

SEQUENCE LISTING

<110> THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

<120> ANTI-MUTATED KRAS T CELL RECEPTORS

<130> 722261

<150> US 62/171,321

<151> 2015-06-05

<150> US 62/084,654

<151> 2014-11-26

<160> 209

<170> PatentIn version 3.5

<210> 1

<211> 189

<212> PRT

<213> Homo sapiens

<400> 1

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Asp	Pro	Thr	Ile	Glu	Asp	Ser	Tyr	Arg	Lys	Gln	Val	Val	Ile	Asp	Gly
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Glu	Thr	Cys	Leu	Leu	Asp	Ile	Leu	Asp	Thr	Ala	Gly	Gln	Glu	Glu	Tyr
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Ser	Ala	Met	Arg	Asp	Gln	Tyr	Met	Arg	Thr	Gly	Glu	Gly	Phe	Leu	Cys
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Val	Phe	Ala	Ile	Asn	Asn	Thr	Lys	Ser	Phe	Glu	Asp	Ile	His	His	Tyr
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Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

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

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
180 185

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<213> Homo sapiens

<400> 2

Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10

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<213> Mus musculus

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Thr Ile Tyr Ser Asn Pro Phe
1 5

<210> 4
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<400> 4

Ser Phe Thr Asp Asn Lys Arg
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<210> 5

<211> 13

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<213> Mus musculus

<400> 5

Cys Ala Leu Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe
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Leu Gly His Asp Thr
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<210> 7

<211> 6

<212> PRT

<213> Mus musculus

<400> 7

Tyr Asn Asn Lys Gln Leu
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<210> 8

<211> 15

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<213> Mus musculus

<400> 8

Cys Ala Ser Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe
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<210> 9
<211> 135
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<213> Mus musculus

<400> 9

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
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Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
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Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

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<213> Mus musculus

<400> 10

Met Gly Cys Arg Leu Leu Ser Cys Val Ala Phe Cys Leu Leu Gly Ile
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Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
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<210> 11
<211> 271
<212> PRT
<213> Mus musculus

<400> 11

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Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

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<213> Mus musculus

<400> 12

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20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<211> 136
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<213> Mus musculus

<400> 13

Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser
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Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
20 25 30

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

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
50 55 60

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
65 70 75 80

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

Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val
100 105 110

Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
115 120 125

Met Thr Leu Arg Leu Trp Ser Ser
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Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser

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		20					25						30		
Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly
		35					40					45			
Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln	Ala	Tyr	Lys	Glu
	50					55					60				
Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser	Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr
65					70					75					80
Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	His
				85					90					95	
Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser	Pro	Lys	Pro	Val
			100					105					110		
Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Ile
		115						120				125			
Thr	Ser	Ala	Ser	Tyr	His	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr
		130				135					140				
Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Gly
145					150					155					160
Leu	Val	Leu	Met	Ala	Met	Val	Lys	Lys	Lys	Asn	Ser				
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gatggagact ccgtgaccca gacagaaggc ctggtcactc tcacagaagg gttgcctgtg 120
atgctgaact gcacctatca gactatttac tcaaatcctt tccttttctg gtatgtgcaa 180
catctcaatg aatccccctg gctactcctg aagagcttca cagacaacaa gaggaccgag 240
caccaagggt tccacgccac tctccataag agcagcagct ctttccatct gcagaagtcc 300
tcagcgcagc tgtcagactc tgccctgtac tactgtgctc tgaggggggaa tgcaggtgcc 360
aagctcacat tcggaggggg aacaaggta acggtcagac ccg 403

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<212> DNA
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aattgtaagc aaactctggg ccacgatact atgtattggt acaagcaaga ctctaagaaa 180
ttgctgaaga ttatgttttag ctacaataat aagcaactca ttgtaaacga aacagttcca 240
aggcgcttct cacctcagtc ttcagataaa gtcatttga atcttcgaat caagtctgta 300
gagccggagg actctgctgt gtatctctgt gccagcagct cccgggactg gagtgcagaa 360
acgctgtatt ttggctcagg aaccagactg actgttctcg 400

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<212> DNA
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<400> 17

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atgctgaact gcacctatca gactattttac tcaaatacctt tccttttctg gtatgtgcaa	180
catctcaatg aatccccctg gctactcctg aagagcttca cagacaacaa gaggaccgag	240
caccaagggg tccacgccac tctccataag agcagcagct ccttccatct gcagaagtcc	300
tcagcgcagc tgtcagactc tgccctgtac tactgtgctc tgaggggggaa tgcaggtgcc	360
aagctcacat tcggaggggg aacaagggtta acggtcagac ccgacatcca gaaccagaa	420
cctgtgtgt accagttaaa agatcctcgg tctcaggaca gcaccctctg cctgttcacc	480
gactttgact cccaaatcaa tgtgccgaaa accatggaat ctggaacgtt catcactgac	540
aaaactgtgc tggacatgaa agctatggat tccaagagca atggggccat tgcctggagc	600
aaccagacaa gcttcacctg ccaagatatc ttcaaagaga ccaacgccac ctaccccagt	660
tcagacgttc cctgtgatgc cacgttgact gagaaaagct ttgaaacaga tatgaaccta	720
aactttcaaa acctgtcagt tatgggactc cgaatcctcc tgctgaaagt agccggattt	780
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<210> 18
 <211> 921
 <212> DNA
 <213> Artificial Sequence

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<400> 18	
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acggctgttt tccagactcc aaactatcat gtcacacagg tgggaaatga agtgtctttc	120
aattgtaagc aaactctggg ccacgatact atgtattggt acaagcaaga ctctaagaaa	180
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aggcgcttct cacctcagtc ttcagataaa gtcatttga atcttcgaat caagtctgta	300
gagccggagg actctgctgt gtatctctgt gccagcagct cccgggactg gagtgcagaa	360

acgctgtatt ttggctcagg aaccagactg actgttctcg aggatctgag aaatgtgact	420
ccaccaagg tctccttggt tgagccatca aaagcagaga ttgcaaaca aaaaaaggct	480
accctcgtgt gcttggccag gggcttcttc cctgaccacg tggagctgag ctggtgggtg	540
aatggcaagg aggtccacag tggggtcagc acggaccctc aggcctacaa ggagagcaat	600
tatagctact gcctgagcag ccgcctgagg gtctctgcta ccttctggca caatcctcga	660
aaccacttcc gctgccaagt gcagttccat gggctttcag aggaggacaa gtggccagag	720
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gtcaagaaaa aaaattcctg a	921

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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gaacgttcat cactgacaaa actgtgctgg acatgaaagc tatggattcc aagagcaatg	180
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aaacagatat gaacctaaac tttcaaaacc tgtcagttat gggactccga atcctcctgc	360
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 <212> DNA
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<223> Synthetic

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tggagctgag ctggtgggtg aatggcaagg aggtccacag tggggtcagc acggaccctc	180
aggcctacaa ggagagcaat tatagctact gcctgagcag ccgcctgagg gtctctgcta	240
ccttctggca caatcctcga aaccacttcc gctgccaaagt gcagttccat gggctttcag	300
aggaggacaa gtggccagag ggctcaccca aacctgtcac acagaacatc agtgcagagg	360
cctggggccg agcagactgt ggaatcactt cagcatccta tcatcagggg gttctgtctg	420
caaccatcct ctatgagatc ctactgggga aggccaccct atatgctgtg ctggtcagtg	480
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catctcaatg aatccccctg gctactcctg aagagcttca cagacaacaa gaggaccgag	240
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cctgtgtgtg accagttaaa agatcctcgg tctcaggaca gcaccctctg cctgttcacc	480
gactttgact cccaaatcaa tgtgccgaaa accatggaat ctggaacgtt catcactgac	540

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aaccagacaa gcttcacctg ccaagatatc ttcaaagaga ccaacgccac ctaccccagt	660
tcagacgttc cctgtgatgc cacgttgact gagaaaagct ttgaaacaga tatgaacct	720
aactttcaaa acctgtcagt tatgggactc cgaatcctcc tgctgaaagt agccggattt	780
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gttttccaga ctccaaacta tcatgtcaca cagggtgggaa atgaagtgtc tttcaattgt	1020
aagcaaaactc tgggccacga tactatgtat tgggtacaagc aagactctaa gaaattgctg	1080
aagattatgt ttagctacaa taataagcaa ctcatgttaa acgaaacagt tccaaggcgc	1140
ttctcacctc agtcttcaga taaagctcat ttgaatcttc gaatcaagtc tgtagagccg	1200
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gtgtgcttgg ccaggggctt cttccctgac cacgtggagc tgagctgggtg ggtgaatggc	1440
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tactgcctga gcagccgcct gagggctctt gctaccttct ggcacaatcc tcgaaaccac	1560
ttccgctgcc aagtgcagtt ccatgggctt tcagaggagg acaagtggcc agagggtca	1620
cccaaacctg tcacacagaa catcagtga gaggcctggg gccgagcaga ctgtggaatc	1680
acttcagcat cctatcatca gggggttctg tctgcaacca tcctctatga gatcctactg	1740
gggaaggcca ccctatatgc tgtgctggtc agtggcctgg tgctgatggc catggtcaag	1800
aaaaaaaaatt cctga	1815

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<400> 22
actattttact caaatccttt c 21

<210> 23
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<212> DNA
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<400> 23
agcttcacag acaacaagag g 21

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ctgggccacg atact 15

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tacaataata agcaactc 18

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Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
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Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 29
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<213> Homo sapiens

<400> 29

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

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

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

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

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
180 185

<210> 30
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<400> 30

Val Val Val Gly Ala Gly Gly Val Gly Lys
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<400> 31

Val Val Gly Ala Gly Gly Val Gly Lys
1 5

<210> 32
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<400> 32

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

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

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

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

Arg Glu Ile Arg Gln Tyr Arg Leu Lys Lys Ile Ser Lys Glu Glu Lys
165 170 175

Thr Pro Gly Cys Val Lys Ile Lys Lys Cys Ile Ile Met
180 185

<210> 33
<211> 10
<212> PRT
<213> Homo sapiens

<400> 33

Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10

<210> 34
<211> 9
<212> PRT
<213> Homo sapiens

<400> 34

Val Val Gly Ala Asp Gly Val Gly Lys
1 5

<210> 35
<211> 9
<212> PRT
<213> Homo sapiens

<400> 35

Val Val Gly Ala Val Gly Val Gly Lys
1 5

<210> 36
<211> 9
<212> PRT
<213> Homo sapiens

<400> 36

Val Val Gly Ala Cys Gly Val Gly Lys
1 5

<210> 37
<211> 10
<212> PRT
<213> Homo sapiens

<400> 37

Val Val Val Gly Ala Cys Gly Val Gly Lys
1 5 10

<210> 38
<211> 9
<212> PRT
<213> Homo sapiens

<400> 38

Val Val Gly Ala Arg Gly Val Gly Lys
1 5

<210> 39
<211> 10
<212> PRT
<213> Homo sapiens

<400> 39

Val Val Val Gly Ala Arg Gly Val Gly Lys
1 5 10

<210> 40
<211> 16
<212> PRT
<213> Mus musculus

<400> 40

Cys Ala Met Arg Glu Asp Thr Gly Ala Asn Thr Gly Lys Leu Thr Phe
1 5 10 15

<210> 41
<211> 15
<212> PRT
<213> Mus musculus

<400> 41

Cys Ala Ser Ser Gln Asp Ser Leu Gly Arg Ala Glu Gln Phe Phe
1 5 10 15

<210> 42
<211> 15
<212> PRT
<213> Mus musculus

<400> 42

Cys Ala Ser Ser Ser Asp Trp Gly Gly Ala Glu Thr Leu Tyr Phe
1 5 10 15

<210> 43
<211> 16
<212> PRT
<213> Mus musculus

<400> 43

Cys Ala Ser Ser Ser Gly Leu Gly Ser Ser Ala Glu Thr Leu Tyr Phe
1 5 10 15

<210> 44
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44
cgggcccaagc ggtccggatc cggagccacc aacttcagcc tgctgaagca ggccggcgac 60

gtggaggaga accccggccc c 81

<210> 45
<211> 604
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 45

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
275 280 285

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Cys Arg Leu Leu
290 295 300

Ser Cys Val Ala Phe Cys Leu Leu Gly Ile Gly Pro Leu Glu Thr Ala
305 310 315 320

Val Phe Gln Thr Pro Asn Tyr His Val Thr Gln Val Gly Asn Glu Val
325 330 335

Ser Phe Asn Cys Lys Gln Thr Leu Gly His Asp Thr Met Tyr Trp Tyr
340 345 350

Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile Met Phe Ser Tyr Asn Asn
355 360 365

Lys Gln Leu Ile Val Asn Glu Thr Val Pro Arg Arg Phe Ser Pro Gln
370 375 380

Ser Ser Asp Lys Ala His Leu Asn Leu Arg Ile Lys Ser Val Glu Pro
385 390 395 400

Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Ser Ser Arg Asp Trp Ser
405 410 415

Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr Arg Leu Thr Val Leu Glu
420 425 430

Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser
435 440 445

Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala
450 455 460

Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
465 470 475 480

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys Glu
485 490 495

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

Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe His
515 520 525

Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro Val
530 535 540

Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile
545 550 555 560

Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr
565 570 575

Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Gly
580 585 590

Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
595 600

<210> 46
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 46

Cys Xaa Leu Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe
1 5 10

<210> 47
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 47

Cys Ala Xaa Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe
1 5 10

<210> 48

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 48

Cys Ala Leu Xaa Gly Asn Ala Gly Ala Lys Leu Thr Phe
1 5 10

<210> 49

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 49

Cys Ala Leu Arg Xaa Asn Ala Gly Ala Lys Leu Thr Phe
1 5 10

<210> 50

<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is Ala, Arg, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 50

Cys Ala Leu Arg Gly Xaa Ala Gly Ala Lys Leu Thr Phe
1 5 10

<210> 51
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 51

Cys Ala Leu Arg Gly Asn Xaa Gly Ala Lys Leu Thr Phe
1 5 10

<210> 52
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 52

Cys Ala Leu Arg Gly Asn Ala Xaa Ala Lys Leu Thr Phe
1 5 10

<210> 53
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 53

Cys Ala Leu Arg Gly Asn Ala Gly Xaa Lys Leu Thr Phe
1 5 10

<210> 54
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 54

Cys Ala Leu Arg Gly Asn Ala Gly Ala Xaa Leu Thr Phe

1 5 10

<210> 55
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 55

Cys Ala Leu Arg Gly Asn Ala Gly Ala Lys Xaa Thr Phe
1 5 10

<210> 56
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.

<400> 56

Cys Ala Leu Arg Gly Asn Ala Gly Ala Lys Leu Xaa Phe
1 5 10

<210> 57
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 57

Cys	Xaa	Ser	Ser	Ser	Arg	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Tyr	Phe
1				5					10					15

<210> 58
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 58

Cys	Ala	Xaa	Ser	Ser	Arg	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Tyr	Phe
1				5					10					15

<210> 59
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,

Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 59

Cys	Ala	Ser	Xaa	Ser	Arg	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Tyr	Phe
1				5					10					15

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 60

Cys	Ala	Ser	Ser	Xaa	Arg	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Tyr	Phe
1				5					10					15

<210> 61

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val,

<400> 61

Cys	Ala	Ser	Ser	Ser	Xaa	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Tyr	Phe
1				5					10					15

<210> 62
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Ala, Arg, Asn, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 62

Cys	Ala	Ser	Ser	Ser	Arg	Xaa	Trp	Ser	Ala	Glu	Thr	Leu	Tyr	Phe
1				5					10					15

<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val.

<400> 63

Cys	Ala	Ser	Ser	Ser	Arg	Asp	Xaa	Ser	Ala	Glu	Thr	Leu	Tyr	Phe
1				5					10					15

<210> 64
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 64

Cys	Ala	Ser	Ser	Ser	Arg	Asp	Trp	Xaa	Ala	Glu	Thr	Leu	Tyr	Phe
1				5				10						15

<210> 65
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 65

Cys	Ala	Ser	Ser	Ser	Arg	Asp	Trp	Ser	Xaa	Glu	Thr	Leu	Tyr	Phe
1				5				10						15

<210> 66
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 66

Cys Ala Ser Ser Ser Arg Asp Trp Ser Ala Xaa Thr Leu Tyr Phe
1 5 10 15

<210> 67
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.

<400> 67

Cys Ala Ser Ser Ser Arg Asp Trp Ser Ala Glu Xaa Leu Tyr Phe
1 5 10 15

<210> 68
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 68

Cys Ala Ser Ser Ser Arg Asp Trp Ser Ala Glu Thr Xaa Tyr Phe
1 5 10 15

<210> 69
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (14)..(14)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val.

<400> 69

Cys	Ala	Ser	Ser	Ser	Arg	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Xaa	Phe
1				5					10					15

<210> 70

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (113)..(113)

<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 70

Met	Arg	Pro	Val	Thr	Cys	Ser	Val	Leu	Val	Leu	Leu	Leu	Met	Leu	Arg
1				5					10					15	

Arg	Ser	Asn	Gly	Asp	Gly	Asp	Ser	Val	Thr	Gln	Thr	Glu	Gly	Leu	Val
			20					25					30		

Thr	Leu	Thr	Glu	Gly	Leu	Pro	Val	Met	Leu	Asn	Cys	Thr	Tyr	Gln	Thr
			35					40				45			

Ile	Tyr	Ser	Asn	Pro	Phe	Leu	Phe	Trp	Tyr	Val	Gln	His	Leu	Asn	Glu
	50					55					60				

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Xaa Leu Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 71
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or val.

<400> 71

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Xaa Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 72
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (115)..(115)
<223> Xaa is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 72

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr

35

40

45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
 50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
 85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
 100 105 110

Ala Leu Xaa Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
 115 120 125

Arg Leu Thr Val Arg Pro Asp
 130 135

<210> 73
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (116)..(116)
 <223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys,
 Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 73

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
 1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
 20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Xaa Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 74
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (117)..(117)
<223> Xaa is Ala, Arg, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 74

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Xaa Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 75
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (118)..(118)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 75

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Xaa Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 76
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 76

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Xaa Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 77

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (120)..(120)

<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 77

Met	Arg	Pro	Val	Thr	Cys	Ser	Val	Leu	Val	Leu	Leu	Leu	Met	Leu	Arg
1				5				10					15		

Arg	Ser	Asn	Gly	Asp	Gly	Asp	Ser	Val	Thr	Gln	Thr	Glu	Gly	Leu	Val
			20					25					30		

Thr	Leu	Thr	Glu	Gly	Leu	Pro	Val	Met	Leu	Asn	Cys	Thr	Tyr	Gln	Thr
		35					40					45			

Ile	Tyr	Ser	Asn	Pro	Phe	Leu	Phe	Trp	Tyr	Val	Gln	His	Leu	Asn	Glu
	50					55					60				

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

His	Gln	Gly	Phe	His	Ala	Thr	Leu	His	Lys	Ser	Ser	Ser	Ser	Phe	His
				85					90					95	

Leu	Gln	Lys	Ser	Ser	Ala	Gln	Leu	Ser	Asp	Ser	Ala	Leu	Tyr	Tyr	Cys
			100					105					110		

Ala	Leu	Arg	Gly	Asn	Ala	Gly	Xaa	Lys	Leu	Thr	Phe	Gly	Gly	Gly	Thr
		115					120					125			

Arg	Leu	Thr	Val	Arg	Pro	Asp
	130					135

<210> 78

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (121)..(121)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or val.

<400> 78

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Xaa Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 79

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (122)..(122)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 79

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Lys Xaa Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 80

<211> 135

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (123)..(123)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.

<400> 80

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Lys Leu Xaa Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp
130 135

<210> 81
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (111)..(111)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 81

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Xaa Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 82
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (112)..(112)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 82

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Xaa
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr

115

120

125

Arg Leu Thr Val Leu Glu
130

<210> 83

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (113)..(113)

<223> X is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 83

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Xaa Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 84
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 84

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Xaa Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 85
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (115)..(115)
<223> Xaa is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 85

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Xaa Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 86
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (116)..(116)
<223> Xaa is Ala, Arg, Asn, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 86

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro

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

<210> 87
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (117)..(117)
 <223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val.

<400> 87

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

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Xaa Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 88
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (118)..(118)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 88

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Xaa Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 89
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 89

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Xaa Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 90
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 90

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr

20

25

30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
 35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
 50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
 65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
 85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
 100 105 110

Ser Ser Arg Asp Trp Ser Ala Xaa Thr Leu Tyr Phe Gly Ser Gly Thr
 115 120 125

Arg Leu Thr Val Leu Glu
 130

<210> 91
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (121)..(121)
 <223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
 Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.

<400> 91

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Xaa Leu Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 92
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (122)..(122)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 92

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Xaa Tyr Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 93
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> 'Synthetic

<220>
<221> MISC_FEATURE
<222> (123)..(123)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,

Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val.

<400> 93

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Xaa Phe Gly Ser Gly Thr
115 120 125

Arg Leu Thr Val Leu Glu
130

<210> 94

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (113)..(113)

<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 94

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Xaa Leu Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 95
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 95

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Xaa Arg Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 96
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (115)..(115)
<223> Xaa is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 96

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Xaa Gly Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 97

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (116)..(116)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 97

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Xaa Asn Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 98
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (117)..(117)
<223> Xaa is Ala, Arg, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 98

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Xaa Ala Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro

210

215

220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
 245 250 255

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

<210> 99
 <211> 271
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (118)..(118)
 <223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
 Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 99

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
 1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
 20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
 35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
 50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Xaa Gly Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 100
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 100

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Xaa Ala Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr

130

135

140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
 145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
 165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
 180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
 195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
 210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
 245 250 255

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

<210> 101

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (120)..(120)

<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
 Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 101

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Xaa Lys Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 102
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (121)..(121)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 102

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu

50

55

60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Xaa Leu Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 103
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (122)..(122)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 103

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Lys Xaa Thr Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 104

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (123)..(123)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.

<400> 104

Met Arg Pro Val Thr Cys Ser Val Leu Val Leu Leu Leu Met Leu Arg
1 5 10 15

Arg Ser Asn Gly Asp Gly Asp Ser Val Thr Gln Thr Glu Gly Leu Val
20 25 30

Thr Leu Thr Glu Gly Leu Pro Val Met Leu Asn Cys Thr Tyr Gln Thr
35 40 45

Ile Tyr Ser Asn Pro Phe Leu Phe Trp Tyr Val Gln His Leu Asn Glu
50 55 60

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

His Gln Gly Phe His Ala Thr Leu His Lys Ser Ser Ser Ser Phe His
85 90 95

Leu Gln Lys Ser Ser Ala Gln Leu Ser Asp Ser Ala Leu Tyr Tyr Cys
100 105 110

Ala Leu Arg Gly Asn Ala Gly Ala Lys Leu Xaa Phe Gly Gly Gly Thr
115 120 125

Arg Leu Thr Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala Val Tyr
130 135 140

Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr
165 170 175

Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys
180 185 190

Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln
195 200 205

Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro
210 215 220

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

Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys
245 250 255

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

<210> 105
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (111)..(111)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 105

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Xaa Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 106
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (112)..(112)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 106

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Xaa
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly

245

250

255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
 260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
 275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
 290 295 300

Asn Ser
 305

<210> 107
 <211> 306
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> MISC_FEATURE
 <222> (113)..(113)
 <223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
 Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 107

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
 20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
 35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
 50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Xaa Ser Arg Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 108
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 108

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro

65		70		75		80									
Arg	Arg	Phe	Ser	Pro	Gln	Ser	Ser	Asp	Lys	Ala	His	Leu	Asn	Leu	Arg
			85						90				95		
Ile	Lys	Ser	Val	Glu	Pro	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser
			100					105					110		
Ser	Xaa	Arg	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Tyr	Phe	Gly	Ser	Gly	Thr
		115					120					125			
Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Arg	Asn	Val	Thr	Pro	Pro	Lys	Val
	130					135					140				
Ser	Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala
145					150					155					160
Thr	Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu
				165					170					175	
Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp
			180					185					190		
Pro	Gln	Ala	Tyr	Lys	Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser	Ser	Arg
		195					200					205			
Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg
	210					215					220				
Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu
225					230					235					240
Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly
				245					250					255	
Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	His	Gln	Gly	Val	Leu
			260					265					270		

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 109
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (115)..(115)
<223> Xaa is Ala, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 109

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Xaa Asp Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 110
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (116)..(116)
<223> Xaa is Ala, Arg, Asn, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 110

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Xaa Trp Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys

290

295

300

Asn Ser
305

<210> 111
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (117)..(117)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val.

<400> 111

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Xaa Ser Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 112
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (118)..(118)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu,
Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val.

<400> 112

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Xaa Ala Glu Thr Leu Tyr Phe Gly Ser Gly Thr

115

120

125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
 145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
 165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
 180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
 195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
 210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
 225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
 245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
 260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
 275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
 290 295 300

Asn Ser
 305

<210> 113
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (119)..(119)
<223> Xaa is Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 113

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Xaa Glu Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 114
<211> 306

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa is Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 114

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Xaa Thr Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 115
<211> 306
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (121)..(121)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val.

<400> 115

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Xaa Leu Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 116
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<221> MISC_FEATURE

<222> (122)..(122)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val.

<400> 116

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Arg Asp Trp Ser Ala Glu Thr Xaa Tyr Phe Gly Ser Gly Thr
115 120 125

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

Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu

165

170

175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 117
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE

<222> (123)..(123)

<223> Xaa is Ala, Arg, Asn, Asp, Cys, Glu, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val.

<400> 117

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

Gly	Pro	Leu	Glu	Thr	Ala	Val	Phe	Gln	Thr	Pro	Asn	Tyr	His	Val	Thr
			20					25					30		

Gln	Val	Gly	Asn	Glu	Val	Ser	Phe	Asn	Cys	Lys	Gln	Thr	Leu	Gly	His
		35					40					45			

Asp	Thr	Met	Tyr	Trp	Tyr	Lys	Gln	Asp	Ser	Lys	Lys	Leu	Leu	Lys	Ile
	50					55					60				

Met	Phe	Ser	Tyr	Asn	Asn	Lys	Gln	Leu	Ile	Val	Asn	Glu	Thr	Val	Pro
65					70					75					80

Arg	Arg	Phe	Ser	Pro	Gln	Ser	Ser	Asp	Lys	Ala	His	Leu	Asn	Leu	Arg
				85					90					95	

Ile	Lys	Ser	Val	Glu	Pro	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys	Ala	Ser
			100					105					110		

Ser	Ser	Arg	Asp	Trp	Ser	Ala	Glu	Thr	Leu	Xaa	Phe	Gly	Ser	Gly	Thr
		115					120					125			

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

Ser	Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln	Lys	Ala
145					150					155					160

Thr	Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val	Glu	Leu
				165					170					175	

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg
195 200 205

Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg
210 215 220

Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu
225 230 235 240

Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly
245 250 255

Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu
260 265 270

Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr
275 280 285

Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys
290 295 300

Asn Ser
305

<210> 118
<211> 23
<212> PRT
<213> Homo sapiens

<400> 118

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu
20

<210> 119
<211> 23
<212> PRT
<213> Homo sapiens

<400> 119

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Asp	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu
						20

<210> 120
<211> 23
<212> PRT
<213> Homo sapiens

<400> 120

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Val	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu
						20

<210> 121
<211> 188
<212> PRT
<213> Homo sapiens

<400> 121

Met	Thr	Glu	Tyr	Lys	Leu	Val	Val	Val	Gly	Ala	Gly	Gly	Val	Gly	Lys
1				5					10					15	

Ser	Ala	Leu	Thr	Ile	Gln	Leu	Ile	Gln	Asn	His	Phe	Val	Asp	Glu	Tyr
				20				25					30		

Asp	Pro	Thr	Ile	Glu	Asp	Ser	Tyr	Arg	Lys	Gln	Val	Val	Ile	Asp	Gly
		35					40					45			

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

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

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
165 170 175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
180 185

<210> 122
<211> 188
<212> PRT
<213> Homo sapiens

<400> 122

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

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

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
165 170 175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
180 185

<210> 123
<211> 188
<212> PRT
<213> Homo sapiens

<400> 123

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr
85 90 95

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

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys
165 170 175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met
180 185

<210> 124

<211> 9

<212> PRT

<213> Homo sapiens

<400> 124

Val Val Val Gly Ala Asp Gly Val Gly
1 5

<210> 125

<211> 6

<212> PRT

<213> Murine

<400> 125

Asp Pro Asn Ser Tyr Tyr
1 5

<210> 126

<211> 7

<212> PRT

<213> Murine

<400> 126

Val Phe Ser Ser Thr Glu Ile
1 5

<210> 127

<211> 16

<212> PRT

<213> Murine

<400> 127

Cys Ala Val Ser Gly Gly Thr Asn Ser Ala Gly Asn Lys Leu Thr Phe
1 5 10 15

<210> 128

<211> 5

<212> PRT

<213> Murine

<400> 128

Leu Gly His Asp Thr
1 5

<210> 129
<211> 6
<212> PRT
<213> Murine

<400> 129

Tyr Asn Asn Lys Gln Leu
1 5

<210> 130
<211> 14
<212> PRT
<213> Murine

<400> 130

Cys Ala Ser Ser Arg Asp Trp Gly Pro Ala Glu Gln Phe Phe
1 5 10

<210> 131
<211> 137
<212> PRT
<213> Murine

<400> 131

Met Lys Thr Val Thr Gly Pro Leu Phe Leu Cys Phe Trp Leu Gln Leu
1 5 10 15

Asn Cys Val Ser Arg Gly Glu Gln Val Glu Gln Arg Pro Pro His Leu
20 25 30

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

Pro Asn Ser Tyr Tyr Phe Phe Trp Tyr Lys Gln Glu Pro Gly Ala Ser
50 55 60

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

Gln Gly Phe Thr Val Leu Leu Asn Lys Lys Asp Lys Arg Leu Ser Leu
85 90 95

Asn Leu Thr Ala Ala His Pro Gly Asp Ser Ala Ala Tyr Phe Cys Ala
100 105 110

Val Ser Gly Gly Thr Asn Ser Ala Gly Asn Lys Leu Thr Phe Gly Ile
115 120 125

Gly Thr Arg Val Leu Val Arg Pro Asp
130 135

<210> 132
<211> 133
<212> PRT
<213> Murine

<400> 132

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Arg Asp Trp Gly Pro Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg
115 120 125

Leu Thr Val Leu Glu
130

<210> 133
<211> 273
<212> PRT
<213> Murine

<400> 133

Met Lys Thr Val Thr Gly Pro Leu Phe Leu Cys Phe Trp Leu Gln Leu
1 5 10 15

Asn Cys Val Ser Arg Gly Glu Gln Val Glu Gln Arg Pro Pro His Leu
20 25 30

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

Pro Asn Ser Tyr Tyr Phe Phe Trp Tyr Lys Gln Glu Pro Gly Ala Ser
50 55 60

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

Gln Gly Phe Thr Val Leu Leu Asn Lys Lys Asp Lys Arg Leu Ser Leu
85 90 95

Asn Leu Thr Ala Ala His Pro Gly Asp Ser Ala Ala Tyr Phe Cys Ala
100 105 110

Val Ser Gly Gly Thr Asn Ser Ala Gly Asn Lys Leu Thr Phe Gly Ile
115 120 125

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

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
145 150 155 160

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

Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp
180 185 190

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

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu
245 250 255

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

Ser

<210> 134
<211> 305
<212> PRT
<213> Murine

<400> 134

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

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr

20

25

30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
 35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
 50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
 65 70 75 80

Arg Arg Phe Ser Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg
 85 90 95

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
 100 105 110

Ser Arg Asp Trp Gly Pro Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg
 115 120 125

Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser
 130 135 140

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
 145 150 155 160

Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser
 165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
 180 185 190

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
 195 200 205

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
 210 215 220

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
225 230 235 240

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
245 250 255

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser
260 265 270

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
275 280 285

Val Leu Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn
290 295 300

Ser
305

<210> 135
<211> 136
<212> PRT
<213> Murine

<400> 135

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

Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
20 25 30

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

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
50 55 60

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
65 70 75 80

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

Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val
100 105 110

Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
115 120 125

Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 136
<211> 172
<212> PRT
<213> Murine

<400> 136

Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser
1 5 10 15

Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala
20 25 30

Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
35 40 45

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys Glu
50 55 60

Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
65 70 75 80

Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe His
85 90 95

Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro Val

100

105

110

Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile
 115 120 125

Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr
 130 135 140

Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Gly
 145 150 155 160

Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
 165 170

<210> 137
 <211> 6
 <212> PRT
 <213> Murine

<400> 137

Asn Asp Met Phe Asp Tyr
 1 5

<210> 138
 <211> 7
 <212> PRT
 <213> Murine

<400> 138

Val Arg Ser Asn Val Asp Lys
 1 5

<210> 139
 <211> 15
 <212> PRT
 <213> Murine

<400> 139

Cys Ala Ala Gly Asp Ser Gly Gly Ser Asn Tyr Lys Leu Thr Phe
 1 5 10 15

<210> 140
<211> 5
<212> PRT
<213> Murine

<400> 140

Asn Ser His Asn Tyr
1 5

<210> 141
<211> 6
<212> PRT
<213> Murine

<400> 141

Ser Tyr Gly Ala Gly Asn
1 5

<210> 142
<211> 14
<212> PRT
<213> Murine

<400> 142

Cys Ala Ser Ala Ser Trp Gly Gly Tyr Ala Glu Gln Phe Phe
1 5 10

<210> 143
<211> 141
<212> PRT
<213> Murine

<400> 143

Met Thr Gly Phe Leu Lys Ala Leu Leu Leu Val Leu Cys Leu Arg Pro
1 5 10 15

Glu Trp Ile Lys Ser Gln Gln Lys Thr Gly Gly Gln Gln Val Lys Gln
20 25 30

Ser Ser Pro Ser Leu Thr Val Gln Glu Gly Gly Ile Leu Ile Leu Asn
35 40 45

Cys Asp Tyr Glu Asn Asp Met Phe Asp Tyr Phe Ala Trp Tyr Lys Lys
50 55 60

Tyr Pro Asp Asn Ser Pro Thr Leu Leu Ile Ser Val Arg Ser Asn Val
65 70 75 80

Asp Lys Arg Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Gly
85 90 95

Lys His Phe Ser Leu His Ile Thr Ala Ser Gln Pro Glu Asp Thr Ala
100 105 110

Val Tyr Leu Cys Ala Ala Gly Asp Ser Gly Gly Ser Asn Tyr Lys Leu
115 120 125

Thr Phe Gly Lys Gly Thr Leu Leu Thr Val Thr Pro Asn
130 135 140

<210> 144
<211> 131
<212> PRT
<213> Murine

<400> 144

Met Gly Ser Arg Leu Phe Leu Val Leu Ser Leu Leu Cys Thr Lys His
1 5 10 15

Met Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Thr Val Thr
20 25 30

Gly Gly Asn Val Thr Leu Ser Cys Arg Gln Thr Asn Ser His Asn Tyr
35 40 45

Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile His
50 55 60

Tyr Ser Tyr Gly Ala Gly Asn Leu Gln Ile Gly Asp Val Pro Asp Gly
65 70 75 80

Tyr Lys Ala Thr Arg Thr Thr Gln Glu Asp Phe Phe Leu Leu Leu Glu
85 90 95

Leu Ala Ser Pro Ser Gln Thr Ser Leu Tyr Phe Cys Ala Ser Ala Ser
100 105 110

Trp Gly Gly Tyr Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr
115 120 125

Val Leu Glu
130

<210> 145
<211> 277
<212> PRT
<213> Murine

<400> 145

Met Thr Gly Phe Leu Lys Ala Leu Leu Leu Val Leu Cys Leu Arg Pro
1 5 10 15

Glu Trp Ile Lys Ser Gln Gln Lys Thr Gly Gly Gln Gln Val Lys Gln
20 25 30

Ser Ser Pro Ser Leu Thr Val Gln Glu Gly Gly Ile Leu Ile Leu Asn
35 40 45

Cys Asp Tyr Glu Asn Asp Met Phe Asp Tyr Phe Ala Trp Tyr Lys Lys
50 55 60

Tyr Pro Asp Asn Ser Pro Thr Leu Leu Ile Ser Val Arg Ser Asn Val
65 70 75 80

Asp Lys Arg Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Gly
85 90 95

Lys His Phe Ser Leu His Ile Thr Ala Ser Gln Pro Glu Asp Thr Ala
100 105 110

Val Tyr Leu Cys Ala Ala Gly Asp Ser Gly Gly Ser Asn Tyr Lys Leu
115 120 125

Thr Phe Gly Lys Gly Thr Leu Leu Thr Val Thr Pro Asn Ile Gln Asn
130 135 140

Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser
145 150 155 160

Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys
165 170 175

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

Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln
195 200 205

Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr
210 215 220

Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe
225 230 235 240

Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu
245 250 255

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser
275

<210> 146
<211> 303
<212> PRT
<213> Murine

<400> 146

Met Gly Ser Arg Leu Phe Leu Val Leu Ser Leu Leu Cys Thr Lys His
1 5 10 15

Met Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Thr Val Thr
20 25 30

Gly Gly Asn Val Thr Leu Ser Cys Arg Gln Thr Asn Ser His Asn Tyr
35 40 45

Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile His
50 55 60

Tyr Ser Tyr Gly Ala Gly Asn Leu Gln Ile Gly Asp Val Pro Asp Gly
65 70 75 80

Tyr Lys Ala Thr Arg Thr Thr Gln Glu Asp Phe Phe Leu Leu Leu Glu
85 90 95

Leu Ala Ser Pro Ser Gln Thr Ser Leu Tyr Phe Cys Ala Ser Ala Ser
100 105 110

Trp Gly Gly Tyr Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr
115 120 125

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

Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val
145 150 155 160

Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
165 170 175

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala
180 185 190

Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val
195 200 205

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

Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro
225 230 235 240

Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp
245 250 255

Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr
260 265 270

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
275 280 285

Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
290 295 300

<210> 147
<211> 136
<212> PRT
<213> Murine

<400> 147

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

Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
20 25 30

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

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
50 55 60

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
65 70 75 80

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

Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val
100 105 110

Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
115 120 125

Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 148

<211> 172

<212> PRT

<213> Murine

<400> 148

Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser
1 5 10 15

Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala
20 25 30

Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
35 40 45

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys Glu
50 55 60

Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr

65		70		75		80									
Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	His
			85						90					95	
Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser	Pro	Lys	Pro	Val
			100					105					110		
Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Ile
		115					120					125			
Thr	Ser	Ala	Ser	Tyr	His	Gln	Gly	Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr
	130					135					140				
Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	Leu	Val	Ser	Gly
145					150					155					160
Leu	Val	Leu	Met	Ala	Met	Val	Lys	Lys	Lys	Asn	Ser				
			165						170						

<210> 149
 <211> 5
 <212> PRT
 <213> Murine

<400> 149

Thr	Thr	Met	Arg	Ser
1				5

<210> 150
 <211> 5
 <212> PRT
 <213> Murine

<400> 150

Leu	Ala	Ser	Gly	Thr
1				5

<210> 151

<211> 15
<212> PRT
<213> Murine

<400> 151

Cys	Ala	Ala	Asp	Ser	Ser	Asn	Thr	Gly	Tyr	Gln	Asn	Phe	Tyr	Phe
1				5					10					15

<210> 152
<211> 5
<212> PRT
<213> Murine

<400> 152

Ser	Gly	His	Leu	Ser
1				5

<210> 153
<211> 6
<212> PRT
<213> Murine

<400> 153

His	Tyr	Asp	Lys	Met	Glu
1				5	

<210> 154
<211> 15
<212> PRT
<213> Murine

<400> 154

Cys	Ala	Ser	Ser	Leu	Thr	Asp	Pro	Leu	Asp	Ser	Asp	Tyr	Thr	Phe
1				5					10					15

<210> 155
<211> 133
<212> PRT
<213> Murine

<400> 155

Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val Gln Ile
1 5 10 15

Cys Trp Val Arg Gly Asp Gln Val Glu Gln Ser Pro Ser Ala Leu Ser
20 25 30

Leu His Glu Gly Thr Asp Ser Ala Leu Arg Cys Asn Phe Thr Thr Thr
35 40 45

Met Arg Ser Val Gln Trp Phe Arg Gln Asn Ser Arg Gly Ser Leu Ile
50 55 60

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

Ser Ala Phe Asp Ser Lys Glu Arg Arg Tyr Ser Thr Leu His Ile Arg
85 90 95

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

Ser Asn Thr Gly Tyr Gln Asn Phe Tyr Phe Gly Lys Gly Thr Ser Leu
115 120 125

Thr Val Ile Pro Asn
130

<210> 156
<211> 143
<212> PRT
<213> Murine

<400> 156

Met Ser Asn Thr Ala Phe Pro Asp Pro Ala Trp Asn Thr Thr Leu Leu
1 5 10 15

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

Val Val Gln Ser Pro Arg Tyr Ile Ile Lys Gly Lys Gly Glu Arg Ser
35 40 45

Ile Leu Lys Cys Ile Pro Ile Ser Gly His Leu Ser Val Ala Trp Tyr
50 55 60

Gln Gln Thr Gln Gly Gln Glu Leu Lys Phe Phe Ile Gln His Tyr Asp
65 70 75 80

Lys Met Glu Arg Asp Lys Gly Asn Leu Pro Ser Arg Phe Ser Val Gln
85 90 95

Gln Phe Asp Asp Tyr His Ser Glu Met Asn Met Ser Ala Leu Glu Leu
100 105 110

Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Leu Thr Asp Pro Leu
115 120 125

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

<210> 157
<211> 269
<212> PRT
<213> Murine

<400> 157

Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val Gln Ile
1 5 10 15

Cys Trp Val Arg Gly Asp Gln Val Glu Gln Ser Pro Ser Ala Leu Ser
20 25 30

Leu His Glu Gly Thr Asp Ser Ala Leu Arg Cys Asn Phe Thr Thr Thr
35 40 45

Met Arg Ser Val Gln Trp Phe Arg Gln Asn Ser Arg Gly Ser Leu Ile
50 55 60

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

Ser Ala Phe Asp Ser Lys Glu Arg Arg Tyr Ser Thr Leu His Ile Arg
85 90 95

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

Ser Asn Thr Gly Tyr Gln Asn Phe Tyr Phe Gly Lys Gly Thr Ser Leu
115 120 125

Thr Val Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu
130 135 140

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
165 170 175

Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
225 230 235 240

Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala
245 250 255

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 158
<211> 316
<212> PRT
<213> Murine

<400> 158

Met Ser Asn Thr Ala Phe Pro Asp Pro Ala Trp Asn Thr Thr Leu Leu
1 5 10 15

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

Val Val Gln Ser Pro Arg Tyr Ile Ile Lys Gly Lys Gly Glu Arg Ser
35 40 45

Ile Leu Lys Cys Ile Pro Ile Ser Gly His Leu Ser Val Ala Trp Tyr
50 55 60

Gln Gln Thr Gln Gly Gln Glu Leu Lys Phe Phe Ile Gln His Tyr Asp
65 70 75 80

Lys Met Glu Arg Asp Lys Gly Asn Leu Pro Ser Arg Phe Ser Val Gln
85 90 95

Gln Phe Asp Asp Tyr His Ser Glu Met Asn Met Ser Ala Leu Glu Leu
100 105 110

Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Leu Thr Asp Pro Leu
115 120 125

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

Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro Ser
145 150 155 160

Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala
165 170 175

Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
180 185 190

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys Glu
195 200 205

Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
210 215 220

Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe His
225 230 235 240

Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro Val
245 250 255

Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile
260 265 270

Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr
275 280 285

Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Thr
290 295 300

Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
305 310 315

<210> 159
<211> 136
<212> PRT
<213> Murine

<400> 159

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

Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
20 25 30

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

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
50 55 60

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
65 70 75 80

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

Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val
100 105 110

Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
115 120 125

Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 160
<211> 173
<212> PRT
<213> Murine

<400> 160

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
1 5 10 15

Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn

35

40

45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys
 50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
 65 70 75 80

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
 85 90 95

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

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
 115 120 125

Ile Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
 130 135 140

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
 145 150 155 160

Thr Leu Val Val Met Ala Met Val Lys Arg Lys Asn Ser
 165 170

<210> 161
 <211> 13
 <212> PRT
 <213> Murine

<400> 161

Cys Ala Ala Leu Asn Thr Gly Tyr Gln Asn Phe Tyr Phe
 1 5 10

<210> 162
 <211> 612
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 162

Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	Gln	Ile
1				5					10					15	

Cys	Trp	Val	Arg	Gly	Asp	Gln	Val	Glu	Gln	Ser	Pro	Ser	Ala	Leu	Ser
			20					25					30		

Leu	His	Glu	Gly	Thr	Asp	Ser	Ala	Leu	Arg	Cys	Asn	Phe	Thr	Thr	Thr
		35					40					45			

Met	Arg	Ser	Val	Gln	Trp	Phe	Arg	Gln	Asn	Ser	Arg	Gly	Ser	Leu	Ile
	50					55					60				

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

Ser	Ala	Phe	Asp	Ser	Lys	Glu	Arg	Arg	Tyr	Ser	Thr	Leu	His	Ile	Arg
				85					90					95	

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

Ser	Asn	Thr	Gly	Tyr	Gln	Asn	Phe	Tyr	Phe	Gly	Lys	Gly	Thr	Ser	Leu
			115				120					125			

Thr	Val	Ile	Pro	Asn	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu
	130					135					140				

Lys	Asp	Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe
145					150					155					160

Asp	Ser	Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile
				165					170					175	

Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
225 230 235 240

Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala
245 250 255

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

Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
275 280 285

Asp Val Glu Glu Asn Pro Gly Pro Met Ser Asn Thr Ala Phe Pro Asp
290 295 300

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

Gly Thr Ser Ser Ala Asn Ser Gly Val Val Gln Ser Pro Arg Tyr Ile
325 330 335

Ile Lys Gly Lys Gly Glu Arg Ser Ile Leu Lys Cys Ile Pro Ile Ser
340 345 350

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

Lys Phe Phe Ile Gln His Tyr Asp Lys Met Glu Arg Asp Lys Gly Asn
370 375 380

Leu Pro Ser Arg Phe Ser Val Gln Gln Phe Asp Asp Tyr His Ser Glu
385 390 395 400

Met Asn Met Ser Ala Leu Glu Leu Glu Asp Ser Ala Val Tyr Phe Cys
405 410 415

Ala Ser Ser Leu Thr Asp Pro Leu Asp Ser Asp Tyr Thr Phe Gly Ser
420 425 430

Gly Thr Arg Leu Leu Val Ile Glu Asp Leu Arg Asn Val Thr Pro Pro
435 440 445

Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln
450 455 460

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

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
485 490 495

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

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His
515 520 525

Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp
530 535 540

Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala
545 550 555 560

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly
565 570 575

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
580 585 590

Leu Tyr Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys
595 600 605

Arg Lys Asn Ser
610

<210> 163
<211> 1839
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 163
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ctgagatgca attttacgac caccatgagg agtgtgcagt ggttccgaca gaattccagg 180
ggcagcctca tcagtttggt ctacttggct tcaggaacaa aggagaatgg gaggctaaag 240
tcagcatttg attctaagga gcggcgctac agcaccctgc acatcaggga tgcccagctg 300
gaggactcag gcacttactt ctgtgctgct gactcttcga acacgggtta ccagaacttc 360
tattttggga aaggaacaag ttgactgtc attccaaaca tccagaaccc agaacctgct 420
gtgtaccagt taaaagatcc tcggtctcag gacagcacc tctgcctgtt caccgacttt 480
gactcccaaa tcaatgtgcc gaaaaccatg gaatctggaa cgttcatcac tgacaaaact 540
gtgctggaca tgaaagctat ggattccaag agcaatgggg ccattgcctg gagcaaccag 600
acaagcttca cctgccaaga tatcttcaaa gagaccaacg ccacctaccc cagttcagac 660
gttccctgtg atgccacgtt gaccgagaaa agctttgaaa cagatatgaa cctgaacttt 720
caaaacctgt cagttatggg actccgaatc ctctgctga aagtagcggg atttaacctg 780
ctcatgacgc tgaggctgtg gtccagtcgg gccaaagcgg cgggatccgg agccaccaac 840
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gccttccctg accccgcctg gaacaccacc ctgctatctt gggttgctct ctttctcctg	960
ggaacaagtt cagcaaattc tggggttgtc cagtctccaa gatacataat caaaggaaaag	1020
ggagaaaaggt ccatttctaaa atgtattccc atctctggac atctctctgt ggcctgggtat	1080
caacagactc aggggcagga actaaagttc ttcattcagc attatgataa aatggagaga	1140
gataaaggaa acctgcccag cagattctca gtccaacagt ttgatgacta tcactctgag	1200
atgaacatga gtgccttggg gctagaggac tctgccgtgt acttctgtgc cagctctctc	1260
acagatccgc tagactccga ctacaccttc ggctcaggga ccaggctttt ggtaatagag	1320
gatctgagaa atgtgactcc acccaaggtc tccttgtttg agccatcaaa agcagagatt	1380
gcaaacaac aaaaggctac cctcgtgtgc ttggccaggg gcttcttccc tgaccacgtg	1440
gagctgagct ggtgggtgaa tggcaaggag gtccacagtg gggtcagcac ggaccctcag	1500
gcctacaagg agagcaatta tagctactgc ctgagcagcc gcctgagggt ctctgctacc	1560
ttctggcaca atcctcgcaa ccacttccgc tgccaagtgc agttccatgg gctttcagag	1620
gaggacaagt ggccagaggg ctcacccaaa cctgtcacac agaacatcag tgcagaggcc	1680
tggggccgag cagactgtgg gattacctca gcacacctatc aacaaggggt cttgtctgcc	1740
accatcctct atgagatcct gctagggaaa gccaccctgt atgctgtgct tgtcagtaca	1800
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<210> 164
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 164
 accacatga ggagt

15

<210> 165
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic

<400> 165
ttggcttcag gaaca 15

<210> 166
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 166
gctgctgact cttcgaacac gggttaccag aacttctat 39

<210> 167
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 167
tctggacatc tctct 15

<210> 168
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 168
cattatgata aaatggag 18

<210> 169
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 169

gccagctctc tcacagatcc gctagactcc gactacacc

39

<210> 170

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 170

atgcagagga acctgggagc tgtgctgggg attctgtggg tgcagatttg ctgggtgaga 60

ggggatcagg tggagcagag tccttcagcc ctgagcctcc acgagggaac cgattctgct 120

ctgagatgca attttacgac caccatgagg agtgtgcagt ggttccgaca gaattccagg 180

ggcagcctca tcagtttggt ctacttggct tcaggaacaa aggagaatgg gaggctaaag 240

tcagcatttg attctaagga gcggcgctac agcaccctgc acatcaggga tgcccagctg 300

gaggactcag gcacttactt ctgtgctgct gactcttcga acacgggtta ccagaacttc 360

tattttggga aaggaacaag ttgactgtc attccaaac 399

<210> 171

<211> 429

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 171

atgtctaaca ctgccttccc tgaccccgcc tggaacacca ccctgctatc ttgggttgct 60

ctcttttctcc tgggaacaag ttcagcaaatt tctgggggttg tccagtctcc aagatacata 120

atcaaaggaa agggagaaaag gtccattcta aaatgtattc ccatctctgg acatctctct 180

gtggcctggg atcaacagac tcaggggcag gaactaaaagt tcttcattca gcattatgat 240

aaaatggaga gagataaagg aaacctgccc agcagattct cagtccaaca gtttcatgac 300

tatcactctg agatgaacat gagtgccttg gagctagagg actctgccgt gtacttctgt 360

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ttggtaata	429

<210> 172
 <211> 807
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 172	
atgcagagga acctgggagc tgtgctgggg attctgtggg tgcagatttg ctgggtgaga	60
ggggatcagg tggagcagag tccttcagcc ctgagcctcc acgagggaac cgattctgct	120
ctgagatgca attttacgac caccatgagg agtgtgcagt ggttccgaca gaattccagg	180
ggcagcctca tcagtttggt ctacttggct tcaggaacaa aggagaatgg gaggctaaag	240
tcagcatttg attctaagga gcggcgctac agcaccctgc acatcaggga tgcccagctg	300
gaggactcag gcacttactt ctgtgctgct gactcttcga acacgggtta ccagaacttc	360
tattttggga aaggaacaag ttgactgtc attccaaaca tccagaaccc agaacctgct	420
gtgtaccagt taaaagatcc tcggtctcag gacagcacc tctgcctgtt caccgacttt	480
gactcccaaa tcaatgtgcc gaaaaccatg gaatctggaa cgttcatcac tgacaaaact	540
gtgctggaca tgaaagctat ggattccaag agcaatgggg ccattgcctg gagcaaccag	600
acaagcttca cctgccaaga tatcttcaaa gagaccaacg ccacctacc cagttcagac	660
gttccctgtg atgccacgtt gaccgagaaa agctttgaaa cagatatgaa cctgaacttt	720
caaaacctgt cagttatggg actccgaatc ctctgctga aagtagcggg atttaacctg	780
ctcatgacgc tgaggctgtg gtccagt	807

<210> 173
 <211> 951
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 173

atgtctaaca ctgccttccc tgaccccgcc tggaacacca ccctgctatc ttgggttgct	60
ctcttttctcc tgggaacaag ttcagcaaata tctgggggttg tccagtctcc aagatacata	120
atcaaaggaa agggagaaaag gtccattcta aaatgtattc ccatctctgg acatctctct	180
gtggcctggt atcaacagac tcaggggcag gaactaaagt tcttcattca gcattatgat	240
aaaatggaga gagataaagg aaacctgccc agcagattct cagtccaaca gtttgatgac	300
tatcactctg agatgaacat gagtgccttg gagctagagg actctgccgt gtacttctgt	360
gccagctctc tcacagatcc gctagactcc gactacacct tcggctcagg gaccaggctt	420
ttggtaatag aggatctgag aaatgtgact ccacccaagg tctccttggt tgagccatca	480
aaagcagaga ttgcaaaca acaaaaggct accctcgtgt gcttggccag gggcttcttc	540
cctgaccacg tggagctgag ctggtgggtg aatggcaagg aggtccacag tggggtcagc	600
acggaccctc aggcctacaa ggagagcaat tatagctact gcctgagcag ccgcctgagg	660
gtctctgcta ctttctggca caatcctcgc aaccacttcc gctgccaagt gcagttccat	720
gggctttcag aggaggacaa gtggccagag ggctcaccca aacctgtcac acagaacatc	780
agtgcagagg cctggggccg agcagactgt gggattacct cagcatccta tcaacaaggg	840
gtcttgtctg ccaccatcct ctatgagatc ctgctaggga aagccaccct gtatgctgtg	900
cttgtcagta cactggtggt gatggctatg gtcaaaagaa agaattcatg a	951

<210> 174

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 174

atccagaacc cagaacctgc tgtgtaccag ttaaaagatc ctcggtctca ggacagcacc	60
ctctgcctgt tcaccgactt tgactcccaa atcaatgtgc cgaaaaccat ggaatctgga	120
acgttcatca ctgacaaaac tgtgctggac atgaaagcta tggattccaa gagcaatggg	180

gccattgcct ggagcaacca gacaagcttc acctgccaaag atatcttcaa agagaccaac	240
gccacctacc ccagttcaga cgttccctgt gatgccacgt tgaccgagaa aagctttgaa	300
acagatatga acctaaactt tcaaaacctg tcagttatgg gactccgaat cctcctgctg	360
aaagtagcgg gatttaacct gctcatgacg ctgaggctgt ggtccagt	408

<210> 175
 <211> 522
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 175	
gaggatctga gaaatgtgac tccacccaag gtctccttgt ttgagccatc aaaagcagag	60
attgcaaaca aacaaaaggc taccctcgtg tgcttggcca ggggcttctt ccctgaccac	120
gtggagctga gctgggtgggt gaatggcaag gaggtccaca gtggggtcag cacggaccct	180
caggcctaca aggagagcaa ttatagctac tgcctgagca gccgcctgag ggtctctgct	240
accttctggc acaatcctcg caaccacttc cgctgccaaag tgcagttcca tgggctttca	300
gaggaggaca agtggccaga gggctcacc aaacctgtca cacagaacat cagtgcagag	360
gcctggggcc gagcagactg tgggattacc tcagcatcct atcaacaagg ggtcttgtct	420
gccaccatcc tctatgagat cctgctaggg aaagccaccc tgtatgctgt gcttgtcagt	480
acactggtgg tgatggctat ggtcaaaaga aagaattcat ga	522

<210> 176
 <211> 1818
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 176	
atgaagacgg tgactggacc tttgttcctg tgcttctggc tgcagctgaa ctgtgtgagc	60
agaggcgagc aggtggagca gcgccctcct cacctgagtg tccgggaggg agacagtgcc	120

gttatcacct gcacctacac agaccctaac agttattact tcttctggta caagcaagag	180
ccgggggcaa gtcttcagtt gcttatgaag gttttctcaa gtacggaaat aaacgaagga	240
caaggattca ctgtcctact gaacaagaaa gacaaacgac tctctctgaa cctcacagct	300
gcccacctg gggactcagc cgcgtacttc tgcgcagtca gtggagggac taacagtgca	360
gggaacaagc taacttttgg aattggaacc aggggtgctgg tcaggccaga catccagaac	420
ccagaacctg ctgtgtacca gttaaaagat cctcggcttc aggacagcac cctctgcctg	480
ttcaccgact ttgactccca aatcaatgtg ccgaaaacca tggaatctgg aacgttcac	540
actgacaaaa ctgtgctgga catgaaagct atggattcca agagcaatgg ggccattgcc	600
tggagcaacc agacaagctt cacctgccaa gatatcttca aagagaccaa cgccacctac	660
cccagttcag acgttccctg tgatgccacg ttgaccgaga aaagctttga aacagatatg	720
aacctaaact ttcaaaacct gtcagttatg ggactccgaa tcctcctgct gaaagtagcg	780
ggatttaacc tgctcatgac gctgaggctg tgggtccagtc gggccaagcg gtccggatcc	840
ggagccacca acttcagcct gctgaagcag gccggcgacg tggaggagaa ccccggtccc	900
atgggctgta ggctcctaag ctgtgtggcc ttctgcctct tgggaatagg ccctttggag	960
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aattgtaagc aaactctggg ccacgatact atgtattggg acaagcaaga ctctaagaaa	1080
ttgctgaaga ttatgtttag ctacaataat aagcaactca ttgtaaacga aacagttcca	1140
aggcgcttct cacctcagtc ttcagataaa gctcatttga atcttcgaat caagtctgta	1200
gagccggagg actctgctgt gtatctctgt gccagcagtc gggactgggg gcctgctgag	1260
cagttcttcg gaccagggac acgactcacc gtcctagagg atctgagaaa tgtgactcca	1320
ccaaggtct ccttgtttga gccatcaaaa gcagagattg caaacaaca aaaggctacc	1380
ctcgtgtgct tggccagggg cttcttccct gaccacgtgg agctgagctg gtgggtgaat	1440
ggcaaggagg tccacagtgg ggtcagcacg gaccctcagg cctacaagga gagcaattat	1500
agctactgcc tgagcagccg cctgagggtc tctgctacct tctggcaca tcctcgaaac	1560
cacttccgct gccaaagtga gttccatggg ctttcagagg aggacaagt gccagagggc	1620

tcacccaaac ctgtcacaca gaacatcagt gcagaggcct ggggccgagc agactgtgga	1680
atcacttcag catcctatca tcaggggggtt ctgtctgcaa ccatcctcta tgagatccta	1740
ctggggaagg ccaccctata tgctgtgctg gtcagtggcc tgggtgctgat ggccatggtc	1800
aagaaaaaaaa attcctga	1818

<210> 177
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 177	
gaccctaaca gttattac	18

<210> 178
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 178	
gttttctcaa gtacggaaat a	21

<210> 179
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 179	
tgcgagtcga gtggagggac taacagtgca gggaacaagc taactttt	48

<210> 180
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 180
 ctgggccacg atact 15

<210> 181
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 181
 tacaataata agcaactc 18

<210> 182
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 182
 tgtgccagca gtcgggactg ggggcctgct gagcagttct tc 42

<210> 183
 <211> 411
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 183
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agaggcgagc aggtggagca gcgccctcct cacctgagtg tccgggaggg agacagtgcc 120

gttatcacct gcacctacac agaccctaac agttattact tcttctggta caagcaagag 180

ccggggggcaa gtcttcagtt gcttatgaag gttttctcaa gtacggaaat aaacgaagga 240

caaggattca ctgtcctact gaacaagaaa gacaaacgac tctctctgaa cctcacagct 300

gccccatcctg gggactcagc cgcgtacttc tgcgcagtca gtggaggggac taacagtgca	360
gggaacaagc taacttttgg aattggaacc aggggtgctgg tcaggccaga c	411

<210> 184
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 184	
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acggctgttt tccagactcc aaactatcat gtcacacagg tgggaaatga agtgtctttc	120
aattgtaagc aaactctggg ccacgatact atgtattggt acaagcaaga ctctaagaaa	180
ttgctgaaga ttatgttttag ctacaataat aagcaactca ttgtaaacga aacagttcca	240
aggcgcttct cacctcagtc ttcagataaa gctcatttga atcttcgaat caagtctgta	300
gagccggagg actctgctgt gtatctctgt gccagcagtc gggactgggg gcctgctgag	360
cagttcttcg gaccagggac acgactcacc gtcctagag	399

<210> 185
 <211> 819
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 185	
atgaagacgg tgactggacc tttgttcctg tgcttctggc tgcagctgaa ctgtgtgagc	60
agaggcgagc aggtggagca gcgccctcct cacctgagtg tccgggaggg agacagtgcc	120
gttatcacct gcacctacac agaccctaac agttattact tcttctggta caagcaagag	180
ccgggggcaa gtcttcagtt gcttatgaag gttttctcaa gtacggaaat aaacgaagga	240
caaggattca ctgtcctact gaacaagaaa gacaaacgac tctctctgaa cctcacagct	300
gccccatcctg gggactcagc cgcgtacttc tgcgcagtca gtggaggggac taacagtgca	360

gggaacaagc taacttttgg aattggaacc aggggtgctgg tcaggccaga catccagaac	420
ccagaacctg ctgtgtacca gttaaaagat cctcggcttc aggacagcac cctctgcctg	480
ttcaccgact ttgactccca aatcaatgtg ccgaaaacca tggaatctgg aacgttcatc	540
actgacaaaa ctgtgctgga catgaaagct atggattcca agagcaatgg ggccattgcc	600
tggagcaacc agacaagctt cacctgccaa gatatcttca aagagaccaa cgccacctac	660
cccagttcag acgttccctg tgatgccacg ttgaccgaga aaagctttga aacagatatg	720
aacctaaact ttcaaaacct gtcagttatg ggactccgaa tcctcctgct gaaagtagcg	780
ggatttaacc tgctcatgac gctgaggctg tgggccagt	819

<210> 186
 <211> 918
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 186	
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acggctgttt tccagactcc aaactatcat gtcacacagg tgggaaatga agtgtctttc	120
aattgtaagc aaactctggg ccacgatact atgtattggc acaagcaaga ctctaagaaa	180
ttgctgaaga ttatgttttag ctacaataat aagcaactca ttgtaaacga aacagttcca	240
aggcgcttct cacctcagtc ttcagataaa gctcatttga atcttcgaat caagtctgta	300
gagccggagg actctgctgt gtatctctgt gccagcagtc gggactgggg gcctgctgag	360
cagttcttcg gaccagggac acgactcacc gtcctagagg atctgagaaa tgtgactcca	420
cccaaggctc ctttgtttga gccatcaaaa gcagagattg caaacaacaa aaaggctacc	480
ctcgtgtgct tggccagggg cttcttccct gaccacgtgg agctgagctg gtgggtgaat	540
ggcaaggagg tccacagtgg ggtcagcacg gaccctcagg cctacaagga gagcaattat	600
agctactgcc tgagcagccg cctgagggtc tctgctacct tctggcacia tcctcgaaac	660
cacttccgct gccaaagtga gttccatggg ctttcagagg aggacaagtg gccagagggc	720

tcacccaaac ctgtcacaca gaacatcagt gcagaggcct ggggccgagc agactgtgga	780
atcacttcag catcctatca tcaggggggtt ctgtctgcaa ccatcctcta tgagatccta	840
ctggggaagg ccaccctata tgctgtgctg gtcagtggcc tgggtgctgat ggccatggtc	900
aagaaaaaaaa attcctga	918

<210> 187
 <211> 408
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 187	
atccagaacc cagaacctgc tgtgtaccag ttaaaagatc ctcggtctca ggacagcacc	60
ctctgcctgt tcaccgactt tgactcccaa atcaatgtgc cgaaaaccat ggaatctgga	120
acgttcatca ctgacaaaac tgtgctggac atgaaaagcta tggattccaa gagcaatggg	180
gccattgcct ggagcaacca gacaagcttc acctgccaaag atatcttcaa agagaccaac	240
gccacctacc ccagttcaga cgttccctgt gatgccacgt tgaccgagaa aagctttgaa	300
acagatatga acctaaactt tcaaaacctg tcagttatgg gactccgaat cctcctgctg	360
aaagtagcgg gatttaacct gctcatgacg ctgaggctgt ggtccagt	408

<210> 188
 <211> 519
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 188	
gatctgagaa atgtgactcc acccaaggctc tccttgtttg agccatcaaa agcagagatt	60
gcaaacaaac aaaaggctac cctcgtgtgc ttggccaggg gcttcttccc tgaccacgtg	120
gagctgagct ggtgggtgaa tggcaaggag gtccacagtg gggtcagcac ggacctcag	180
gcctacaagg agagcaatta tagctactgc ctgagcagcc gcctgagggt ctctgctacc	240

ttctggcaca atcctcgaaa ccacttccgc tgccaagtgc agttccatgg gctttcagag	300
gaggacaagt ggccagaggg ctcacccaaa cctgtcacac agaacatcag tgcagaggcc	360
tggggccgag cagactgtgg aatcacttca gcatcctatc atcaggggggt tctgtctgca	420
accatcctct atgagatcct actgggggaag gccaccctat atgctgtgct ggtcagtggc	480
ctggtgctga tggccatggg caagaaaaaa aattcctga	519

<210> 189
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 189	
aatgatatgt ttgactat	18

<210> 190
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 190	
gtacgctcaa atgtggataa g	21

<210> 191
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 191	
tgcgcagcag gtgacagtgg aggcagcaat tacaaaactga cattt	45

<210> 192
 <211> 15

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 192
 aatagccaca actac 15

<210> 193
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 193
 tcatatgggtg ctggcaac 18

<210> 194
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 194
 tgtgccagcg cgagctgggg gggctatgct gagcagttct tc 42

<210> 195
 <211> 423
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

<400> 195
 atgactggct tcctgaaggc cttgctgttg gttctgtgcc tgcggccaga atggataaag 60
 agtcaacaga agactgggtgg ccagcaagtt aaacaaagct ctccatcgct gactgttcaa 120
 gagggaggga tattgacccct gaattgtgat tacgagaatg atatgtttga ctattttgcc 180
 tggtaaaaa aataccctga caacagcccc acactcctga tatccgtacg ctcaaattgtg 240

gataagaggg aagacggaag attcacagtt ttcttgaaca aaagcggcaa acacttctca	300
ctgcacatca cagcctccca gcctgaagac acagcagtggt acctctgcgc agcagggtgac	360
agtggaggca gcaattacaa actgacattt gggaaaggaa ctctcttaac tgtgactcca	420
aac	423

<210> 196
 <211> 393
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 196	
atgggctcca ggctctttct ggtcttgagc ctcctgtgta caaaacacat ggaggctgca	60
gtcacccaaa gccctagaaa caagggtgaca gtaacaggag gaaacgtgac attgagctgt	120
cgccagacta atagccacaa ctacatgtac tggatatcggc aggacactgg gcatgggctg	180
aggctgatcc attactcata tgggtgctggc aaccttcaaa taggagatgt ccctgatggg	240
tacaaggcca ccagaacaac gcaagaagac ttcttcctcc tgctggaatt ggcttctccc	300
tctcagacat ctttgtactt ctgtgccagc gcgagctggg ggggctatgc tgagcagttc	360
ttcggaccag ggacacgact caccgtccta gag	393

<210> 197
 <211> 831
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 197	
atgactggct tcctgaaggc cttgctgttg gttctgtgcc tgcggccaga atggataaag	60
agtcaacaga agactgggtg ccagcaagtt aaacaaagct ctccatcgct gactgttcaa	120
gagggaggga tattgatcct gaattgtgat tacgagaatg atatgtttga ctattttgcc	180
tggtaaaaa aataccctga caacagcccc acactcctga tatccgtacg ctcaaattgtg	240

gataagaggg aagacggaag attcacagtt ttcttgaaca aaagcggcaa acacttctca	300
ctgcacatca cagcctccca gcctgaagac acagcagtgt acctctgcgc agcaggtgac	360
agtggaggca gcaattacaa actgacattt gggaaaggaa ctctcttaac tgtgactcca	420
aacatccaga acccagaacc tgctgtgtac cagttaaaag atcctcggtc tcaggacagc	480
accctctgcc tgttcaccga ctttgactcc caaatcaatg tgccgaaaac catggaatct	540
ggaacgttca tcaactgacaa aactgtgctg gacatgaaag ctatggattc caagagcaat	600
ggggccattg cctggagcaa ccagacaagc ttcacctgcc aagatatctt caaagagacc	660
aacgccacct accccagttc agacgttccc tgtgatgcca cggtgaccga gaaaagcttt	720
gaaacagata tgaacctaaa ctttcaaaac ctgtcagtta tgggactccg aatcctcctg	780
ctgaaagtag cgggatttaa cctgctcatg acgctgaggc tgtggtccag t	831

<210> 198
 <211> 912
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 198	
atgggctcca ggctctttct ggtcttgagc ctcctgtgta caaaacacat ggaggctgca	60
gtcacccaaa gccctagaaa caaggtgaca gtaacaggag gaaacgtgac attgagctgt	120
cgccagacta atagccacaa ctacatgtac tggatatcggc aggacactgg gcatgggctg	180
aggctgatcc attactcata tggtgctggc aaccttcaaa taggagatgt ccctgatggg	240
tacaaggcca ccagaacaac gcaagaagac ttcttcctcc tgctggaatt ggcttctccc	300
tctcagacat ctttgtactt ctgtgccagc gcgagctggg ggggctatgc tgagcagttc	360
ttcggaccag ggacacgact caccgtccta gaggatctga gaaatgtgac tccaccaag	420
gtctccttgt ttgagccatc aaaagcagag attgcaaaca aacaaaaggc taccctcgtg	480
tgcttgacca ggggcttctt ccctgaccac gtggagctga gctggtgggt gaatggcaag	540
gagggtccaca gtgggggtcag cacggaccct caggcctaca aggagagcaa ttatagctac	600

tgctgagca gccgcctgag ggtctctgct accttctggc acaatcctcg aaaccacttc	660
cgctgccaag tgcagttcca tgggctttca gaggaggaca agtggccaga gggctcaccc	720
aaacctgtca cacagaacat cagtgcagag gcctggggcc gagcagactg tggaatcact	780
tcagcatcct atcatcaggg ggttctgtct gcaaccatcc tctatgagat cctactgggg	840
aaggccaccc tatatgctgt gctggtcagt ggcctgggtg tgatggccat ggtcaagaaa	900
aaaaattcct ga	912

<210> 199
 <211> 408
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 199	
atccagaacc cagaacctgc tgtgtaccag ttaaaagatc ctcggtctca ggacagcacc	60
ctctgcctgt tcaccgactt tgactcccaa atcaatgtgc cgaaaaccat ggaatctgga	120
acgttcatca ctgacaaaac tgtgctggac atgaaagcta tggattccaa gagcaatggg	180
gccattgcct ggagcaacca gacaagcttc acctgccaa atatcttcaa agagaccaac	240
gccacctacc ccagttcaga cgttccctgt gatgccacgt tgaccgagaa aagctttgaa	300
acagatatga acctaaactt tcaaaacctg tcagttatgg gactccgaat cctcctgctg	360
aaagtagcgg gatttaacct gctcatgacg ctgaggctgt ggtccagt	408

<210> 200
 <211> 519
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 200	
gatctgagaa atgtgactcc acccaaggct tccttgtttg agccatcaaa agcagagatt	60
gcaaacaac aaaaggctac cctcgtgtgc ttggccaggg gcttcttccc tgaccacgtg	120

gagctgagct ggtgggtgaa tggcaaggag gtccacagtg gggtcagcac ggaccctcag	180
gcctacaagg agagcaatta tagctactgc ctgagcagcc gcctgagggt ctctgctacc	240
ttctggcaca atcctcgaaa ccacttccgc tgccaagtgc agttccatgg gctttcagag	300
gaggacaagt ggccagaggg ctcacccaaa cctgtcacac agaacatcag tgcagaggcc	360
tggggccgag cagactgtgg aatcacttca gcatcctatc atcaggggggt tctgtctgca	420
accatcctct atgagatcct actgggggaag gccaccctat atgctgtgct ggtcagtggc	480
ctggtgctga tggccatggt caagaaaaaa aattcctga	519

<210> 201
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 201

Met	Lys	Thr	Val	Thr	Gly	Pro	Leu	Phe	Leu	Cys	Phe	Trp	Leu	Gln	Leu
1				5					10					15	

Asn	Cys	Val	Ser	Arg	Gly	Glu	Gln	Val	Glu	Gln	Arg	Pro	Pro	His	Leu
			20					25						30	

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

Pro	Asn	Ser	Tyr	Tyr	Phe	Phe	Trp	Tyr	Lys	Gln	Glu	Pro	Gly	Ala	Ser
	50					55					60				

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

Gln	Gly	Phe	Thr	Val	Leu	Leu	Asn	Lys	Lys	Asp	Lys	Arg	Leu	Ser	Leu
				85					90					95	

Asn Leu Thr Ala Ala His Pro Gly Asp Ser Ala Ala Tyr Phe Cys Ala
100 105 110

Val Ser Gly Gly Thr Asn Ser Ala Gly Asn Lys Leu Thr Phe Gly Ile
115 120 125

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

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
145 150 155 160

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

Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp
180 185 190

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

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu
245 250 255

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

Ser Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
275 280 285

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Cys Arg
290 295 300

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

Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr Gln Val Gly Asn
325 330 335

Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His Asp Thr Met Tyr
340 345 350

Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile Met Phe Ser Tyr
355 360 365

Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro Arg Arg Phe Ser
370 375 380

Pro Gln Ser Ser Asp Lys Ala His Leu Asn Leu Arg Ile Lys Ser Val
385 390 395 400

Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser Ser Arg Asp Trp
405 410 415

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

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
435 440 445

Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
450 455 460

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
465 470 475 480

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys
485 490 495

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
500 505 510

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
515 520 525

His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
530 535 540

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
545 550 555 560

Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr Ile Leu
565 570 575

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
580 585 590

Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
595 600 605

<210> 202
<211> 1824
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202
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agtcaacaga agactggtgg ccagcaagtt aaacaaagct ctccatcgct gactgttcaa 120
gagggaggga tattgatcct gaattgtgat tacgagaatg atatgtttga ctattttgcc 180
tggtacaaaa aataccctga caacagcccc acactcctga tatccgtacg ctcaaatgtg 240
gataagaggg aagacggaag attcacagtt ttcttgaaca aaagcggcaa acacttctca 300
ctgcacatca cagcctccca gcctgaagac acagcagtgt acctctgcgc agcaggtgac 360
agtggaggca gcaattacaa actgacattt gggaaaggaa ctctcttaac tgtgactcca 420

aacatccaga acccagaacc tgctgtgtac cagttaaaag atcctcggtc tcaggacagc	480
accctctgcc tgttcaccga ctttgactcc caaatcaatg tgccgaaaac catggaatct	540
ggaacgttca tcaactgacaa aactgtgctg gacatgaaag ctatggattc caagagcaat	600
ggggccattg cctggagcaa ccagacaagc ttcacctgcc aagatatctt caaagagacc	660
aacgccacct accccagttc agacgttccc tgtgatgcca cgttgaccga gaaaagcttt	720
gaaacagata tgaacctaaa ctttcaaaac ctgtcagtta tgggactccg aatcctcctg	780
ctgaaagtag cgggatttaa cctgctcatg acgctgaggc tgtggtccag tcgggccaag	840
cgggccggat ccggagccac caacttcagc ctgctgaagc aggccggcga cgtggaggag	900
aaccccggcc ccatgggctc caggctcttt ctggcttga gcctcctgtg tacaaaacac	960
atggaggctg cagtcaccca aagccctaga aacaagggtga cagtaacagg aggaaacgtg	1020
acattgagct gtcgccagac taatagccac aactacatgt actggtatcg gcaggacact	1080
gggcatgggc tgaggctgat ccattactca tatggtgctg gcaaccttca aataggagat	1140
gtccctgatg ggtacaaggc caccagaaca acgcaagaag acttcttcct cctgctggaa	1200
ttggcttctc cctctcagac atctttgtac ttctgtgcca gcgcgagctg ggggggctat	1260
gctgagcagt tcttcggacc agggacacga ctcaccgtcc tagaggatct gagaaatgtg	1320
actccaccca aggtctcctt gtttgagcca tcaaaagcag agattgcaaa caaacaaaag	1380
gctaccctcg tgtgcttggc caggggcttc ttccctgacc acgtggagct gagctggtgg	1440
gtgaatggca aggaggtcca cagtggggtc agcacggacc ctcaggccta caaggagagc	1500
aattatagct actgcctgag cagccgcctg agggctctctg ctaccttctg gcacaatcct	1560
cgaaaccact tccgctgcca agtgcagttc catgggcttt cagaggagga caagtggcca	1620
gagggctcac ccaaacctgt cacacagaac atcagtgcag aggcctgggg ccgagcagac	1680
tgtggaatca cttcagcatc ctatcatcag ggggttctgt ctgcaaccat cctctatgag	1740
atcctactgg ggaaggccac cctatatgct gtgctgggtca gtggcctggt gctgatggcc	1800
atggtcaaga aaaaaaattc ctga	1824

<210> 203
<211> 607
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 203

Met Thr Gly Phe Leu Lys Ala Leu Leu Leu Val Leu Cys Leu Arg Pro
1 5 10 15

Glu Trp Ile Lys Ser Gln Gln Lys Thr Gly Gly Gln Gln Val Lys Gln
20 25 30

Ser Ser Pro Ser Leu Thr Val Gln Glu Gly Gly Ile Leu Ile Leu Asn
35 40 45

Cys Asp Tyr Glu Asn Asp Met Phe Asp Tyr Phe Ala Trp Tyr Lys Lys
50 55 60

Tyr Pro Asp Asn Ser Pro Thr Leu Leu Ile Ser Val Arg Ser Asn Val
65 70 75 80

Asp Lys Arg Glu Asp Gly Arg Phe Thr Val Phe Leu Asn Lys Ser Gly
85 90 95

Lys His Phe Ser Leu His Ile Thr Ala Ser Gln Pro Glu Asp Thr Ala
100 105 110

Val Tyr Leu Cys Ala Ala Gly Asp Ser Gly Gly Ser Asn Tyr Lys Leu
115 120 125

Thr Phe Gly Lys Gly Thr Leu Leu Thr Val Thr Pro Asn Ile Gln Asn
130 135 140

Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser
145 150 155 160

Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys
165 170 175

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

Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln
195 200 205

Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr
210 215 220

Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe
225 230 235 240

Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu
245 250 255

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn
275 280 285

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

Met Gly Ser Arg Leu Phe Leu Val Leu Ser Leu Leu Cys Thr Lys His
305 310 315 320

Met Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Thr Val Thr
325 330 335

Gly Gly Asn Val Thr Leu Ser Cys Arg Gln Thr Asn Ser His Asn Tyr
340 345 350

Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile His
355 360 365

Tyr Ser Tyr Gly Ala Gly Asn Leu Gln Ile Gly Asp Val Pro Asp Gly
370 375 380

Tyr Lys Ala Thr Arg Thr Thr Gln Glu Asp Phe Phe Leu Leu Leu Glu
385 390 395 400

Leu Ala Ser Pro Ser Gln Thr Ser Leu Tyr Phe Cys Ala Ser Ala Ser
405 410 415

Trp Gly Gly Tyr Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr
420 425 430

Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe
435 440 445

Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val
450 455 460

Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
465 470 475 480

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala
485 490 495

Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val
500 505 510

Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val
515 520 525

Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro
530 535 540

Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp
545 550 555 560

Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser Ala Thr
565 570 575

Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu
580 585 590

Val Ser Gly Leu Val Leu Met Ala Met Val Lys Lys Lys Asn Ser
595 600 605

<210> 204
<211> 16
<212> PRT
<213> Murine

<400> 204

Cys Ala Val Ser Gly Gly Thr Asn Ser Ala Gly Asn Lys Leu Thr Phe
1 5 10 15

<210> 205
<211> 14
<212> PRT
<213> Murine

<400> 205

Cys Ala Ser Ala Ser Trp Gly Gly Tyr Ala Glu Gln Phe Phe
1 5 10

<210> 206
<211> 14
<212> PRT
<213> Murine

<400> 206

Cys Thr Cys Ser Ala Asp Arg Gly Ala Glu Thr Leu Tyr Phe
1 5 10

<210> 207
<211> 15
<212> PRT
<213> Murine

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> Wherein X is alanine, arginine, asparagine, asparatic acid,
 cysteine, glutamic acid, glutamine, histidine, isoleucine,
 leucine, lysine, methionine, phenylalanine, proline, serine,
 threonine, tryptophan, tyrosine, or valine

<400> 207

Cys	Ala	Ala	Asp	Ser	Ser	Asn	Thr	Xaa	Tyr	Gln	Asn	Phe	Tyr	Phe
1				5					10					15

<210> 208
 <211> 133
 <212> PRT
 <213> Murine

<220>
 <221> MISC_FEATURE
 <222> (116)..(116)
 <223> Wherein X is alanine, arginine, asparagine, asparatic acid,
 cysteine, glutamic acid, glutamine, histidine, isoleucine,
 leucine, lysine, methionine, phenylalanine, proline, serine,
 threonine, tryptophan, tyrosine, or valine

<400> 208

Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	Gln	Ile
1				5					10					15	

Cys	Trp	Val	Arg	Gly	Asp	Gln	Val	Glu	Gln	Ser	Pro	Ser	Ala	Leu	Ser
			20					25					30		

Leu	His	Glu	Gly	Thr	Asp	Ser	Ala	Leu	Arg	Cys	Asn	Phe	Thr	Thr	Thr
		35					40					45			

Met	Arg	Ser	Val	Gln	Trp	Phe	Arg	Gln	Asn	Ser	Arg	Gly	Ser	Leu	Ile
	50					55				60					

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

Ser Ala Phe Asp Ser Lys Glu Arg Arg Tyr Ser Thr Leu His Ile Arg
85 90 95

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

Ser Asn Thr Xaa Tyr Gln Asn Phe Tyr Phe Gly Lys Gly Thr Ser Leu
115 120 125

Thr Val Ile Pro Asn
130

<210> 209
<211> 269
<212> PRT
<213> Murine

<220>
<221> MISC_FEATURE
<222> (116)..(116)
<223> Wherein X is alanine, arginine, asparagine, asparatic acid,
cysteine, glutamic acid, glutamine, histidine, isoleucine,
leucine, lysine, methionine, phenylalanine, proline, serine,
threonine, tryptophan, tyrosine, or valine

<400> 209

Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val Gln Ile
1 5 10 15

Cys Trp Val Arg Gly Asp Gln Val Glu Gln Ser Pro Ser Ala Leu Ser
20 25 30

Leu His Glu Gly Thr Asp Ser Ala Leu Arg Cys Asn Phe Thr Thr Thr
35 40 45

Met Arg Ser Val Gln Trp Phe Arg Gln Asn Ser Arg Gly Ser Leu Ile
50 55 60

Ser Leu Phe Tyr Leu Ala Ser Gly Thr Lys Glu Asn Gly Arg Leu Lys

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