacac tgtatctgca gatgaacagc ctgaagcccg aggacaccgc cgtgtactat 1500
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cttcaaggaa acggtggttc tggctcgaaa cagcgtatca ctgagaccga gtcgccttat 2640
caggagctcc agggctcagag gtcggatgtc tacagcgacc tcaacacaca gggtggttct 2700
ggttaa 2706
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<210> 207

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 207

Met	Gly	Gly	Ala	Ile	Ser	Lys	Lys	Gln	Tyr	Lys	Arg	Gly	Gly	Asn	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Glu	Gly	Tyr	Ser	Gln	Ser	Leu	Gly	Ala	Ser	Gly	Lys
		35					40					45			
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Pro	Gln	Lys	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Tyr	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Thr	Glu	Arg	Ala	Lys	Leu
65					70					75					80
Gly	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Glu	Asp	Asp	Asp
				85					90					95	
Leu	Ile	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr
			100					105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120						125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Asn	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Met
	130					135					140				
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	His	Tyr	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180				185					190			
Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Tyr	Gln	Trp	Asp	Asp	Pro	Trp	Gly
		195				200					205				
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Glu	Leu	Ala	Tyr	Ser	Tyr	Lys
	210					215					220				
Ala	Phe	Ile	Lys	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230				235						240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Leu	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 208

<211> 259

<212> PRT

<213> Simian immunodeficiency virus

<400> 208

Met	Gly	Gly	Ala	Ile	Ser	Met	Arg	Arg	Ser	Arg	Pro	Ser	Gly	Asp	Leu
1				5					10					15	
Arg	Gln	Arg	Leu	Leu	Arg	Ala	Arg	Gly	Glu	Thr	Ser	Gly	Arg	Leu	Leu
			20					25					30		
Gly	Glu	Glu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Pro	Gly	Gly	Leu	Asp	Lys
		35					40					45			
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Gly	Gln	Lys	Tyr	Asn	Gln	Gly	Ala
	50					55					60				
Pro	Trp	Arg	Asn	Pro	Ala	Lys	Glu	Arg	Glu	Lys	Leu	Ala	Tyr	Arg	Lys
65					70					75					80

Gln	Asn	Met	Asp	Asp	Ile	Asp	Glu	Glu	Asp	Asp	Asp	Leu	Val	Gly	Val	
				85					90					95		
Ser	Val	Arg	Pro	Lys	Val	Pro	Leu	Arg	Thr	Met	Ser	Tyr	Lys	Leu	Ala	
			100					105					110			
Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Ile	
		115					120					125				
Tyr	Tyr	Ser	Ala	Arg	Arg	His	Arg	Ile	Leu	Asp	Ile	Tyr	Leu	Glu	Lys	
	130					135					140					
Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asp	Tyr	Thr	Ser	Gly	Pro	Gly	
145					150					155					160	
Ile	Arg	Tyr	Pro	Lys	Thr	Phe	Gly	Trp	Leu	Trp	Lys	Leu	Val	Pro	Val	
				165					170					175		
Asn	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Glu	His	Tyr	Leu	Met	His	
			180					185					190			
Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Pro	Trp	Gly	Glu	Val	Leu	Val	
		195					200					205				
Trp	Lys	Phe	Asp	Pro	Thr	Leu	Ala	Tyr	Thr	Tyr	Glu	Ala	His	Val	Arg	
	210					215					220					
Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser	Glu	Glu	Glu	Val	
225					230					235					240	
Arg	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Leu	Asn	Met	Ala	Asp	Lys	Lys	
				245					250					255		
Glu	Thr	Arg														

<210> 209

<211> 243

<212> PRT

<213> Simian immunodeficiency virus

<400> 209

Met	Gly	Ser	Val	Lys	Ser	Arg	Met	Gln	Gln	Ser	Ala	Trp	Glu	Asp	Arg	
1				5				10						15		
Leu	Glu	Thr	Gly	Trp	Trp	Lys	Arg	Arg	Gly	Lys	Tyr	Thr	Pro	Phe	Pro	
			20					25					30			
Asp	Ala	Leu	Leu	Arg	Ala	Ser	Leu	Pro	Ser	Arg	Gly	Gly	Phe	Asp	Lys	
	35					40					45					
Ala	Trp	Arg	Ser	Thr	Leu	Thr	Glu	Pro	Ile	Asp	Pro	His	Gly	Pro	Asp	
	50				55					60						
Arg	Asp	Trp	Gly	His	Ser	Gly	Gly	Gln	Lys	Trp	Ser	Pro	Gly	Asp	Met	
65				70					75					80		
Val	Tyr	Asp	Glu	Gly	Asp	Thr	Gly	Leu	Val	Gly	Phe	Pro	Val	Cys	Pro	
			85					90					95			
Gln	Thr	Pro	Leu	Arg	Pro	Leu	Thr	Tyr	Lys	Leu	Ala	Ile	Asp	Leu	Ser	
		100						105					110			
His	Leu	Ile	Lys	Glu	Lys	Gly	Gly	Leu	Gln	Gly	Met	Asn	Phe	Asp	Ser	
	115					120						125				
Arg	Arg	Asp	Glu	Ile	Leu	His	Leu	Tyr	Leu	Lys	Asn	Glu	His	Gly	Val	
	130				135						140					
Ile	Asp	Arg	Ile	Asn	Tyr	Thr	Ser	Gly	Pro	Gly	Thr	Arg	Tyr	Pro	Leu	
145				150						155					160	
Ile	Phe	Gly	Trp	Leu	Trp	Glu	Leu	Ala	Pro	Asn	Asp	Ile	Glu	Gly	Tyr	
				165				170						175		

Leu	Ser	Asp	Glu	Glu	Asp	Thr	Leu	Leu	Leu	His	Pro	Ala	Ala	Gly	Lys
			180					185					190		
Gly	Ala	Ser	Glu	Asp	Ile	His	Gly	Glu	Asn	Leu	Ile	Trp	Asn	Phe	Asn
		195					200					205			
Ser	His	Leu	Ala	Tyr	Thr	Pro	Gly	Trp	Glu	Leu	Ala	Arg	Arg	Gln	Leu
	210					215					220				
Glu	Ala	Gln	Thr	Gly	Lys	Pro	Gln	Thr	Val	Lys	Gln	Ala	Leu	Thr	Gly
225					230					235					240
Lys	Gly	Ser													

<210> 210
 <211> 231
 <212> PRT
 <213> Simian immunodeficiency virus

Met	Gly	Gly	Arg	Asn	Ser	Lys	Thr	Gln	Ser	Ser	Gly	Gln	Glu	Glu	Asn
1				5					10					15	
Trp	Gly	Lys	His	Phe	Lys	Gly	Gly	Gln	Arg	Trp	Arg	Tyr	Arg	Tyr	Leu
			20					25					30		
Gly	Glu	Glu	Ser	Glu	Lys	Phe	Leu	Pro	Tyr	Gln	Pro	Glu	Ser	Asp	Lys
		35				40					45				
Glu	Leu	Asn	Cys	Ser	Leu	Thr	Glu	Glu	Thr	Phe	Ile	Gly	Asn	Pro	Arg
	50				55					60					
Arg	Glu	Ile	Lys	Cys	Thr	Gln	Arg	Gln	Gln	Gln	Asp	Phe	Asp	Gln	Gln
65				70					75					80	
Glu	Glu	Val	Gly	Phe	Pro	Val	Lys	Pro	Arg	Val	Pro	Ile	Arg	Asp	Pro
			85					90					95		
Thr	Tyr	Lys	Leu	Met	Ile	Asp	Tyr	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
			100					105					110		
Gly	Leu	Glu	Asp	Ile	Phe	Tyr	Ser	Ala	Arg	Arg	His	Ala	Ile	Leu	Glu
		115					120					125			
Leu	His	Ala	Gln	Asn	Glu	Trp	Gly	Ile	Ile	Pro	Gly	Trp	Leu	Gln	Tyr
	130					135					140				
Thr	Glu	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Lys	Tyr	Phe	Gly	Phe	Leu	Phe
145				150						155				160	
Lys	Leu	Val	Pro	Val	Glu	Ile	Ala	Asp	Pro	Asp	Tyr	Glu	Asn	Asp	Glu
			165					170						175	
Arg	Asn	Ile	Leu	Leu	His	Asp	Ala	His	Gln	Gly	Gln	Met	Glu	Asp	Pro
		180					185					190			
Tyr	Lys	Glu	Arg	Leu	Val	Trp	Lys	Phe	Asp	Ser	Gln	Leu	Ala	Tyr	Cys
		195					200					205			
Tyr	Lys	Ala	Gly	His	Glu	Ala	His	Thr	Lys	Glu	Thr	His	Thr	Arg	Arg
	210					215					220				
Cys	Met	Phe	Pro	Lys	Arg	Lys									
225					230										

<210> 211
 <211> 226
 <212> PRT
 <213> Simian immunodeficiency virus

<400> 211

Met	Gly	Gly	Lys	Asn	Ser	Lys	Gln	Gln	Gln	Gln	Arg	Ser	Leu	Trp	Leu
1				5				10						15	
Trp	Ser	Lys	Leu	Arg	Glu	Ala	Pro	Glu	Ile	Arg	Tyr	Asp	Met	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Ser	Ile	Gln	Glu	Glu	Cys	Ala	Lys
		35				40						45			
Ser	Leu	Ser	Asp	Gly	Leu	Ile	Lys	Gln	Gly	Asp	Ser	Ser	Arg	Thr	Glu
	50				55					60					
Glu	Gly	Ile	Lys	Leu	Arg	His	Pro	Gly	Lys	Gln	Pro	Ser	Trp	Tyr	Asp
65				70						75					80
Asp	Asp	Glu	Glu	Glu	Val	Gly	Phe	Pro	Val	Lys	Pro	Arg	Val	Pro	Leu
				85					90					95	
Arg	Ala	Met	Thr	Tyr	Lys	Ile	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys
			100					105					110		
Glu	Lys	Gly	Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Lys	Lys
		115				120						125			
Ile	Leu	Asp	Leu	Tyr	Ala	Leu	Asn	Glu	Trp	Gly	Ile	Val	Asp	Gly	Trp
	130					135						140			
Gln	Asn	Tyr	Thr	Asp	Gly	Pro	Gly	Pro	Arg	Tyr	Pro	Lys	Thr	Phe	Gly
145				150						155					160
Phe	Cys	Phe	Lys	Leu	Val	Pro	Val	His	Pro	Ser	Asp	Glu	Ala	Gln	Asn
				165					170					175	
Asp	Glu	His	His	Cys	Leu	Leu	His	Pro	Met	Gln	Val	Ala	Trp	Glu	Asp
			180					185					190		
Asp	Pro	Trp	Lys	Glu	Ile	Leu	Val	Trp	Lys	Phe	Asp	Pro	Leu	Leu	Ala
		195				200						205			
Val	Asp	Tyr	Ala	Ala	Trp	Arg	Leu	His	Pro	Glu	Gln	Val	Thr	Ser	Thr
	210					215					220				
Ser	Ala														
225															

<210> 212

<211> 226

<212> PRT

<213> Simian immunodeficiency virus

<400> 212

Met	Gly	Gly	Lys	Asn	Ser	Lys	Gln	Gln	Gln	Gln	Arg	Ser	Leu	Trp	Leu
1				5				10						15	
Trp	Ser	Lys	Leu	Arg	Glu	Ala	Pro	Glu	Ile	Arg	Tyr	Asp	Met	Leu	Ser
			20					25					30		
Asp	Pro	Leu	Ile	Gly	Gln	Ser	Ser	Ser	Ile	Gln	Glu	Glu	Cys	Ala	Lys
		35				40						45			
Ser	Leu	Ser	Asp	Gly	Leu	Ile	Lys	Gln	Gly	Asp	Ser	Ser	Arg	Thr	Glu
	50				55					60					
Glu	Gly	Ile	Lys	Leu	Arg	His	Pro	Gly	Lys	Gln	Pro	Ser	Trp	Tyr	Asp
65				70						75					80
Asp	Asp	Glu	Glu	Glu	Val	Gly	Phe	Pro	Val	Arg	Pro	Arg	Val	Pro	Leu
				85					90					95	
Arg	Thr	Met	Thr	Tyr	Lys	Met	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys
			100					105					110		

Glu	Lys	Gly	Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	Lys	Lys
		115					120					125			
Ile	Leu	Asp	Leu	Tyr	Ala	Leu	Asn	Glu	Trp	Gly	Ile	Val	Asp	Gly	Trp
	130					135					140				
Gln	Asn	Tyr	Thr	Asp	Gly	Pro	Gly	Glu	Arg	Tyr	Pro	Lys	Thr	Phe	Gly
145					150					155					160
Phe	Cys	Phe	Lys	Leu	Val	Pro	Val	His	Pro	Ser	Asp	Glu	Ala	Gln	Asn
			165						170					175	
Asp	Glu	Asn	His	Cys	Leu	Leu	His	Pro	Met	Gln	Val	Ala	Trp	Glu	Asp
		180					185					190			
Asp	Pro	Trp	Lys	Glu	Ile	Leu	Val	Trp	Lys	Phe	Asp	Pro	Leu	Leu	Ala
	195					200					205				
Val	Asp	Tyr	Ala	Ala	Trp	Arg	Leu	His	Pro	Glu	Gln	Val	Pro	Ser	Thr
	210					215					220				
Ser	Ala														
225															

<210> 213

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 213

Met	Gly	Ala	Ala	Gly	Ser	Lys	Lys	Arg	Ser	Arg	Gln	Gln	Arg	Gly	Leu
1				5				10					15		
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Lys	Leu	Trp
			20					25					30		
Asp	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Glu	Leu	Gly	Arg
		35				40					45				
Asp	Trp	Asn	Leu	His	Ser	Ser	Glu	Gly	Gln	Gly	Tyr	Ser	Glu	Gly	Gln
	50				55					60					
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu
65					70				75						80
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu
			85					90					95		
Leu	Ile	Gly	Val	Ala	Val	His	Pro	Lys	Val	Pro	Leu	Arg	Ala	Met	Ser
		100					105					110			
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120					125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Ile
	130					135				140					
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145				150						155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys
			165					170					175		
Leu	Val	Pro	Val	Glu	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
		180				185						190			
Tyr	Leu	Val	His	Pro	Ala	Gln	Ile	Ser	Gln	Trp	Asp	Asp	Pro	Trp	Gly
	195					200					205				
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Ser	Gln	Leu	Ala	Tyr	Arg	Tyr	Glu
	210				215					220					
Ala	Phe	Ile	Arg	His	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230				235						240

Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Thr	Arg	Gly	Leu	Leu	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 214
 <211> 263
 <212> PRT
 <213> Simian immunodeficiency virus

<400> 214															
Met	Gly	Ala	Ala	Gly	Ser	Lys	Lys	Gln	Ser	Arg	Gln	Gln	Arg	Gly	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Lys	Leu	Trp
			20					25					30		
Gly	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Gln	Gly	Glu	Leu	Gly	Arg
		35					40					45			
Asp	Trp	Asn	Leu	His	Ser	Ser	Glu	Gly	Gln	Gly	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Lys	Lys	Leu
65					70					75					80
Lys	Tyr	Lys	Gln	Gln	Asn	Met	Asn	Asn	Val	Asn	Asp	Asp	Asp	Asp	Glu
			85						90					95	
Leu	Ile	Gly	Val	Ser	Val	His	Pro	Lys	Val	Pro	Leu	Arg	Ala	Met	Ser
			100					105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120						125			
Leu	Glu	Gly	Val	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Ile
	130					135					140				
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Glu	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180					185					190		
Cys	Leu	Met	His	Pro	Ala	Gln	Ile	Ser	Gln	Trp	Asp	Asp	Pro	Trp	Gly
		195				200						205			
Glu	Ala	Leu	Ala	Trp	Lys	Phe	Asp	Ser	Gln	Leu	Ala	Tyr	Arg	Tyr	Glu
	210					215					220				
Ala	Phe	Ile	Arg	His	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230					235					240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Phe	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 215
 <211> 263
 <212> PRT
 <213> Simian immunodeficiency virus

<400> 215

Met	Gly	Ala	Ala	Gly	Ser	Lys	Lys	Arg	Ser	Arg	Gln	Gln	Arg	Gly	Leu
1				5				10					15		
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Ile	Tyr	Gly	Lys	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Glu	Leu	Gly	Arg
		35					40					45			
Asp	Trp	Asn	Leu	His	Ser	Phe	Glu	Gly	Gln	Gly	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu
65					70				75						80
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu
				85					90						95
Leu	Ile	Gly	Val	Ser	Val	His	Ser	Lys	Val	Pro	Leu	Arg	Ala	Met	Ser
			100					105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115					120					125			
Leu	Glu	Gly	Val	Tyr	Tyr	Ser	Asn	Arg	Arg	His	Arg	Ile	Leu	Asp	Ile
	130					135					140				
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Ser	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180				185					190			
Tyr	Leu	Val	His	Pro	Ala	Gln	Ile	Ser	Gln	Trp	Asp	Asp	Pro	Trp	Gly
	195						200					205			
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Ser	Gln	Leu	Ala	Tyr	Arg	Tyr	Glu
	210					215					220				
Ala	Phe	Ile	Arg	His	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230				235						240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Phe	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 216

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 216

Met	Gly	Ala	Ala	Gly	Ser	Lys	Lys	Arg	Ser	Arg	Gln	Gln	Arg	Gly	Leu
1				5				10					15		
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Lys	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Gln	Gly	Glu	Leu	Gly	Arg
		35					40					45			
Asp	Trp	Asn	Leu	His	Ser	Ser	Glu	Gly	Gln	Gly	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu
65					70				75						80
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu
				85					90						95

Leu	Ile	Gly	Val	Ala	Val	His	Pro	Lys	Val	Pro	Leu	Arg	Ala	Met	Ser	
			100					105					110			
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
		115					120					125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Ile	
	130					135					140					
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	
145					150					155					160	
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys	
			165						170					175		
Leu	Ile	Pro	Val	Ala	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His	
			180					185					190			
Cys	Leu	Met	His	Pro	Ala	Gln	Ile	Ser	Gln	Trp	Asp	Asp	Pro	Trp	Gly	
	195						200					205				
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Ser	Gln	Leu	Ala	Tyr	Arg	Tyr	Glu	
	210					215					220					
Ala	Phe	Ile	Arg	His	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser	
225					230				235						240	
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Leu	Lys	Met	
			245						250					255		
Ala	Asp	Lys	Lys	Glu	Thr	Ser										
			260													

<210> 217

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 217

Met	Gly	Ala	Ala	Gly	Ser	Lys	Lys	Arg	Ser	Arg	Gln	Gln	Arg	Gly	Leu	
1				5				10						15		
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp	
			20					25					30			
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Glu	Leu	Gly	Arg	
	35					40						45				
Asp	Trp	Asn	Leu	His	Ser	Ser	Glu	Gly	Gln	Gly	Tyr	Ser	Glu	Gly	Gln	
	50				55					60						
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu	
65					70				75						80	
Glu	Tyr	Arg	Gln	Gln	Asn	Arg	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asn	Glu	
			85						90					95		
Leu	Ile	Gly	Val	Ser	Val	His	Pro	Lys	Val	Pro	Leu	Arg	Ala	Met	Ser	
			100					105					110			
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
	115						120					125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Gly	His	Arg	Ile	Leu	Asp	Ile	
	130					135					140					
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Val	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	
145					150					155					160	
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys	
			165						170					175		
Leu	Val	Pro	Val	Ser	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His	
			180					185						190		

<210> 219
 <211> 263
 <212> PRT
 <213> Simian immunodeficiency virus

<400> 219

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Met Gly Ala Ala Gly Ser Lys Lys Arg Ser Arg Gln Gln Arg Gly Leu
 1          5          10          15
Arg Glu Arg Leu Leu Gln Ala Arg Gly Glu Thr Tyr Gly Lys Leu Trp
 20          25          30
Lys Gly Leu Glu Asp Gly Tyr Ser Gln Ser Arg Gly Glu Leu Gly Arg
 35          40          45
Asp Trp Asn Leu His Ser Phe Glu Gly Gln Gly Tyr Ser Glu Gly Gln
 50          55          60
Phe Met Asn Thr Pro Trp Arg Asn Pro Ala Arg Glu Arg Glu Lys Leu
 65          70          75          80
Lys Tyr Arg Gln Gln Asn Met Asp Asn Val Asp Asp Asp Asp Asp Glu
 85          90          95
Leu Ile Gly Val Ser Val His Ser Lys Val Pro Leu Arg Ala Met Ser
100          105          110
Tyr Lys Leu Ala Ile Asp Met Ser His Phe Ile Lys Glu Lys Gly Gly
115          120          125
Leu Glu Gly Ile Tyr Tyr Ser Glu Arg Arg His Arg Ile Leu Asp Ile
130          135          140
Tyr Leu Glu Lys Glu Glu Gly Ile Ile Pro Asp Trp Gln Asn Tyr Thr
145          150          155          160
Ser Gly Pro Gly Ile Arg Tyr Pro Met Phe Phe Gly Trp Leu Trp Lys
165          170          175
Leu Val Pro Val Asp Val Ser Asp Glu Ala Gln Glu Asp Glu Thr Tyr
180          185          190
Cys Leu Val His Pro Ala Gln Ile Ser Gln Trp Asp Asp Pro Trp Gly
195          200          205
Glu Val Leu Ala Trp Lys Phe Asp Ser Gln Leu Ala Tyr Arg Tyr Glu
210          215          220
Ala Phe Ile Lys His Pro Glu Glu Phe Gly Ser Lys Ser Gly Leu Ser
225          230          235          240
Glu Glu Lys Val Lys Arg Arg Leu Thr Ala Arg Gly Leu Phe Lys Met
245          250          255
Ala Asp Lys Lys Glu Thr Ser
260

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<210> 220
 <211> 263
 <212> PRT
 <213> Simian immunodeficiency virus

<400> 220

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Met Gly Ala Ala Gly Ser Lys Lys Gln Ser Arg Gln Gln Arg Gly Leu
 1          5          10          15
Arg Glu Lys Leu Leu Pro Ala Arg Gly Glu Thr Tyr Gly Lys Leu Trp
 20          25          30
Glu Gly Leu Glu Asp Gly Tyr Ser Gln Ser Gln Gly Glu Leu Gly Arg
 35          40          45

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Asp	Trp	Asn	Leu	His	Ser	Ser	Glu	Gly	Gln	Gly	Tyr	Ser	Glu	Gly	Gln
50						55					60				
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu
65					70					75					80
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu
				85					90					95	
Leu	Ile	Gly	Val	Ser	Val	His	Pro	Lys	Val	Pro	Leu	Arg	Ala	Met	Ser
			100					105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120						125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Asn	Arg	Arg	His	Arg	Ile	Leu	Asp	Ile
	130					135					140				
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Val	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Glu	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180					185					190		
Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Pro	Trp	Gly
		195					200					205			
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Ser	Gln	Leu	Ala	Tyr	Arg	Tyr	Glu
	210					215					220				
Ala	Phe	Ile	Arg	Asn	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230					235					240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Thr	Arg	Gly	Leu	Leu	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 221

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 221

Met	Gly	Ala	Ala	Gly	Ser	Lys	Lys	Gln	Ser	Arg	Arg	His	Gly	Arg	Leu
1				5				10					15		
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Lys	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Glu	Leu	Gly	Arg
		35					40					45			
Asp	Trp	Asn	Leu	His	Ser	Phe	Glu	Gly	Gln	Gly	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu
65					70					75					80
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu
				85					90					95	
Leu	Ile	Gly	Val	Ser	Val	Tyr	Ser	Lys	Val	Pro	Leu	Arg	Ala	Met	Ser
			100					105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120						125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Asn	Arg	Arg	His	Arg	Ile	Leu	Asp	Ile
	130					135					140				

<210> 223
 <211> 263
 <212> PRT
 <213> Simian immunodeficiency virus

<400> 223
 Met Gly Gly Ala Ile Ser Met Arg Arg Ser Arg Pro Ser Gly Asp Leu
 1 5 10 15
 Arg Gln Arg Leu Leu Arg Ala Arg Gly Glu Thr Tyr Gly Arg Leu Leu
 20 25 30
 Gly Glu Val Glu Asp Gly Tyr Ser Gln Ser Pro Gly Gly Leu Asp Lys
 35 40 45
 Gly Leu Ser Ser Leu Ser Cys Glu Gly Gln Lys Tyr Asn Gln Gly Gln
 50 55 60
 Tyr Met Asn Thr Pro Trp Arg Asn Pro Ala Glu Glu Arg Glu Lys Leu
 65 70 75 80
 Ala Tyr Arg Lys Gln Asn Met Asp Asp Ile Asp Glu Glu Asp Asp Asp
 85 90 95
 Leu Val Gly Val Ser Val Arg Pro Lys Val Pro Leu Arg Thr Met Ser
 100 105 110
 Tyr Lys Leu Ala Ile Asp Met Ser His Phe Ile Lys Glu Lys Gly Gly
 115 120 125
 Leu Glu Gly Ile Tyr Tyr Ser Ala Arg Arg His Arg Ile Leu Asp Ile
 130 135 140
 Tyr Leu Glu Lys Glu Glu Gly Ile Ile Pro Asp Trp Gln Asp Tyr Thr
 145 150 155 160
 Ser Gly Pro Gly Ile Arg Tyr Pro Lys Thr Phe Gly Trp Leu Trp Lys
 165 170 175
 Leu Val Pro Val Asn Val Ser Asp Glu Ala Gln Glu Asp Glu Glu His
 180 185 190
 Tyr Leu Met His Pro Ala Gln Thr Ser Gln Trp Asp Asp Pro Trp Gly
 195 200 205
 Glu Val Leu Ala Trp Lys Phe Asp Pro Thr Leu Ala Tyr Thr Tyr Glu
 210 215 220
 Ala Tyr Val Arg Tyr Pro Glu Glu Phe Gly Ser Lys Ser Gly Leu Ser
 225 230 235 240
 Glu Glu Glu Val Arg Arg Arg Leu Thr Ala Arg Gly Leu Leu Asn Met
 245 250 255
 Ala Asp Lys Lys Glu Thr Arg
 260

<210> 224
 <211> 263
 <212> PRT
 <213> Simian immunodeficiency virus

<400> 224
 Met Gly Gly Ala Ile Ser Arg Lys Gln Cys Arg Arg Gly Gly Asp Leu
 1 5 10 15
 Arg Glu Arg Leu Leu Gln Ala Arg Gly Glu Thr Tyr Gly Arg Leu Trp
 20 25 30

Glu	Gly	Leu	Glu	Glu	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Ala	Ser	Gly	Lys	
		35					40					45				
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Pro	Gln	Lys	Tyr	Ser	Glu	Gly	Gln	
	50					55					60					
Tyr	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Thr	Glu	Arg	Glu	Lys	Leu	
65					70					75					80	
Gly	Tyr	Arg	Gln	Gln	Asn	Arg	Asp	Asp	Val	Asp	Asp	Glu	Asp	Asp	Asp	
			85						90					95		
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr	
		100					105						110			
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
	115					120						125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Lys	Arg	His	Arg	Ile	Leu	Asp	Met	
	130					135					140					
Tyr	Met	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	
145					150					155					160	
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Tyr	Phe	Gly	Trp	Leu	Trp	Lys	
			165						170					175		
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His	
		180					185						190			
Cys	Leu	Val	His	Pro	Ala	Gln	Thr	His	Gln	Trp	Asp	Asp	Pro	Trp	Gly	
	195					200						205				
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Glu	Leu	Ala	Tyr	Ser	Tyr	Lys	
	210					215					220					
Ala	Phe	Ile	Lys	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser	
225					230				235						240	
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Ile	Lys	Met	
			245						250					255		
Ala	Asp	Lys	Lys	Glu	Thr	Ser										
		260														

<210> 225

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 225

Met	Gly	Gly	Ala	Ile	Ser	Arg	Lys	Gln	Cys	Arg	Arg	Gly	Gly	Asp	Leu	
1				5					10					15		
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp	
	20							25					30			
Glu	Gly	Leu	Glu	Glu	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Ala	Ser	Gly	Lys	
	35					40						45				
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Pro	Gln	Lys	Tyr	Ser	Glu	Gly	Gln	
	50					55					60					
Tyr	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Thr	Glu	Arg	Glu	Lys	Leu	
65					70					75					80	
Gly	Tyr	Arg	Gln	Gln	Asn	Arg	Asp	Asp	Val	Asp	Asp	Glu	Asp	Asp	Asp	
			85						90					95		
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr	
		100					105						110			
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
	115					120						125				

Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Met
130						135					140				
Tyr	Met	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145						150				155					160
Ser	Gly	Pro	Gly	Thr	Arg	Tyr	Pro	Met	Tyr	Phe	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180					185					190		
Cys	Leu	Val	His	Pro	Ala	Gln	Thr	His	Gln	Trp	Asp	Asp	Pro	Trp	Gly
	195					200						205			
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Glu	Leu	Ala	Tyr	Ser	Tyr	Lys
	210					215					220				
Ala	Phe	Ile	Lys	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230					235					240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Ile	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 226

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 226

Met	Gly	Gly	Ala	Ile	Ser	Arg	Lys	Gln	Cys	Arg	Arg	Gly	Gly	Asp	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Glu	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Ala	Ser	Gly	Lys
		35				40						45			
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Pro	Gln	Lys	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Tyr	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Thr	Glu	Arg	Glu	Lys	Leu
65					70					75					80
Gly	Tyr	Arg	Gln	Gln	Asp	Met	Asp	Asp	Val	Asp	Asp	Glu	Asp	Asp	Asp
			85						90					95	
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr
		100						105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120						125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Met
	130					135					140				
Tyr	Met	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145						150				155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Tyr	Tyr	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180					185					190		
Cys	Leu	Val	His	Pro	Ala	Gln	Thr	His	Gln	Trp	Asp	Asp	Pro	Trp	Gly
	195					200						205			
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Glu	Leu	Ala	Tyr	Ser	Tyr	Lys
	210					215					220				

Ala	Phe	Ile	Lys	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230					235					240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Ile	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 227

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 227

Met	Gly	Gly	Val	Ile	Ser	Lys	Lys	Gln	Cys	Arg	Arg	Gly	Gly	Asn	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Glu	Gly	Tyr	Ser	Gln	Ser	Leu	Gly	Ala	Ser	Gly	Lys
		35				40						45			
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Pro	Gln	Lys	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Tyr	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Ala	Glu	Arg	Ala	Lys	Leu
65					70				75						80
Gly	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asn	Glu	Asp	Asp	Asp
			85					90						95	
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr
			100					105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120						125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Asn	Glu	Lys	Arg	His	Arg	Ile	Leu	Asp	Met
	130					135					140				
Tyr	Met	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Thr	Arg	Tyr	Pro	Met	Tyr	Tyr	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180					185					190		
Cys	Leu	Met	His	Pro	Ala	Gln	Thr	His	Gln	Trp	Asp	Asp	Pro	Trp	Gly
		195				200						205			
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Glu	Leu	Ala	Tyr	Ser	Tyr	Lys
	210					215					220				
Ala	Phe	Ile	Lys	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230					235					240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Ile	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 228

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 228

Met	Gly	Gly	Val	Ile	Ser	Lys	Lys	Gln	Cys	Arg	Arg	Gly	Gly	Asn	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Glu	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Ala	Ser	Gly	Lys
		35					40					45			
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Pro	Gln	Lys	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Tyr	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Ala	Glu	Arg	Ala	Lys	Leu
65					70				75						80
Gly	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Glu	Asp	Asp	Asp
				85					90					95	
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr
			100					105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115				120						125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Asn	Glu	Lys	Arg	His	Arg	Ile	Leu	Asp	Met
	130					135					140				
Tyr	Met	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Thr	Arg	Tyr	Pro	Met	Tyr	Tyr	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His
			180				185					190			
Cys	Leu	Met	His	Pro	Ala	Gln	Thr	His	Gln	Trp	Asp	Asp	Pro	Trp	Gly
		195				200						205			
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Glu	Leu	Ala	Tyr	Ser	Tyr	Lys
	210					215					220				
Ala	Phe	Ile	Lys	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser
225					230					235					240
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Ile	Lys	Met
				245					250					255	
Ala	Asp	Lys	Lys	Glu	Thr	Ser									
			260												

<210> 229

<211> 263

<212> PRT

<213> Simian immunodeficiency virus

<400> 229

Met	Gly	Gly	Val	Ile	Ser	Lys	Lys	Gln	Cys	Arg	Arg	Gly	Gly	Asn	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Glu	Gly	Tyr	Ser	Gln	Ser	Leu	Gly	Ala	Ser	Gly	Lys
		35					40					45			
Gly	Leu	Ser	Ser	Leu	Ser	Cys	Glu	Pro	Gln	Lys	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Tyr	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Ala	Glu	Arg	Ala	Lys	Leu
65					70					75					80

Gly	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Lys	Asp	Asp	Asp	
			85						90				95			
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr	
			100					105					110			
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
		115					120					125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Asn	Glu	Lys	Arg	His	Arg	Ile	Leu	Asp	Met	
	130					135					140					
Tyr	Met	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	
145					150					155					160	
Ser	Gly	Pro	Gly	Thr	Arg	Tyr	Pro	Met	Tyr	Tyr	Gly	Trp	Leu	Trp	Lys	
				165					170					175		
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Thr	His	
			180					185					190			
Cys	Leu	Met	His	Pro	Ala	Gln	Thr	His	Gln	Trp	Asp	Asp	Pro	Trp	Gly	
	195						200					205				
Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Glu	Leu	Ala	Tyr	Ser	Tyr	Lys	
	210					215					220					
Ala	Phe	Ile	Lys	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	Gly	Leu	Ser	
225					230					235					240	
Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	Ile	Lys	Met	
				245					250					255		
Ala	Asp	Lys	Lys	Glu	Thr	Ser										
			260													

<210> 230

<211> 240

<212> PRT

<213> Simian immunodeficiency virus

<400> 230

Met	Gly	Ser	Val	Lys	Ser	Lys	Leu	Leu	Gly	Glu	Thr	Ala	Ser	Gln	Arg	
1				5					10					15		
Leu	Gln	Gly	Ser	His	Gly	Gly	Gly	Arg	Met	Val	Tyr	Trp	Arg	Leu	Arg	
			20					25					30			
Asp	Gly	Gln	Val	Lys	Arg	Ser	Gln	Leu	Ser	Pro	Gly	Ala	Arg	Gly	Lys	
		35					40					45				
Asp	Leu	Asn	Ile	Ala	Leu	Leu	Asp	Glu	Glu	Trp	Gln	Ala	Thr	Gly	Ala	
	50					55					60					
Asp	Tyr	Met	Gly	Lys	Ala	Leu	Thr	Gln	Gly	Glu	Val	Trp	Tyr	Glu	Lys	
65				70						75				80		
Glu	Gln	Glu	Glu	Asn	Asp	Met	Glu	Leu	Val	Gly	Phe	Pro	Val	Arg	Pro	
				85					90					95		
Lys	Val	Pro	Leu	Arg	Thr	Cys	Thr	Tyr	Lys	Leu	Gly	Ile	Asp	Phe	Ser	
			100					105					110			
Phe	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Lys	Gly	Ile	Phe	Tyr	Asn	Lys	
		115					120					125				
Arg	Arg	His	Ala	Ile	Leu	Asn	Leu	Tyr	Ala	His	Asn	Glu	Trp	Gly	Ile	
	130					135					140					
Leu	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Glu	Gly	Pro	Gly	Thr	Arg	Tyr	Pro	
145					150					155					160	
Leu	Cys	Phe	Gly	Ile	Leu	Trp	Lys	Leu	Cys	Pro	Val	Glu	Ile	His	Glu	
				165					170					175		

Asp	Asp	Thr	Glu	Asp	Gly	His	Leu	Leu	Pro	His	Pro	Ala	Tyr	Asp	Gly
			180					185					190		
Gln	Ala	Glu	Asp	Pro	Trp	Gly	Glu	Ser	Leu	Val	Trp	Val	Phe	Asp	Glu
		195					200					205			
Lys	Leu	Ala	Tyr	Thr	Pro	Gly	Ala	Lys	Met	Ala	Glu	Trp	Asp	Arg	Leu
	210					215					220				
Glu	Arg	Glu	Lys	Arg	Met	Leu	Leu	Ala	Pro	Pro	Gln	Thr	Ala	Ser	Ser
225					230					235					240

<210> 231

<211> 240

<212> PRT

<213> Simian immunodeficiency virus

<400> 231

Met	Gly	Ser	Val	Lys	Ser	Lys	Leu	Leu	Gly	Glu	Thr	Ala	Ser	Gln	Arg
1				5					10					15	
Leu	Gln	Gly	Ser	Pro	Gly	Ala	Gly	Arg	Leu	Val	Tyr	Trp	Arg	Leu	Arg
			20					25					30		
Asp	Gly	Gln	Cys	Arg	Gln	Leu	Gln	Arg	Ser	Arg	Gly	Glu	Arg	Gly	Lys
		35					40					45			
Gly	Leu	Asn	Ile	Ala	Leu	Leu	Asp	Ala	Gly	Trp	Gln	Ala	Ser	Asp	Ala
	50					55					60				
Asn	Trp	Met	Gly	Lys	Ala	Leu	Ser	Glu	Gly	Glu	Val	Trp	Tyr	Glu	Lys
65				70						75				80	
Glu	Gln	Glu	Glu	Asn	Asp	Met	Glu	Leu	Val	Gly	Phe	Pro	Val	Arg	Pro
				85					90					95	
Gln	Val	Pro	Leu	Arg	Pro	Cys	Asn	Tyr	Lys	Leu	Gly	Ile	Asp	Phe	Ser
			100					105					110		
Phe	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Lys	Gly	Ile	Phe	Tyr	Asn	Asn
		115					120					125			
Arg	Arg	His	Ala	Ile	Leu	Asn	Leu	Tyr	Ala	His	Asn	Glu	Trp	Gly	Ile
		130				135					140				
Leu	Pro	Asp	Trp	Gln	Ser	Tyr	Thr	Glu	Gly	Pro	Gly	Thr	Arg	Tyr	Pro
145					150					155					160
Leu	Cys	Phe	Gly	Ile	Leu	Trp	Lys	Leu	Cys	Pro	Val	Glu	Ile	His	Glu
				165					170					175	
Asp	Asp	Thr	Glu	Asp	Gly	His	Leu	Leu	Met	His	Pro	Ala	Tyr	Asp	Gly
			180					185					190		
Gln	Gln	Glu	Asp	Pro	Trp	Gly	Glu	Ala	Leu	Val	Trp	Val	Phe	Asp	Glu
		195					200					205			
Lys	Leu	Ala	Tyr	Thr	Pro	Gly	Ala	Lys	Met	Ala	Glu	Tyr	Asp	Arg	Leu
	210					215					220				
Glu	Arg	Lys	Lys	Lys	Glu	Leu	Leu	Ala	Pro	Pro	Gln	Thr	Ala	Ser	Ser
225					230					235					240

<210> 232

<211> 2886

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 232

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gcaacaggag cggactacat gggcaaggca ttaacacaag gagaggtttg gtatgaaaaa 240
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aaggccggtg tgcgtttgtc tatatgttat tttccaccat attgccgtct tttggcaatg 840
tgagggcccg gaaacctggc cctgtcttct tgacgagcat tcctaggggt ctttcccctc 900
tcgccaaagg aatgcaaggt ctgttgaatg tcgtgaagga agcagttcct ctggaagctt 960
cttgaagaca aacaacgtct gtagcgaccc tttgcaggca gcggaacccc ccacctggcg 1020
acaggtgcct ctgcggccaa aagccacgtg tataagatac acctgcaaag gcggcacaac 1080
cccagtgcca cgttgtgagt tggatagttg tggaaagagt caaatggctc tcctcaagcg 1140
tattcaacaa ggggctgaag gatgcccaga aggtacccca ttgtatggga tctgatctgg 1200
ggcctcgggt cacatgcttt acatgtgttt agtcgagggt aaaaaaacgt ctaggcccc 1260
cgaaccagg ggacgtggtt ttcttttgaa aaacacgatg ataatatggc cacaggatcc 1320
gccgccacca tggccctgcc agtgaccgcc ttgctccttc ccctggctct tctgctgcac 1380
gctgctagac ctgaggtgca gctgcagcag agcggagctg agctggtgaa gcctggcgct 1440
agcgtgaaga tgagctgcaa ggccagcggc tacaccttca ccagctataa catgcactgg 1500
gtgaagcaga cccctggaca gggactggag tggatcggag ctatctaccc tggaaacgga 1560
gacacctcat acaaccagaa gttcaaggga aaggctaccc tgaccgctga caagagcagc 1620
agcaccgctt acatgcagct gagctcactg accagcgagg actccgccga ctactactgc 1680
gccagaagca actactacgg aagcagctac tggttcttcg acgtgtgggg agctggaacc 1740
accgtgaccg tgtcaagcgg cggcggaggc tccggaggcg gaggatctgg cggcggcggc 1800
agcgacatcg tgctgaccga gagccctgct atcctgtctg ccagccctgg agagaaggtg 1860
accatgacct gcagagctag cagcagcgtg aactacatgg actggtatca gaaaaagccc 1920
ggcagctcac ctaagccttg gatctacgt accagcaact tagccagcgg cgtgcctgct 1980
agattctccg gaagcggctc tggaaaccagc tactccctta ccatcagcag agtggaggct 2040
gaggacgtg ctacctacta ctgccagcag tggagcttca accctcctac cttcggagga 2100
ggaaccaagc tggagatcaa gactagtacc acgacgccag cgccgcgacc accaacaccg 2160
gcgccacca tcgctcgca gccctgtcc ctgcgccag aggcgtgccg gccagcggcg 2220
ggggcgcgag tgcacacgag ggggctggac ttgcctgtg atatctacat ctggcgccc 2280
ttggccggga cttgtggggt ctttctctctg tctgtggtta tcacccttta ctgcaaacgg 2340
ggcagaaaga aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact 2400
caagaggaag atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg 2460
ggtgaaaatt tgtattttca atctggtggt gacacacaag ctctgttgag gaatgaccag 2520
gtctatcagc ccctccgaga tcgagatgat gctcagtaca gccaccttgg aggaaacggg 2580
ggttctggtg agaggccacc acctgttccc aaccagact atgagcccat ccggaaaggc 2640
cagcgggacc tgtattctgg cctgaatcag agaggtgggt ctggtgacaa gcagactctg 2700
ttgccaatg accagctcta ccagcccctc aaggatcgag aagatgacca gtacagccac 2760
cttcaaggaa acgggtggtt tggtcggaaa cagcgtatca ctgagaccga gtcgccttat 2820
caggagctcc agggtcagag gtcggatgtc tacagcgacc tcaacacaca ggttggttct 2880
ggttaa
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<210> 233

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 233
actcacgctg gatagcctcc 20

<210> 234
<211> 723
<212> DNA
<213> Simian immunodeficiency virus

<400> 234
atgggttcag tgaaatccaa gctgcttggc gagacggcat cacagcgctt gcaaggttca 60
catggtggtg gacgaatggt gtattggcgg ctgcgcgatg ggcaggtgaa gcgatcgcag 120
ctatccccag gcgcacgagg caaggacttg aatattgctt tacttgatga agaattggcaa 180
gcaacaggag cggactacat gggcaaggca ttaacacaag gagaggtttg gtatgaaaaa 240
gaacaagaag aaaatgacat ggaactagtg ggcttccctg tgaggcctaa agttccgttg 300
agaacctgta cttataaact aggtatagac ttctcgttct ttttgaaaga aaaggaggga 360
ctgaagggga tatttttaca caaacgtagg catgcaatct tgaatctgta tgcccacaat 420
gaatggggca tactgccaga ctggcagaac tacacagagg gaccaggaac aagataccca 480
ttgtgctttg gtatcctgtg gaaactctgc ccagtagaga tccatgagga tgacacggag 540
gacggacatc tcctcccgcg tccagcatat gatgggcagg cagaagaccc atggggagaa 600
tccctggtct gggtctttga tgagaagctg gcctacaccc ccggagcgaa gatggccgag 660
tgggacaggt tggagagaga gaagcggatg ctgctagctc caccgcaaac cgcattcctc 720
tga 723

<210> 235
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> 3, 4, 5, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18, 19, 21, 22,
26, 27, 29, 30, 32, 33, 34, 36, 37, 38, 39, 41, 43, 45,
46, 48, 49, 50, 51, 52, 53, 54, 55, 57, 58, 59, 60, 61,
62, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 78,
81
<223> Xaa = Any Amino Acid or absent

<220>
<221> VARIANT
<222> 82, 83, 84, 85, 86, 87, 89, 90, 91, 94, 96, 97, 99, 101,
102, 104, 106, 111, 113, 120, 137, 141, 145, 147, 148, 149,
151, 166, 170, 171, 182, 186, 193, 195, 197, 202, 203, 205,
208, 209, 216, 221, 222, 226, 228, 230, 231, 232, 233
<223> Xaa = Any Amino Acid or absent

<220>

<221> VARIANT

<222> 234, 238, 239, 243, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269

<223> Xaa = Any Amino Acid or absent

<400> 235

Met	Gly	Xaa	Xaa	Xaa	Ser	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu
1				5				10					15		
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Ala	Arg	Gly	Xaa	Xaa	Tyr	Xaa	Xaa	Leu	Xaa
			20					25					30		
Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Ser	Xaa	Gly	Xaa	Xaa	Gly	Xaa
		35					40				45				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa
	50					55					60				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Arg	Xaa	Lys	Leu
65					70				75						80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Asp	Asp	Xaa	Asp	Xaa
				85				90					95		
Xaa	Leu	Xaa	Gly	Xaa	Xaa	Val	Xaa	Pro	Xaa	Val	Pro	Leu	Arg	Xaa	Met
			100					105					110		
Xaa	Tyr	Lys	Leu	Ala	Ile	Asp	Xaa	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly
		115				120						125			
Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Xaa	Arg	Arg	His	Xaa	Ile	Leu	Asp
	130					135					140				
Xaa	Tyr	Xaa	Xaa	Xaa	Glu	Xaa	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr
145					150					155					160
Thr	Ser	Gly	Pro	Gly	Xaa	Arg	Tyr	Pro	Xaa	Xaa	Phe	Gly	Trp	Leu	Trp
				165					170					175	
Lys	Leu	Val	Pro	Val	Xaa	Val	Ser	Asp	Xaa	Glu	Ala	Gln	Glu	Asp	Glu
			180					185					190		
Xaa	His	Xaa	Leu	Xaa	His	Pro	Ala	Gln	Xaa	Xaa	Gln	Xaa	Asp	Asp	Xaa
		195					200					205			
Xaa	Pro	Trp	Gly	Glu	Val	Leu	Xaa	Trp	Lys	Phe	Asp	Xaa	Xaa	Leu	Ala
	210					215					220				
Tyr	Xaa	Tyr	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Glu	Glu	Xaa	Xaa	Ser
225					230					235					240
Lys	Ser	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			245					250						255	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			260					265							

<210> 236

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 3, 4, 5, 8, 10, 12, 13, 14, 15, 22, 30, 32, 33, 37, 43, 45,
46, 49, 51, 52, 53, 55, 57, 59, 61, 62, 65, 75, 78, 81,
87, 89, 91, 94, 102, 104, 106, 113, 145, 147, 170, 171,
182, 186, 197, 202, 203, 208, 209, 221, 222, 226, 228, 230

<223> Xaa = Any Amino Acid or absent

<220>

<221> VARIANT

<222> 231, 232, 233, 234, 250, 255, 259, 260, 268, 269

<223> Xaa = Any Amino Acid or absent

<400> 236

Met	Gly	Xaa	Xaa	Xaa	Ser	Lys	Xaa	Gln	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	Leu
1				5				10						15	
Arg	Glu	Arg	Leu	Leu	Xaa	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Xaa	Leu	Xaa
			20					25					30		
Xaa	Gly	Leu	Glu	Xaa	Gly	Tyr	Ser	Gln	Ser	Xaa	Gly	Xaa	Xaa	Gly	Lys
		35				40						45			
Xaa	Leu	Xaa	Xaa	Xaa	Ser	Xaa	Glu	Xaa	Gln	Xaa	Tyr	Xaa	Xaa	Gly	Gln
	50				55						60				
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Xaa	Glu	Arg	Xaa	Lys	Leu
65					70					75					80
Xaa	Tyr	Arg	Gln	Gln	Asn	Xaa	Asp	Xaa	Asp	Xaa	Asp	Asp	Xaa	Asp	Asp
			85					90					95		
Glu	Leu	Val	Gly	Val	Xaa	Val	Xaa	Pro	Xaa	Val	Pro	Leu	Arg	Ala	Met
			100					105					110		
Xaa	Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly
		115				120						125			
Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp
	130					135					140				
Xaa	Tyr	Xaa	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr
145				150						155					160
Thr	Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Xaa	Xaa	Phe	Gly	Trp	Leu	Trp
			165						170					175	
Lys	Leu	Val	Pro	Val	Xaa	Val	Ser	Asp	Xaa	Glu	Ala	Gln	Glu	Asp	Glu
			180				185						190		
Thr	His	Cys	Leu	Xaa	His	Pro	Ala	Gln	Xaa	Xaa	Gln	Trp	Asp	Asp	Xaa
	195					200						205			
Xaa	Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Xaa	Xaa	Leu	Ala
	210				215						220				
Tyr	Xaa	Tyr	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Glu	Glu	Phe	Gly	Ser
225				230						235					240
Lys	Ser	Gly	Leu	Ser	Glu	Glu	Glu	Val	Xaa	Arg	Arg	Leu	Thr	Xaa	Arg
			245					250						255	
Gly	Leu	Xaa	Xaa	Met	Ala	Asp	Lys	Lys	Glu	Thr	Xaa	Xaa			
			260					265							

<210> 237

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 3, 5, 10, 12, 13, 14, 15, 30, 33, 37, 43, 46, 49, 51, 52, 53, 55, 57, 59, 65, 75, 78, 81, 89, 94, 106, 145, 147, 171, 182, 186, 197, 202, 203, 208, 209, 221, 222, 226, 228, 230, 233, 234, 255, 259, 269

<223> Xaa = Any Amino Acid or absent

<400> 237

Met	Gly	Xaa	Ala	Xaa	Ser	Lys	Lys	Gln	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	Leu
1				5				10						15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Xaa	Leu	Trp
			20					25					30		
Xaa	Gly	Leu	Glu	Xaa	Gly	Tyr	Ser	Gln	Ser	Xaa	Gly	Glu	Xaa	Gly	Lys
		35				40						45			
Xaa	Leu	Xaa	Xaa	Xaa	Ser	Xaa	Glu	Xaa	Gln	Xaa	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Xaa	Glu	Arg	Xaa	Lys	Leu
65					70					75					80
Xaa	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Xaa	Asp	Val	Asp	Asp	Xaa	Asp	
			85					90					95		
Glu	Leu	Val	Gly	Val	Ser	Val	His	Pro	Xaa	Val	Pro	Leu	Arg	Ala	Met
			100					105					110		
Thr	Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly
		115				120						125			
Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp
	130				135						140				
Xaa	Tyr	Xaa	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr
145				150						155					160
Thr	Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Xaa	Phe	Gly	Trp	Leu	Trp
			165					170					175		
Lys	Leu	Val	Pro	Val	Xaa	Val	Ser	Asp	Xaa	Glu	Ala	Gln	Glu	Asp	Glu
		180					185						190		
Thr	His	Cys	Leu	Xaa	His	Pro	Ala	Gln	Xaa	Xaa	Gln	Trp	Asp	Asp	Xaa
	195					200						205			
Xaa	Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Xaa	Xaa	Leu	Ala
	210				215						220				
Tyr	Xaa	Tyr	Xaa	Ala	Xaa	Phe	Ile	Xaa	Xaa	Pro	Glu	Glu	Phe	Gly	Ser
225				230						235					240
Lys	Ser	Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Xaa	Arg
			245					250					255		
Gly	Leu	Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa			
		260					265								

<210> 238

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 5, 10, 12, 13, 14, 15, 37, 43, 46, 49, 51, 52, 53, 55, 57, 59, 65, 75, 81, 89, 94, 145, 171, 182, 186, 197, 202, 203, 208, 209, 222, 226, 228, 230, 233, 234, 259, 269

<223> Xaa = Any Amino Acid or absent

<400> 238

Met	Gly	Gly	Ala	Xaa	Ser	Lys	Lys	Gln	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Xaa	Gly	Tyr	Ser	Gln	Ser	Xaa	Gly	Glu	Xaa	Gly	Lys
		35				40						45			
Xaa	Leu	Xaa	Xaa	Xaa	Ser	Xaa	Glu	Xaa	Gln	Xaa	Tyr	Ser	Glu	Gly	Gln
	50				55						60				
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Xaa	Glu	Arg	Glu	Lys	Leu
65					70				75						80
Xaa	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Xaa	Asp	Val	Asp	Asp	Xaa	Asp	Asp
			85					90						95	
Glu	Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met
			100					105					110		
Thr	Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly
		115				120						125			
Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp
	130				135						140				
Xaa	Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr
145				150						155					160
Thr	Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Xaa	Phe	Gly	Trp	Leu	Trp
			165					170						175	
Lys	Leu	Val	Pro	Val	Xaa	Val	Ser	Asp	Xaa	Glu	Ala	Gln	Glu	Asp	Glu
			180					185					190		
Thr	His	Cys	Leu	Xaa	His	Pro	Ala	Gln	Xaa	Xaa	Gln	Trp	Asp	Asp	Xaa
		195				200						205			
Xaa	Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Xaa	Leu	Ala
	210				215						220				
Tyr	Xaa	Tyr	Xaa	Ala	Xaa	Phe	Ile	Xaa	Xaa	Pro	Glu	Glu	Phe	Gly	Ser
225				230						235					240
Lys	Ser	Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg
			245					250						255	
Gly	Leu	Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa			
			260					265							

<210> 239

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 5, 13, 14, 15, 49, 52, 53, 55, 65, 75, 81, 89, 94, 171, 186, 208, 209, 222, 226, 230, 259, 269

<223> Xaa = Any Amino Acid or absent

<400> 239

Met	Gly	Gly	Ala	Xaa	Ser	Lys	Lys	Gln	Ser	Arg	Arg	Xaa	Xaa	Xaa	Leu
1				5				10					15		
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25				30			
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Glu	Leu	Gly	Lys
		35					40					45			
Xaa	Leu	Asn	Xaa	Xaa	Ser	Xaa	Glu	Gly	Gln	Lys	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Xaa	Glu	Arg	Glu	Lys	Leu
65					70				75						80
Xaa	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Xaa	Asp	Val	Asp	Asp	Xaa	Asp	Asp
				85				90						95	
Glu	Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met
			100					105					110		
Thr	Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly
		115					120					125			
Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp
	130					135					140				
Ile	Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr
145					150					155					160
Thr	Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Xaa	Phe	Gly	Trp	Leu	Trp
				165				170						175	
Lys	Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Xaa	Glu	Ala	Gln	Glu	Asp	Glu
			180					185					190		
Thr	His	Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Xaa
		195					200					205			
Xaa	Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Xaa	Leu	Ala
	210					215					220				
Tyr	Xaa	Tyr	Glu	Ala	Xaa	Phe	Ile	Arg	Tyr	Pro	Glu	Glu	Phe	Gly	Ser
225					230					235					240
Lys	Ser	Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg
				245				250						255	
Gly	Leu	Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa			
			260					265							

<210> 240

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 15, 65, 89, 186, 208, 209, 226, 230, 259, 269

<223> Xaa = Any Amino Acid or absent

<400> 240

Met	Gly	Gly	Ala	Gly	Ser	Lys	Lys	Gln	Ser	Arg	Arg	Gln	Gly	Xaa	Leu
1				5				10						15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Glu	Leu	Gly	Lys
		35					40					45			
Asp	Leu	Asn	Ser	His	Ser	Cys	Glu	Gly	Gln	Lys	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu
65					70					75					80
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Xaa	Asp	Val	Asp	Asp	Asp	Asp	Asp
				85					90					95	
Glu	Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met
			100					105					110		
Thr	Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly
		115					120						125		
Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp
	130					135					140				
Ile	Tyr	Leu	Glu	Lys	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	
145					150					155					160
Thr	Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp
				165					170					175	
Lys	Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Xaa	Glu	Ala	Gln	Glu	Asp	Glu
			180					185					190		
Thr	His	Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Xaa
		195					200						205		
Xaa	Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Gln	Leu	Ala
	210					215					220				
Tyr	Xaa	Tyr	Glu	Ala	Xaa	Phe	Ile	Arg	Tyr	Pro	Glu	Glu	Phe	Gly	Ser
225					230					235					240
Lys	Ser	Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg
				245					250					255	
Gly	Leu	Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa			
			260					265							

<210> 241

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 65, 89, 186, 208, 209, 230, 259, 269

<223> Xaa = Any Amino Acid or absent

<400> 241

Met Gly Gly Ala Gly Ser Lys Lys Gln Ser Arg Arg Gln Gly Gly Leu

1				5					10					15			
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp		
			20					25					30				
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Arg	Gly	Glu	Leu	Gly	Lys		
		35					40					45					
Asp	Leu	Asn	Ser	His	Ser	Cys	Glu	Gly	Gln	Lys	Tyr	Ser	Glu	Gly	Gln		
	50					55					60						
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu		
65				70					75						80		
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Xaa	Asp	Val	Asp	Asp	Asp	Asp	Asp		
			85					90					95				
Glu	Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met		
			100					105					110				
Thr	Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly		
		115				120						125					
Gly	Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp		
	130				135						140						
Ile	Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr		
145				150						155					160		
Thr	Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp		
				165					170					175			
Lys	Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Xaa	Glu	Ala	Gln	Glu	Asp	Glu		
			180					185					190				
Thr	His	Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Xaa		
		195				200						205					
Xaa	Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Gln	Leu	Ala		
	210					215					220						
Tyr	Arg	Tyr	Glu	Ala	Xaa	Phe	Ile	Arg	Tyr	Pro	Glu	Glu	Phe	Gly	Ser		
225				230					235					240			
Lys	Ser	Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg		
			245					250					255				
Gly	Leu	Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa					
			260					265									

<210> 242

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 3, 4, 5, 10, 12, 13, 14, 15, 30, 33, 37, 43, 46, 49, 51, 52, 53, 55, 57, 59, 65, 75, 81, 144, 146, 170, 181, 191, 196, 201, 202, 207, 208, 221, 225, 227, 231, 232, 253, 257, 267

<223> Xaa = Any Amino Acid or absent

<400> 242

Met	Gly	Xaa	Xaa	Xaa	Ser	Lys	Lys	Gln	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	Leu		
1				5				10						15			

Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Xaa	Leu	Trp
			20					25					30		
Xaa	Gly	Leu	Glu	Xaa	Gly	Tyr	Ser	Gln	Ser	Xaa	Gly	Glu	Xaa	Gly	Lys
	35					40					45				
Xaa	Leu	Xaa	Xaa	Xaa	Ser	Xaa	Glu	Xaa	Gln	Xaa	Tyr	Ser	Glu	Gly	Gln
	50				55						60				
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Xaa	Glu	Arg	Glu	Lys	Leu
65					70					75					80
Xaa	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu
			85					90					95		
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr
		100						105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
	115					120						125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Xaa
130						135					140				
Tyr	Xaa	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Xaa	Phe	Gly	Trp	Leu	Trp	Lys
			165						170					175	
Leu	Val	Pro	Val	Xaa	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Xaa	Thr
		180						185					190		
His	Cys	Leu	Xaa	His	Pro	Ala	Gln	Xaa	Xaa	Gln	Trp	Asp	Asp	Xaa	Xaa
	195					200						205			
Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Xaa	Leu	Ala	Tyr
	210					215					220				
Xaa	Tyr	Xaa	Ala	Phe	Ile	Xaa	Xaa	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser
225					230					235					240
Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Xaa	Arg	Gly	Leu
			245						250					255	
Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa					
		260						265							

<210> 243

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 3, 5, 10, 12, 13, 14, 15, 30, 37, 43, 46, 49, 51, 52, 53, 55, 57, 59, 65, 75, 81, 144, 170, 191, 196, 201, 202, 207,

208, 221, 225, 227, 231, 232, 253, 257, 267

<223> Xaa = Any Amino Acid or absent

<400> 243

Met	Gly	Xaa	Ala	Xaa	Ser	Lys	Lys	Gln	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	Leu
1				5					10					15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Xaa	Leu	Trp
			20					25					30		

Glu	Gly	Leu	Glu	Xaa	Gly	Tyr	Ser	Gln	Ser	Xaa	Gly	Glu	Xaa	Gly	Lys
		35					40					45			
Xaa	Leu	Xaa	Xaa	Xaa	Ser	Xaa	Glu	Xaa	Gln	Xaa	Tyr	Ser	Glu	Gly	Gln
	50					55					60				
Xaa	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Xaa	Glu	Arg	Glu	Lys	Leu
65					70					75					80
Xaa	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu
			85						90					95	
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr
		100						105					110		
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly
		115					120					125			
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Xaa
	130					135					140				
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Xaa	Phe	Gly	Trp	Leu	Trp	Lys
				165					170					175	
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Xaa	Thr
			180					185					190		
His	Cys	Leu	Xaa	His	Pro	Ala	Gln	Xaa	Xaa	Gln	Trp	Asp	Asp	Xaa	Xaa
	195						200					205			
Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Xaa	Leu	Ala	Tyr
	210					215					220				
Xaa	Tyr	Xaa	Ala	Phe	Ile	Xaa	Xaa	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser
225					230					235					240
Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Xaa	Arg	Gly	Leu
				245					250					255	
Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa					
			260					265							

<210> 244

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 5, 13, 14, 15, 37, 46, 49, 52, 53, 55, 57, 59, 65, 75, 81, 170, 191, 201, 202, 207, 208, 221, 225, 227, 231, 257, 267

<223> Xaa = Any Amino Acid or absent

<400> 244

Met	Gly	Gly	Ala	Xaa	Ser	Lys	Lys	Gln	Ser	Arg	Arg	Xaa	Xaa	Xaa	Leu
1				5				10						15	
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp
			20					25					30		
Glu	Gly	Leu	Glu	Xaa	Gly	Tyr	Ser	Gln	Ser	Gln	Gly	Glu	Xaa	Gly	Lys
		35				40					45				
Xaa	Leu	Asn	Xaa	Xaa	Ser	Xaa	Glu	Xaa	Gln	Xaa	Tyr	Ser	Glu	Gly	Gln

50		55		60	
Xaa Met Asn Thr Pro Trp Arg Asn Pro Ala Xaa Glu Arg Glu Lys Leu					
65		70		75	80
Xaa Tyr Arg Gln Gln Asn Met Asp Asp Val Asp Asp Asp Asp Asp Glu					
		85		90	95
Leu Val Gly Val Ser Val His Pro Arg Val Pro Leu Arg Ala Met Thr					
		100		105	110
Tyr Lys Leu Ala Ile Asp Met Ser His Phe Ile Lys Glu Lys Gly Gly					
		115		120	125
Leu Glu Gly Ile Tyr Tyr Ser Glu Arg Arg His Arg Ile Leu Asp Leu					
		130		135	140
Tyr Leu Glu Lys Glu Glu Gly Ile Ile Pro Asp Trp Gln Asn Tyr Thr					
145		150		155	160
Ser Gly Pro Gly Ile Arg Tyr Pro Met Xaa Phe Gly Trp Leu Trp Lys					
		165		170	175
Leu Val Pro Val Asp Val Ser Asp Glu Ala Gln Glu Asp Glu Xaa Thr					
		180		185	190
His Cys Leu Val His Pro Ala Gln Xaa Xaa Gln Trp Asp Asp Xaa Xaa					
		195		200	205
Pro Trp Gly Glu Val Leu Ala Trp Lys Phe Asp Pro Xaa Leu Ala Tyr					
		210		215	220
Xaa Tyr Xaa Ala Phe Ile Xaa Tyr Pro Glu Glu Phe Gly Ser Lys Ser					
225		230		235	240
Gly Leu Ser Glu Glu Glu Val Lys Arg Arg Leu Thr Ala Arg Gly Leu					
		245		250	255
Xaa Lys Met Ala Asp Lys Lys Glu Thr Ser Xaa					
		260		265	

<210> 245

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 5, 13, 15, 53, 55, 59, 65, 81, 170, 191, 207, 208, 225, 257, 267

<223> Xaa = Any Amino Acid or absent

<400> 245

Met Gly Gly Ala Xaa Ser Lys Lys Gln Ser Arg Arg Xaa Gly Xaa Leu	
1	5
Arg Glu Arg Leu Leu Gln Ala Arg Gly Glu Thr Tyr Gly Arg Leu Trp	
	20
Glu Gly Leu Glu Asp Gly Tyr Ser Gln Ser Gln Gly Glu Leu Gly Lys	
	35
Gly Leu Asn Ser Xaa Ser Xaa Glu Gly Gln Xaa Tyr Ser Glu Gly Gln	
	50
Xaa Met Asn Thr Pro Trp Arg Asn Pro Ala Arg Glu Arg Glu Lys Leu	
65	70
	75
	80

Xaa	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu	
				85					90					95		
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr	
			100					105					110			
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
		115					120					125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Leu	
	130					135					140					
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	
145					150					155					160	
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Xaa	Phe	Gly	Trp	Leu	Trp	Lys	
			165					170						175		
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Xaa	Thr	
			180				185						190			
His	Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Xaa	Xaa	
	195					200						205				
Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Gln	Leu	Ala	Tyr	
	210					215					220					
Xaa	Tyr	Glu	Ala	Phe	Ile	Arg	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	
225					230					235					240	
Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	
			245					250						255		
Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa						
		260					265									

<210> 246

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 59, 191, 207, 208, 225, 257, 267

<223> Xaa = Any Amino Acid or absent

<400> 246

Met	Gly	Gly	Ala	Gly	Ser	Lys	Lys	Gln	Ser	Arg	Arg	Gln	Gly	Gly	Leu	
1				5				10					15			
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp	
			20				25						30			
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Gln	Gly	Glu	Leu	Gly	Lys	
		35				40						45				
Gly	Leu	Asn	Ser	His	Ser	Cys	Glu	Gly	Gln	Xaa	Tyr	Ser	Glu	Gly	Gln	
	50				55					60						
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu	
65				70				75							80	
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu	
			85					90					95			
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr	
			100				105						110			

Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
		115					120					125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Leu	
	130					135					140					
Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	
145					150					155					160	
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys	
				165					170						175	
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Xaa	Thr	
		180					185					190				
His	Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Xaa	Xaa	
	195						200					205				
Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Gln	Leu	Ala	Tyr	
	210					215					220					
Xaa	Tyr	Glu	Ala	Phe	Ile	Arg	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser	
225					230					235					240	
Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu	
				245					250					255		
Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa						
			260					265								

<210> 247

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> 59, 191, 207, 208, 257, 267

<223> Xaa = Any Amino Acid or absent

<400> 247

Met	Gly	Gly	Ala	Gly	Ser	Lys	Lys	Gln	Ser	Arg	Arg	Gln	Gly	Gly	Leu	
1				5				10					15			
Arg	Glu	Arg	Leu	Leu	Gln	Ala	Arg	Gly	Glu	Thr	Tyr	Gly	Arg	Leu	Trp	
		20					25					30				
Glu	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Gln	Ser	Gln	Gly	Glu	Leu	Gly	Lys	
		35				40					45					
Gly	Leu	Asn	Ser	His	Ser	Cys	Glu	Gly	Gln	Xaa	Tyr	Ser	Glu	Gly	Gln	
	50				55					60						
Phe	Met	Asn	Thr	Pro	Trp	Arg	Asn	Pro	Ala	Arg	Glu	Arg	Glu	Lys	Leu	
65				70				75							80	
Lys	Tyr	Arg	Gln	Gln	Asn	Met	Asp	Asp	Val	Asp	Asp	Asp	Asp	Asp	Glu	
			85					90					95			
Leu	Val	Gly	Val	Ser	Val	His	Pro	Arg	Val	Pro	Leu	Arg	Ala	Met	Thr	
		100					105					110				
Tyr	Lys	Leu	Ala	Ile	Asp	Met	Ser	His	Phe	Ile	Lys	Glu	Lys	Gly	Gly	
	115					120						125				
Leu	Glu	Gly	Ile	Tyr	Tyr	Ser	Glu	Arg	Arg	His	Arg	Ile	Leu	Asp	Leu	
	130					135					140					

Tyr	Leu	Glu	Lys	Glu	Glu	Gly	Ile	Ile	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
145					150					155					160
Ser	Gly	Pro	Gly	Ile	Arg	Tyr	Pro	Met	Phe	Phe	Gly	Trp	Leu	Trp	Lys
				165					170						175
Leu	Val	Pro	Val	Asp	Val	Ser	Asp	Glu	Ala	Gln	Glu	Asp	Glu	Xaa	Thr
			180					185					190		
His	Cys	Leu	Val	His	Pro	Ala	Gln	Thr	Ser	Gln	Trp	Asp	Asp	Xaa	Xaa
	195						200					205			
Pro	Trp	Gly	Glu	Val	Leu	Ala	Trp	Lys	Phe	Asp	Pro	Gln	Leu	Ala	Tyr
	210					215					220				
Arg	Tyr	Glu	Ala	Phe	Ile	Arg	Tyr	Pro	Glu	Glu	Phe	Gly	Ser	Lys	Ser
225					230					235					240
Gly	Leu	Ser	Glu	Glu	Glu	Val	Lys	Arg	Arg	Leu	Thr	Ala	Arg	Gly	Leu
				245					250					255	
Xaa	Lys	Met	Ala	Asp	Lys	Lys	Glu	Thr	Ser	Xaa					
			260					265							