

SEQUENCE LISTING

<110> SIAMAB THERAPEUTICS, INC.

<120> GLYCAN-INTERACTING COMPOUNDS AND METHODS OF USE

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<160> 266

<170> PatentIn version 3.5

<210> 1

<211> 115

<212> PRT

<213> Mus sp.

<400> 1

Gln	Val	Gln	Leu	Leu	Gln	Tyr	Asp	Ala	Glu	Leu	Val	Lys	Pro	Gly	Gly
1			5						10					15	

Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	His
			20					25					30		

Ala	Ile	His	Trp	Val	Lys	Gln	Lys	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			

Gly	Tyr	Phe	Ser	Pro	Gly	Asn	Asp	Asp	Ile	Lys	Tyr	Ser	Glu	Lys	Phe
	50					55					60				

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 2
<211> 106
<212> PRT
<213> Mus sp.

<400> 2
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Lys Lys
100 105

<210> 3
<211> 115
<212> PRT

<213> Mus sp.

<400> 3

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 4

<211> 108

<212> PRT

<213> Mus sp.

<400> 4

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1 5 10 15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Ile Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

50

55

60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 5

<211> 115

<212> PRT

<213> Mus sp.

<400> 5

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Val Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Leu Ile Gly Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 6

<211> 107
<212> PRT
<213> Mus sp.

<400> 6

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Ser Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Phe Leu Ile
35 40 45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Arg Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 7
<211> 115
<212> PRT
<213> Mus sp.

<400> 7

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Leu Ser Pro Gly Asn Asp Asp Ile Lys Tyr Ser Glu Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Gly Gly Asp His Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 8
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<212> PRT
<213> Mus sp.

<400> 8
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Phe
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 9
<211> 115
<212> PRT

<213> Mus sp.

<400> 9

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Gln Arg Gln Leu Gly Gln Gly Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 10

<211> 113

<212> PRT

<213> Mus sp.

<400> 10

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Tyr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50

55

60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Asn
 85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg

<210> 11

<211> 115

<212> PRT

<213> Mus sp.

<400> 11

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Gly Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Glu Arg Ser Met Ile Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ala

115

<210> 12
<211> 112
<212> PRT
<213> Mus sp.

<400> 12
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Thr Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Phe Ser Gln Ser Leu Val Gln Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Cys Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

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

<210> 13
<211> 114
<212> PRT
<213> Mus sp.

<400> 13
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Ile Ser Tyr Tyr Gly Ile Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110

Ser Ser

<210> 14

<211> 107

<212> PRT

<213> Mus sp.

<400> 14

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

Glu Ser Val Thr Ile Thr Cys Arg Leu Ser Glu Asp Ile Tyr Ser Asn
20 25 30

Leu Ala Trp Phe Gln Gln Arg Pro Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

Tyr Lys Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100 105

<210> 15
 <211> 114
 <212> PRT
 <213> Mus sp.

<400> 15
 Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Val Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

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

Ser Ser

<210> 16
 <211> 107
 <212> PRT
 <213> Mus sp.

<400> 16
 Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
 1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser His
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val

35

40

45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile His Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
 85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 17

<211> 115

<212> PRT

<213> Mus sp.

<400> 17

Gln Ile Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Thr
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

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

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Val Gly Tyr Ala Leu Asp Tyr Trp Gly Leu Gly Thr Thr Leu Thr
 100 105 110

Val Ser Ser

115

<210> 18
<211> 108
<212> PRT
<213> Mus sp.

<400> 18
Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1 5 10 15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 19
<211> 115
<212> PRT
<213> Mus sp.

<400> 19
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Thr
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Glu Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Ser Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 20
<211> 114
<212> PRT
<213> Mus sp.

<400> 20
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Arg Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg

<210> 21

<211> 114

<212> PRT

<213> Mus sp.

<400> 21

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Met Gln Met Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

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

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

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser

<210> 22

<211> 114

<212> PRT

<213> Mus sp.

<400> 22

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

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser

20

25

30

Gly Asn Gln Lys Ser Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Ser Trp Ala Ser Thr Arg Asp Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Ser
 85 90 95

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Arg

<210> 23
 <211> 115
 <212> PRT
 <213> Mus sp.

<220>
 <221> MOD_RES
 <222> (9)..(9)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (111)..(111)
 <223> Any amino acid

<400> 23
 Gln Val Gln Leu Gln Gln Ser Asp Xaa Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

Met Gln Leu Asn Ser Leu Ser Ser Asp Asp Ser Ala Val Tyr Phe Cys
85 90 95

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Xaa Thr
100 105 110

Val Ser Ala
115

<210> 24
<211> 114
<212> PRT
<213> Mus sp.

<400> 24
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Arg
20 25 30

Gly Asn His Lys Asn Tyr Leu Thr Trp Tyr Arg Gln Lys Pro Gly Leu
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Ala Leu Thr
65 70 75 80

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

Asp Tyr Thr Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg

<210> 25

<211> 115

<212> PRT

<213> Mus sp.

<400> 25

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 26

<211> 114

<212> PRT

<213> Mus sp.

<400> 26

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
 20 25 30

Gly Lys Thr Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

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

Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Arg

<210> 27
 <211> 115
 <212> PRT
 <213> Mus sp.

<400> 27
 Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Thr Glu Lys Phe
 50 55 60

Lys Gly Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 28
<211> 115
<212> PRT
<213> Mus sp.

<400> 28
Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asp Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 29
<211> 115
<212> PRT
<213> Mus sp.

<400> 29

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 30

<211> 115

<212> PRT

<213> Mus sp.

<400> 30

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 31
<211> 108
<212> PRT
<213> Mus sp.

<400> 31
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Leu Pro
65 70 75 80

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

Met Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 32
<211> 115

<212> PRT

<213> Mus sp.

<400> 32

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 33

<211> 115

<212> PRT

<213> Mus sp.

<400> 33

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Thr Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 34
<211> 107
<212> PRT
<213> Mus sp.

<400> 34
Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 35
<211> 115
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<400> 35

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Ile Glu Lys Phe
50 55 60

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

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

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<400> 36

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

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Asn Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35 40 45

Phe Gly Ala Ser Asn Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65 70 75 80

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

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
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<210> 37

<211> 109

<212> PRT

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<400> 37

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

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Asn Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65 70 75 80

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

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

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<211> 115

<212> PRT

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<400> 38

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Ser Val Lys Ile Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser
115

<210> 39

<211> 105

<212> PRT

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<400> 39

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

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

Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Tyr Thr Val Gln Ala
 65 70 75 80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Gly Tyr Ser Ser Pro Trp
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Lys
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<400> 40
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 20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Asp Trp Ile
 35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Cys
 65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

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

Thr Val Ser Ser
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<400> 41
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Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Asn
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Ile Ala Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Lys Val Leu Ile
 35 40 45

Tyr Ser Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
 65 70 75 80

Glu Asp Leu Thr Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Phe Pro Leu
 85 90 95

Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys
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<400> 42
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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Asp Trp Ile
 35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

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

Thr Val Ser Ser
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<210> 54
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1 5

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Glu Asn Val Val Asn Tyr
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Gln Ser Asp Tyr Ser Tyr Pro Tyr Thr
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Gln Gln Gly Tyr Ser Ser Pro Trp Thr
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Gly

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Gly

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Val

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Thr

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 aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240
 atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatccatt 300

actacgtctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 152
<211> 323
<212> DNA
<213> Mus sp.

<400> 152
aacattgtaa tgaccaatc tcccaaacc atgtccatgt cagtaggaga gagggtcacc 60
ttgacctgca aggccagtga gaatgtgggt atttatgttt cctgggtatca acagaaacca 120
gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180
cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240
gaagaccttg cagattatca ctgtggacag gggttacagct atccgtacac gttcggaggg 300
gggaccaagc tggaaataaa acg 323

<210> 153
<211> 345
<212> DNA
<213> Mus sp.

<400> 153
caggttcagt tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60
tcctgcaagg cttctggcta caccttcact gaccatgcca ttcattgggt gaagcagaag 120
cctgaacagg gcctggaatg gattggatat gtttctcccg gaaatgggtga tattaagtac 180
aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240
atgcagctca acagcctgac atcggaggat tctgcagtgt atttctgtaa aagatcttta 300
attggagact attggggcca aggcaccact ctcacagtct cctca 345

<210> 154
<211> 322
<212> DNA
<213> Mus sp.

<400> 154
gacattgtga tgaccagtc tcaaaaattc atgtcctcat cagtaggaga cagggtcacc 60
atcacctgca aggccagtca gaatgtgggt actgctgtag cctgggtatca acagaaacca 120
ggacaatctc ctaaatttct gatttactcg gcatccaatc ggtacactgg agtccttgat 180
cgcttcacag gcagtggatc tgggacagat ttcactctca cgatcagcaa tatgcagtct 240

gaagacctgg cagattat	ctgccagcaa tatagcagct atcgtctgac gttcggtgga	300
ggcaccaagc tggaaatcaa ac		322

<210> 155
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 155		
caggttcagc tgcagcagtc tgacgctgaa ttggtgaaac ctggggcttc agtgaagata		60
tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag		120
cctgaacagg gcctggaatg gattggatat ctttctcccg gaaatgatga tattaagtac		180
agtgagaagt tcaaggacaa ggccacactg actgcagaca aatcctccag cactgcctac		240
atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatccata		300
gggggggacc actggggcca aggcaccact ctcacagtct cctca		345

<210> 156
 <211> 323
 <212> DNA
 <213> Mus sp.

<400> 156		
gacatccaga tgaaccagtc tccatccagt ctgtctgcat cccttgagaga cacaattacc		60
atcacttgcc atgccagtca gaacattaat gtttggttaa actggtacca gcagaaacca		120
ggaaatattc ctaaactatt gatctataag gcttccaact tgcacacagg cgtcccatca		180
aggttttagtg gcagtggatc tggaacaggt ttcacattaa ccatcggcag cctgcagcct		240
gaagacattg ccacttacta ctgtcaacag ggtcaaagtt atccgttcac gttcggaggg		300
gggaccaagc tggaaataaa acg		323

<210> 157
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 157		
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata		60
tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaaacagaag		120

cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtat	180
aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac	240
atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtca aagacaactg	300
ggacaaggct actggggcca aggcaccact ctcacagtct cctca	345

<210> 158
 <211> 338
 <212> DNA
 <213> Mus sp.

<400> 158 gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc	60
atctcttgca gatctagtca gagccttgta cacagttatg gaaacaccta ttacattgg	120
tacctgcaga agccaggcca gtctccaaag ctctgattt acaaagtttc caaccgattt	180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc	240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaaatac acatgttccg	300
tacacgttcg gaggggggac caagctggaa ataaaacg	338

<210> 159
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 159 caggttcagc tgcagcagtc tgacgctgag ttggggaaac ctggggcttc agtgaagata	60
tcctgcaagg cttctggcta caccttcagt gaccatgcta ttcactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atctctcccg gaaacgatga tattaagtac	180
aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac	240
atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtga aagatcgatg	300
attgggggttt actggggcca agggactctg gtcactgtct ctgca	345

<210> 160
 <211> 337
 <212> DNA
 <213> Mus sp.

<400> 160 gatgttgtga tgacccaaac tccactctcc ctgactgtca gtcttggcga tcaagcctcc	60
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atctcttgca gatttagtca gaggccttgta caaagtaatg gaaataccta tttacagtgg	120
tatctgcaga agccaggcca gtctccaaag ctcctgattt acaaagtctc caaccgattt	180
tgtgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc	240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgctccg	300
ctcacgttcg gtgctgggac caagctggag ctgaaac	337

<210> 161
 <211> 342
 <212> DNA
 <213> Mus sp.

<400> 161	
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tcctgcaaga cttctggcta caccttcact gaccatgcaa ttactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac	180
aatgagaagt tcaagggcaa ggccaccctg actgcagaca aatcctccag cactgcctat	240
atgcagctca gcagcctgac acctgaggat tctgcagtgt atttctgtaa aatatcttac	300
tacggtattt ggggccaagg caccactctc acagtctcct ca	342

<210> 162
 <211> 322
 <212> DNA
 <213> Mus sp.

<400> 162	
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atcacatgtc gactaagtga agatatttac agtaatttag catggtttca gcagagaccg	120
ggaaaatctc ctcagctcct ggtttataaa gcaacaaact tagcagacgg tgtgccatca	180
aggttcagtg gcagtggatc aggcacacag tattccctca agatcaacag cctgcagtct	240
gaagattttg ggacttatta ctgtcaacat ttttggggta ctccattcac gttcggctcg	300
gggaccaagg tggaaataaa ac	322

<210> 163
 <211> 342
 <212> DNA
 <213> Mus sp.

<400> 163
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 60
tcctgcaagg cttctggcta caccttcact gaccatgcta ttactgggt gaagcagaag 120
cctgaacagg gcctggaatg gattggatat ttttctcccg gaaatgatga tattaagtat 180
aatgagaagt tcaaggtcaa ggccacactg actgcagaca aatcctccag cactgcctac 240
atgcaactca ccagcctgac atctgaagat tctgcagtgt atttctgtaa aagatcttac 300
tacggtgatt ggggccaagg caccactctc acagtctcct ca 342

<210> 164
<211> 322
<212> DNA
<213> Mus sp.

<400> 164
gacatccaga tgactcagtc tccagcctcc ctatctgttt ctgtgggaga aactgtcacc 60
atcacatgtc gagcaagtga gaatatttac agtcatttag catggtatca acagaaacag 120
ggaaaatctc ctcaactcct ggtctatggt gcaactaact tagcagatgg tgtgccatca 180
aggttcagtg gcagtggatc aggcacacag ttttccctca agatccacag cctgcagtct 240
gaagattttg ggagttatta ctgtcaacat ttttggggtg ctccattcac gttcggctcg 300
gggacaaaagt tggaaataaa ac 322

<210> 165
<211> 345
<212> DNA
<213> Mus sp.

<400> 165
caaattcagc tgcagcagtc tgacgctgag ttggtgaaac ctgggacttc agtgaagatg 60
tcctgcaagg cttctggcta caccttcact gaccatgcta ttactgggt gaagcagaag 120
cctgaacagg gcctggaatg gattggatat ttttctcccg gaaatgatga tattaagtat 180
aatgtgaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac 240
atgcagctca acagcctgac atctgaagat tctgcagtgt atttctgttc ggtgggatac 300
gcccttgact actggggcct aggcaccact ctacagtct cctca 345

<210> 166

<211> 323
 <212> DNA
 <213> Mus sp.

<400> 166
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 ttgacctgca aggccagtga gaatgtggtt acttatgttt cctggtatca acagaaacca 120
 gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180
 cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240
 gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300
 gggaccaagc tggaaataaa acg 323

<210> 167
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 167
 caggttcagc tgcaacagtc tgacgctgag ttggtgaaac ctgggactac agtgaagata 60
 tcctgcaagg cttctggcta cactttcact gaccatgcta ttcactgggt gaaggagaag 120
 cctgaacagg gcctggaatg gatcggatat atttctcccg gaaatgatga tattaagtac 180
 agtgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcttac 240
 atgcagctca acagcctgac atctgatgat tctgcagtgt atttctgtaa aagatcgctt 300
 agtacgcctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 168
 <211> 477
 <212> DNA
 <213> Mus sp.

<400> 168
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 ggcatcagac cagcatgggc atcaaggtgg aatcacagac tctggtcttc atatccatac 120
 tgtttgggtt atatggagct gatgggaaca cattaatgac ccaatctccc acatccatgt 180
 acatgtcagt aggagagagg gtcaccttga cttgcaaggc cagtgagaat gagattaatt 240
 atgtttcctg gtatcaacag aaaccagagc agtctcctaa actgttgata tacggggcat 300
 ccaaccggtg ctctggggtc cccgatcgct tcacaggcag tggatctgca acagatttca 360

ctctgaccat cagcagtgtg caggctgaag accttgcaga ttatccctgt ggagcaaggg	420
attaactagc tatccgtaca cgttcggagg ggggaccaag ctggaaataa aacgggc	477

<210> 169
 <211> 341
 <212> DNA
 <213> Mus sp.

<400> 169	
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atgagctgca ggtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc	120
tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg	180
gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc	240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat	300
ccgtacacgt tcggaggggg gaccaagctg gaaataaaac g	341

<210> 170
 <211> 343
 <212> DNA
 <213> Mus sp.

<400> 170	
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata	60
tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gatgcagatg	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgggtga tgttaagtac	180
agtgaagagt tcaagggcag ggccacactg actgcagaca aatcctccag ctctgcctac	240
atgcagctca acagcctgac atctgaggat tctgcagttt atttctgtaa aagatcgctt	300
agtacgcctt actggggcca agggactctg gtcactgtct ctg	343

<210> 171
 <211> 341
 <212> DNA
 <213> Mus sp.

<400> 171	
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atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagag ctacttgacc	120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctcctgggc atccactagg	180
gattctggggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc	240
atcagcagtg tgcaggctga agacctggca gtttattact gtcagagtga ttatagttat	300
ccgtacacgt tcggagggggg gaccaagctg gaaataaaac g	341

<210> 172
 <211> 345
 <212> DNA
 <213> Mus sp.

<220>
 <221> modified_base
 <222> (26)..(26)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (332)..(332)
 <223> a, c, t, g, unknown or other

<400> 172	
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tcctgtaagg cttctggcta caccttcact gaccatgcta ttactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat ttttctcccg gaaatgatga tattaagtac	180
aatgagaagt ttaggggcaa ggccacactg actgcagaca aatcctccag cactgcctac	240
atgcagctca acagcctgtc atctgatgat tctgcagtgt atttctgtaa aagatcgctt	300
agtacgcctt actggggcca agggactctg gncactgtct ctgca	345

<210> 173
 <211> 341
 <212> DNA
 <213> Mus sp.

<400> 173	
gacattgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaagtcact	60
atgagctgca agtccagtca gagtctgtta aaccgtggaa atcataagaa ctacttgacc	120
tggtaccggc agaaaccagg gctgcctcct aaactgttga tttactgggc atccactagg	180
gaatctggggg tccctgatcg cttcacaggc agtggatctg gaacagattt cgctctcacc	240
atcagcagtg ttcaggctga agacctggca gtttattact gtcagaatga ttatacttat	300

ccgtacacgt tcggaggggg gaccaagctg gagataaaac g 341

<210> 174
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 174
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 tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120
 cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180
 aatgagaagt tcaaggtcaa ggccacactg actgcagaca aatcctccag cactgcctac 240
 atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgatt 300
 actacgcctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 175
 <211> 341
 <212> DNA
 <213> Mus sp.

<400> 175
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 atgagctgca agtccagtca gagtctgtta aacagtggaa aaacaaagaa ctacttgacg 120
 tgggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gtaagaatga ttatagttat 300
 ccgtacacgt tcggaggggg gaccaagctg gaaataaaac g 341

<210> 176
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 176
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 tcctgcaaga cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag 120
 cctgaacagg gcctggaatg gattggatat atctctcccg gaaatgatga tattaagtac 180

actgagaagt tcaagggcaa ggtcacactg actgcagaca aatcctccag cactgcctac	240
atgcagctca acagcctgac atctgaggat tctgcagtct atttctgtaa aagatcgatt	300
actacgcctt actggggcca agggactctg gtcactgtct ctgca	345

<210> 177
 <211> 480
 <212> DNA
 <213> Mus sp.

<220>
 <221> modified_base
 <222> (153)..(153)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (285)..(286)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (289)..(289)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (297)..(298)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (332)..(332)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (405)..(405)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (412)..(412)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (429)..(429)
 <223> a, c, t, g, unknown or other

<400> 177

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cttcatatcc agtacgctcg gggactatgg agnggaacag tacattttta tgaccaatg	180
tcccaaaggc aagaacatgt cagtaggaga gagggtcact cagagtgcaa ggccaggaga	240
aatcaaaaaca cttatgtttc ctggtatcaa cagaaaccag agcannctnt aaaatgnnga	300
ttacgggggca tccaaccggg aatctggggg cncgatcgc ttcacaggca gtggatctgg	360
aacagatttc actctcacca tcagcagtgt gcaggctgaa gaccnggcag tnttcactgt	420
ggacagggnt acagttatcc gtacacgttc ggagggggga ccaagctgaa aaaaacgggc	480

<210> 178

<211> 345

<212> DNA

<213> Mus sp.

<400> 178

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tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggatga tattaagtac	180
gatgagaagt ttaagggcaa ggccacactg actgcagaca aatcctcctc cactgcctac	240
atgcagctca acagcctgac atctgaagat tctgcagtgt atttctgtaa aagatcgatt	300
actacctctt actggggcca agggactctg gtcactgtct ctgca	345

<210> 179

<211> 345

<212> DNA

<213> Mus sp.

<400> 179

caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata	60
tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgatga tattaagtac	180
aatgagaagt tcaagggcaa ggccacactg actgcagaca agtcctccag cactgcctac	240
atgcagctca acagcctgac atctgaggat tctgcagtgt ttttctgtaa aagatcgatt	300
actacctctt actggggcca agggactctg gtcactgtct ctgca	345

<210> 180
 <211> 483
 <212> DNA
 <213> Mus sp.

<220>
 <221> modified_base
 <222> (3)..(3)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (137)..(137)
 <223> a, c, t, g, unknown or other

<220>
 <221> modified_base
 <222> (193)..(193)
 <223> a, c, t, g, unknown or other

<400> 180
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 tggggggggct ggtgttntgc tttttaggtg tgagatgtga catccagatg aaccagtctc 180
 catccagtct gtntgcatcc tttggagaca caattacat catttgccat tccagtcaga 240
 acattaatgt ttggttaaga tgggtaccagc agaaaccagg aaatattcct aaaatattga 300
 tatataaggg ttccaacttg tacacaggcg tcccatcaag gtttagtggc agtggatttg 360
 gaacaggttt cacattaacc atcagcagcg tgcagcggga agacattgcc acttactact 420
 gtcaacagga tcaaagttat ccgtacacgt tcggaggggg gaccaagctg aaataaaacg 480
 ggc 483

<210> 181
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 181
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 tcctgcaagg cttctggcta catcttcact gaccatgcta ttactgggt gaagcagaag 120
 cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac	240
atgcatctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgatt	300
actacctctt actggggcca agggactctg gtcactgtct ctgca	345

<210> 182
 <211> 323
 <212> DNA
 <213> Mus sp.

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ggaaatattc ctaaactctt gatctataag gcttccaact tgcacacagg cgtcccatca	180
aggttttagtg gcagtggatc tggaacagggt ttcacattaa ccatcagcag cctgctgcct	240
gaagacgttg ccacttacta ctgtcaacag gatcaaagtt atccgtatat gttcggaggg	300
gggaccaagc tggaataaaa acg	323

<210> 183
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 183	
caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata	60
tcctgcaagg cttctggcta caccttact gaccatgcta ttcactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgatga tattaagtac	180
aatgagaagt ttaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac	240
atgctgctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgatt	300
actacctctt actggggcca agggactctg gtcactgtct ctgca	345

<210> 184
 <211> 323
 <212> DNA
 <213> Mus sp.

<400> 184	
aacattgtaa tgaccaatc tcccaaattc atgtccatgt cagtaggaga gagggtcacc	60
ttgacctgca aggccagtga gaatgtggtt acttatgttt cctggtatca acagaaacca	120

gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat	180
cgcttcacag gcagtggatc tgcaacagat ttcactttga ccatcagcag tgtgcaggct	240
gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg	300
gggaccaagc tggaaataaa acg	323

<210> 185
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 185	
caggttcaac tgcagcagtc tgacgtgag ttggtgaaac ctggggcttc agtgaagata	60
tcctgcaagg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgggtga tattaagtac	180
aatgagaagt tcaagggtaa ggccacactg actgcagaca cttcctccac cactgcctac	240
atgcagctca acagcctgac atctgaggat tctgcaatgt atttctgtaa aagatccatt	300
actacgtctt actggggcca agggactctg gtcactgtct ctgca	345

<210> 186
 <211> 321
 <212> DNA
 <213> Mus sp.

<400> 186	
gacatccaga tgaaccagtc tccatccagt ctgtctgcat cccttgagga cacaattacc	60
atcacttgcc atgccagtca gaacattaat gtttggttaa gctggtacca gcagaaacca	120
ggaaatattc ctaaactatt gatctataag gcttccaatt tgtatacagg cgtcccatca	180
aggtttagtg gcagtggatc tggaacagg ttcacattaa ccatcagcag cctgcagcct	240
gaagacgttg ccacgtacta ctgtcaacac gatcaaagtt atccgtacac gttcggaggg	300
gggaccaagc tggaaataaa a	321

<210> 187
 <211> 345
 <212> DNA
 <213> Mus sp.

<400> 187

caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata	60
tcctgcaagg cttctggcta catcttcact gaccatgcaa ttcactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatgggtga tattaagtac	180
attgagaagt tcaggggcaa ggccacactg actgcagaca aatcctccag cactgcctac	240
atgcagctca acagcctgac atctgaggat tctgcagtgt atttctgtaa aagatcgctt	300
agtacgcctt actggggcca agggactctg gtcactgtct ctgca	345

<210> 188
 <211> 329
 <212> DNA
 <213> Mus sp.

<400> 188	
aacatttttaa tgaccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc	60
ttgacctgca aggccagtga gaatgtgggt aattatgttt cctggtatca acagaaacca	120
gagcagtctc ctaaactgct gatattcggg gcatccaacc ggtactctgg ggtccccgat	180
cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct	240
gaagaccttg cagattatca ctgtggaagc aagtggatta ctagctatcc gtacacgttc	300
ggagggggga ccaagctgga aataaaacg	329

<210> 189
 <211> 326
 <212> DNA
 <213> Mus sp.

<400> 189	
aacatttttaa tgaccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc	60
ttgacctgca aggccagtga gaatgtgggt aattatgttt cctggtatca acagaaacca	120
gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtactctgg ggtccccgat	180
cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct	240
gaagaccttg cagattatca ctgtggagca agggttacta gctatccgta cacgttcgga	300
ggggggacca agctggaaat aaaacg	326

<210> 190
 <211> 345
 <212> DNA

<213> Mus sp.

<400> 190

caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctgggacttc agtgaagata	60
tcctgcaggg cttctggcta caccttcact gaccatgcta ttcactgggt gaagcagaag	120
cctgaacagg gcctggaatg gattggatat atttctcccg gaaatggtga tattaagtac	180
aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cactgcctac	240
atgcagctca acagcctgac atctgacgat tctgcagtgt atttctgtaa aagatccatt	300
actacgcctt actggggcca aggcaccact ctcacagtct cctca	345

<210> 191

<211> 315

<212> DNA

<213> Mus sp.

<400> 191

agttttgtga tgaccagac tcccaaattc ctgcttgtgt cagcaggaga cagggttacc	60
ataacctgca aggccagtca gagtgtgaat aataatgtag cttggtacca acagaagcca	120
gggcagtctc ctaaacagct gatatactat gcatccaatc gctacactgg agtccctgat	180
cgcttcactg gcagtggata tgggacggat ttcactttca ccatctacac tgtgcaggct	240
gaagacctgg cagtttattt ctgtcagcag ggttatagct ctccgtggac gttcgggtgga	300
ggcaccaagc tgaaa	315

<210> 192

<211> 330

<212> PRT

<213> Mus sp.

<400> 192

Ala	Lys	Thr	Thr	Ala	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Val	Cys	Gly
1				5				10						15	

Asp	Thr	Thr	Gly	Ser	Ser	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr
			20					25					30		

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

Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
85 90 95

Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
100 105 110

Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
115 120 125

Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
130 135 140

Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
145 150 155 160

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

Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
180 185 190

His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
195 200 205

Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
210 215 220

Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
225 230 235 240

Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
245 250 255

Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
260 265 270

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

Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
 290 295 300

Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
 305 310 315 320

Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 325 330

<210> 193
 <211> 107
 <212> PRT
 <213> Mus sp.

<400> 193
 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 1 5 10 15

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

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 35 40 45

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 50 55 60

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 65 70 75 80

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

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 100 105

<210> 194
 <211> 330
 <212> PRT

<213> Homo sapiens

<400> 194

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 195
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 195
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 196

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 196

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Lys Gln Lys Pro Glu Gln Gly Leu Asp Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Lys Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Cys
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

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

Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala
115 120 125

Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu
130 135 140

Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly
145 150 155 160

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

Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro
180 185 190

Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys
195 200 205

Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro
210 215 220

Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro
245 250 255

Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val
260 265 270

Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr
275 280 285

Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala
290 295 300

Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys
305 310 315 320

Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser
325 330 335

Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro

340

345

350

Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val
 355 360 365

Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly
 370 375 380

Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp
 385 390 395 400

Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp
 405 410 415

Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His
 420 425 430

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

<210> 197

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 hybrid polynucleotide

<400> 197

atggagaccg acaccctgct gctctgggtg ctgctgctct gggtgcccg ctccaccgga 60

caggttcagc tgcagcagtc tgacgctgag ttggtgaaac ctggggcttc agtgaagata 120

tcctgcaagg cttctggcta caccttcact gaccatgcta ttactgggt gaagcaaaag 180

cctgaacagg gcctggactg gattggatat atttctcccg gaaatggtga tattaagtac 240

aatgagaagt tcaaggacaa ggtcacactg actgcagaca aatcctccag cactgcctgc 300

atgcacctca acagcctgac atctgaggat tctgcagtgt atttctgcaa aagatcccta 360

ctagctcttg actactgggg ccaaggcacc actctcacag tctcctcagc taaaacaaca 420

gccccatcgg tctatccact ggcccctgtg tgtggagata caactggctc ctcggtgact 480

ctaggatgcc tgggtcaagg ttatttcct gagccagtga ccttgacctg gaactctggt 540

tccctgtcca gtggtgtgca caccttccca gctgtcctgc agtctgacct ctacaccctc	600
agctcaagcg tgactgtaac cagctcgacc tggcccagcc agtccatcac ctgcaatgtg	660
gcccacccgg caagcagcac caaggtggac aagaaaattg agcccagagg gcccaacaatc	720
aagccctgtc ctccatgcaa atgcccagca cctaacctct tgggtggacc atccgtcttc	780
atcttccctc caaagatcaa ggatgtactc atgatctccc tgagcccat agtcacatgt	840
gtagtcgttg atgtgagcga ggatgaccca gatgtccaga tcagctggtt tgtgaacaac	900
gtggaagtgc aactgctca gacacagacg catagagagg attacaacag tactctccgg	960
gttgtcagtg ccctcccat ccagcaccag gactggatga gtggcaagga gttcaaatgc	1020
aaggtcaaca acaaagacct ccagcgccc atcgagagaa ccatctcaaa acccaaaggg	1080
tcagtaagag ctccacaggt atatgtcttg cctccaccag aagaggagat gactaagaaa	1140
caggtcactc tgacctgcat ggtcacagac ttcatgcctg aagacattta cgtggagtgg	1200
accaacaacg ggaaaacaga gctaaactac aagaactg aaccagtcct ggactctgat	1260
ggttcttact tcatgtacag caagctgaga gtggagaaga agaactgggt ggagagaaat	1320
agctactcct gttcagtggt ccacgagggt ctgcacaatc accacacgac taagagcttc	1380
tcccggactc cgggtaaata g	1401

<210> 198

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 198

Asp	Ile	Val	Met	Thr	Gln	Ser	His	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Gly	Thr	Asn
			20					25					30		

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

Tyr Ser Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Thr Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Phe Pro Leu
85 90 95

Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
100 105 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
115 120 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130 135 140

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

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 199

<211> 705

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polynucleotide

<400> 199

atggagaccg acaccctgct gctctgggtg ctgctgctct gggtgcccgg ctccaccgga	60
gacattgtga tgaccagtc tcacaaattc atgtccacat cagtaggaga cagggtcagc	120
atcacctgca aggccagtca ggatgtgggc actaatatag cctggatatca acagaaacca	180
ggccgatctc ctaaagtact gatttactcg gcatccaccc ggcacactgg agtccttgat	240
cgcttcacag gcagtggatc tgggacagat ttcactctca ccattagcaa tgtgcagtct	300
gaagacttga cagattatct ctgtcagcaa tatagcagct ttcctctcac gttcgggtgtt	360
gggaccaagc tggagctgaa acgggcagat gctgcaccaa ctgtatccat cttcccacca	420
tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac	480
cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgtcctg	540
aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg	600
ttgaccaagg acgagtatga acgacataac agctatacct gtgaggccac tcacaagaca	660
tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttga	705

<210> 200
 <211> 296
 <212> DNA
 <213> Homo sapiens

<400> 200	
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc	60
tcctgcaagg cttctgggta cacctttacc agctatggta tcagctgggt gcgacaggcc	120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat	180
gcacagaagc tccagggcag agtcacatg accacagaca catccacgag cacagcctac	240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagaga	296

<210> 201
 <211> 286
 <212> DNA
 <213> Homo sapiens

<400> 201	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc	60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca	180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctc 286

<210> 202
<211> 305
<212> DNA
<213> Homo sapiens

<400> 202
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctgctca ttactgggc atctaccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300
cctcc 305

<210> 203
<211> 98
<212> PRT
<213> Homo sapiens

<400> 203
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg

<210> 204

<211> 95

<212> PRT

<213> Homo sapiens

<400> 204

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
85 90 95

<210> 205

<211> 102

<212> PRT

<213> Homo sapiens

<400> 205

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

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

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Cys
100

<210> 206
<211> 25
<212> PRT
<213> Homo sapiens

<400> 206
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 207
<211> 22
<212> PRT
<213> Homo sapiens

<400> 207
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
1 5 10 15

Arg Val Thr Ile Thr Cys
20

<210> 208
<211> 23
<212> PRT
<213> Homo sapiens

<400> 208
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys
20

<210> 209
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 209
 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 1 5 10

<210> 210
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 210
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 1 5 10 15

<210> 211
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 211
 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 1 5 10 15

<210> 212
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 212
 Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
 1 5 10 15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 20 25 30

<210> 213
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 213
 Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 214
<211> 32
<212> PRT
<213> Homo sapiens

<400> 214
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
20 25 30

<210> 215
<211> 11
<212> PRT
<213> Homo sapiens

<400> 215
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 216
<211> 10
<212> PRT
<213> Homo sapiens

<400> 216
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 217
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 217
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser His
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 218

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 218

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser His
20 25 30

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

Tyr Gly Ala Thr Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 219
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 219
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser His
20 25 30

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

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Trp Gly Ala Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 220
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 220

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Ser Ser

<210> 221

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 221

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Ser Ser

<210> 222

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 222

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Ser Ser

<210> 223

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 223

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Ser Ser

<210> 224

<211> 114

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 224

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Val Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Ser Ser

<210> 225

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 225

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

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 226

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 226

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

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 227
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 227
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Met Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 228
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 228

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

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Gln Ser Tyr Pro Tyr
85 90 95

Phe Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 229

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 229

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

Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln His Ile Asn Phe Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Phe Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 230

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 230

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 231
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 hybrid polypeptide

<400> 231
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 232
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 hybrid polypeptide

<400> 232

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

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

Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 233

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 hybrid polypeptide

<400> 233

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 234
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 234
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 235
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 235
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Arg
20 25 30

Gly Asn His Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Asp Tyr Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 236
<211> 113
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 236

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

Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Arg
20 25 30

Gly Asn His Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Asp Tyr Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 237

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 237

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 238

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 238

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 239

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 239

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 240
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 240
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 241
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 241

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

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

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

Lys Arg Ser Leu Ser Thr Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 242

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 hybrid polypeptide

<400> 242

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
 20 25 30

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

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 243

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 243

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20 25 30

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

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 244
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 244

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

Asp Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Pro
65 70 75 80

Glu Asp Leu Ala Thr Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 245
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 245

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

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 246

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 246

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

Asp Arg Val Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 247

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 247

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

Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Asn Leu Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 248

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 248

Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Asn Leu Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asp Gln Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 249

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 hybrid polypeptide

<400> 249

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 250

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 250

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 251
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 251
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Met Tyr Phe Cys
85 90 95

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 252
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 252

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

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

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 253

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 253

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

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

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Met Tyr Phe Cys
85 90 95

Lys Arg Ser Ile Thr Thr Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 254

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 254

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Asn
20 25 30

Ile Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 255

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 255

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Asn
20 25 30

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

Tyr Ser Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 256

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 256

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Thr Val Ser Ser
115

<210> 257

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 257

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Thr Val Ser Ser
115

<210> 258
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 258
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Asn Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser
65 70 75 80

Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Thr Val Ser Ser
115

<210> 259
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 259
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Met Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Thr Val Ser Ser
115

<210> 260
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
hybrid polypeptide

<400> 260

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Ser Pro Gly Ser Gly Asp Ile Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser
65 70 75 80

Met His Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Thr Val Ser Ser
115

<210> 261

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 261

Cys Gln Phe Asp Leu Ser Thr Arg Arg Leu Lys Cys
1 5 10

<210> 262

<211> 12

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 262

Cys Gln Tyr Asn Leu Ser Ser Arg Ala Leu Lys Cys
1 5 10

<210> 263

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 263

Met Ala Asn Val Gln Leu Asn Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

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

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

Trp Val Ser Asp Ile Ser Pro Ser Gly Ala Val Lys Ala Tyr Ser Asp
50 55 60

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

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

Phe Cys Thr Lys Val Gln Ser Pro Arg Thr Arg Ile Pro Ala Pro Ser
100 105 110

Ser Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 264
<211> 122
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 264

Met Ala Asn Val Gln Leu Asn Glu Ser Gly Gly Gly Leu Val Gln Pro
1 5 10 15

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

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

Trp Val Ser Glu Ile Ser Pro Ser Gly Ala Val Lys Ala Tyr Ser Asp
50 55 60

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

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

Phe Cys Thr Lys Val Gln Ser Pro Arg Thr Arg Ile Pro Ala Pro Ser
100 105 110

Ser Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 265
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 265

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 266

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 266

Asp Tyr Lys Asp Asp Asp Asp Lys

1 5