

SEQUENCE LISTING

<110> SASINAPAS CO.,LTD.

<120> Modified peptides

<130> D0282-00004

<150> PCT/IB2016/057193

<151> 2016-11-30

<160> 79

<170> PatentIn version 3.5

<210> 1

<211> 29

<212> PRT

<213> unknown

<220>

<223> SMAP-29 sheep

<400> 1

Arg	Gly	Leu	Arg	Arg	Leu	Gly	Arg	Lys	Ile	Ala	His	Gly	Val	Lys	Lys
1				5					10					15	

Tyr	Gly	Pro	Thr	Val	Leu	Arg	Ile	Ile	Arg	Ile	Ala	Gly
			20					25				

<210> 2

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> sequence, which is not part of the sequence motif, if the sequence motif contains at least three non-adjacent histidine residues

<400> 2

Ala	Ala	Leu	Thr	His
1				5

<210> 3

<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Example for intrasequential pairwise block of amino acids of the first group

<400> 3

Leu Lys Arg Glu
1

<210> 4
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Example for intrasequential triplet block of amino acids of the first group

<400> 4

Leu Lys Arg Lys Glu
1 5

<210> 5
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Example for N-terminal triplet block of amino acids of the first group

<400> 5

Lys Arg Lys Glu
1

<210> 6
<211> 4
<212> PRT
<213> Artificial sequence

<220>

<223> Example for C-terminal triplet block of amino acids of the first group

<400> 6

Leu Lys Arg Lys

1

<210> 7

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Example of a sequence precluded from the sequence motif, if a triplet of amino acids of the first group is present

<400> 7

Arg Arg Arg Gly Leu Arg His

1

5

<210> 8

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Example of sequence not allowable within the sequence motif

<400> 8

Lys Arg Lys Lys

1

<210> 9

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Example of sequence not allowable within the sequence motif

<400> 9

Arg Arg Arg Arg

1

<210> 10
<211> 18
<212> PRT
<213> Unknown

<220>
<223> SMAP-29 sheep;aa1-18

<400> 10

Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys Lys
1 5 10 15

Tyr Gly

<210> 11
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from Cecropin A (A. aegypti)

<400> 11

Gly Gly Leu Lys Lys Leu Gly Lys Lys Leu Lys Lys Ala Gly Lys Arg
1 5 10 15

Val Phe Lys Ala Ala Lys Lys Ala Leu
20 25

<210> 12
<211> 28
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from BMAP-28

<400> 12

Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Leu Arg Ala Trp Lys Lys
1 5 10 15

Tyr Gly Pro Ile Ile Val Pro Ile Ile Arg Ile Gly
20 25

<210> 13
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated peptide deriving from MSI-78 (4-20) peptide

<400> 13

Arg Phe Leu Arg Arg Ala Arg Arg Phe Gly Arg Ala Phe Val Arg Ile
1 5 10 15

Leu

<210> 14
<211> 26
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from magainin

<400> 14

Gly Ile Lys Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala Phe
1 5 10 15

Lys Lys Val Ile Arg Gly Gly Gly Gly Ser
20 25

<210> 15
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from HPA-NT3 peptide

<400> 15

Lys Arg Leu Lys Lys Leu Ala Lys Lys Ile Trp Lys Trp Gly Arg Arg
1 5 10 15

Gly Pro Gly Ser
20

<210> 16

<211> 29

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 298-326 of the alpha subunit of stonustoxin

<400> 16

Ile Lys Leu Ile Lys Arg Val Ile Lys Lys Phe Lys Lys Ile Phe Arg
1 5 10 15

Lys Tyr Pro Leu Thr Val Lys Lys Gly Ile Ala Val Gly
20 25

<210> 17

<211> 27

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 26-48 of CagL protein

<400> 17

Gly Leu Lys Lys Leu Lys Arg Val Tyr Arg Lys Trp Val Lys Ala Val
1 5 10 15

Lys Lys Val Leu Lys Leu Gly Gly Gly Gly Ser
20 25

<210> 18

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 26-48 of CagL protein

<400> 18

Gly	Leu	Lys	Val	Leu	Lys	Lys	Ala	Tyr	Arg	Arg	Ile	Arg	Lys	Ala	Val
1				5					10					15	

Arg	Lys	Ile	Leu	Lys	Ala
				20	

<210> 19

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 178-198 of IE1 protein

<400> 19

Tyr	Lys	Arg	Ala	Phe	Lys	Lys	Val	Leu	Lys	Arg	Ile	Arg	Arg	Tyr	Ala
1				5					10					15	

Lys Arg Ser

<210> 20

<211> 24

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence

<400> 20

Gly	Phe	Phe	Lys	Lys	Ala	Trp	Arg	Lys	Val	Lys	His	Ala	Gly	Arg	Arg
1				5					10					15	

Val	Leu	Lys	Thr	Ala	Lys	Gly	Val
							20

<210> 21
<211> 20
<212> PRT
<213> unknown

<220>
<223> CAP18AA

<400> 21

Gly Leu Arg Lys Ala Leu Arg Lys Phe Arg Asn Lys Ile Lys Glu Ala
1 5 10 15

Leu Lys Lys Ile
20

<210> 22
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence

<400> 22

Gly Leu Arg Lys Ala Leu Arg Lys Phe Arg Lys Lys Ile Lys Glu Ala
1 5 10 15

Leu Lys Lys Ile
20

<210> 23
<211> 29
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence

<400> 23

Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala Arg Gly Val Lys Lys
1 5 10 15

Tyr Gly Pro Thr Val Leu Arg Ile Ile Arg Ile Ala Gly
20 25

<210> 24
<211> 136
<212> PRT
<213> Unknown

<220>
<223> S394 endolysin without N-terminal methionine

<400> 24

Ser Phe Lys Phe Gly Lys Asn Ser Glu Lys Gln Leu Ala Thr Val Lys
1 5 10 15

Pro Glu Leu Gln Lys Val Ala Arg Arg Ala Leu Glu Leu Ser Pro Tyr
20 25 30

Asp Phe Thr Ile Val Gln Gly Ile Arg Thr Val Ala Gln Ser Ala Gln
35 40 45

Asn Ile Ala Asn Gly Thr Ser Phe Leu Lys Asp Pro Ser Lys Ser Lys
50 55 60

His Val Thr Gly Asp Ala Ile Asp Phe Ala Pro Tyr Ile Asn Gly Lys
65 70 75 80

Ile Asp Trp Lys Asp Leu Glu Ala Phe Trp Ala Val Lys Lys Ala Phe
85 90 95

Glu Gln Ala Gly Lys Glu Leu Gly Ile Lys Leu Arg Phe Gly Ala Asp
100 105 110

Trp Asn Ser Ser Gly Asp Tyr His Asp Glu Ile Asp Arg Gly Thr Tyr
115 120 125

Asp Gly Gly His Val Glu Leu Val
130 135

<210> 25
 <211> 259
 <212> PRT
 <213> artificial sequence

 <220>
 <223> mutated KZ144 with C14S, C23S and C50S, without N-terminal methionine

 <400> 25

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

Thr Leu Leu Asn Leu Ser Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile
 20 25 30

Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn
 35 40 45

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

Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro
 65 70 75 80

Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val
 85 90 95

Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser
 100 105 110

Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala
 115 120 125

Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu
 130 135 140

Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu
 145 150 155 160

Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys
165 170 175

Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp
180 185 190

Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg
195 200 205

Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys
210 215 220

Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro
225 230 235 240

Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala
245 250 255

His Arg Lys

<210> 26
<211> 327
<212> PRT
<213> unknown

<220>
<223> OBPgpLYS fragment

<400> 26

Lys Asn Ser Glu Lys Asn Ala Ser Ile Ile Met Ser Ile Gln Arg Thr
1 5 10 15

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

Glu Lys Cys Arg Gly Ala Ile Ile Leu Met Leu Asn Lys Val Tyr Pro
35 40 45

Asn Phe Ser Thr Asn Lys Leu Pro Ser Asn Thr Tyr Glu Ala Glu Ser
50 55 60

Val Phe Thr Phe Leu Gln Thr Ala Leu Ala Gly Val Gly Leu Tyr Thr
65 70 75 80

Ile Thr Ile Asp Gly Lys Trp Gly Gly Thr Ser Gln Gly Ala Ile Asp
85 90 95

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

Ser Thr Leu Pro Leu Gly Leu Ala Thr Val Met Ser Lys His Met Ser
115 120 125

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

Glu Val Tyr Ile Asp Pro Leu Asn Glu Thr Met Asp Ile Phe Glu Ile
145 150 155 160

Asn Thr Pro Leu Arg Ile Ala His Phe Met Ala Gln Ile Leu His Glu
165 170 175

Thr Ala Cys Phe Lys Tyr Thr Glu Glu Leu Ala Ser Gly Lys Ala Tyr
180 185 190

Glu Gly Arg Ala Asp Leu Gly Asn Thr Arg Pro Gly Asp Gly Pro Leu
195 200 205

Phe Lys Gly Arg Gly Leu Leu Gln Ile Thr Gly Arg Leu Asn Tyr Val
210 215 220

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

Ile Thr Ser Ser Val Thr Cys Ala Gln Gln Leu Ser Glu Ser Pro Leu
245 250 255

Leu Ala Ala Leu Ala Ser Gly Tyr Phe Trp Arg Phe Ile Lys Pro Lys
260 265 270

Leu Asn Glu Thr Ala Asp Lys Asp Asp Ile Tyr Trp Val Ser Val Tyr
275 280 285

Val Asn Gly Tyr Ala Lys Gln Ala Asn Pro Tyr Tyr Pro Asn Arg Asp
290 295 300

Lys Glu Pro Asn His Met Lys Glu Arg Val Gln Met Leu Ala Val Thr
305 310 315 320

Lys Lys Ala Leu Gly Ile Val
325

<210> 27

<211> 237

<212> PRT

<213> unknown

<220>

<223> Tail baseplate protein of Vibrio phage ICP1 without N-terminal
methionine

<400> 27

Ile Leu Lys Arg Gly Ser Ser Gly Ala Asp Val Lys Asn Met Gln Glu
1 5 10 15

Tyr Leu Thr Ala Leu Gly Tyr Asp Thr Lys Gly Val Glu Gly Thr Phe
20 25 30

Glu Gly Gly Thr Glu Ser Ala Val Lys Ala Phe Gln Lys Asp Met Ser
35 40 45

Phe Thr Val Val Asp Gly Ile Ile Gly Asn Gln Thr Ala Lys His Leu
50 55 60

Val Asp Met Tyr Tyr Gly Lys Val Val Pro Phe Gly Tyr Val Thr Asn
65 70 75 80

Thr Pro Trp Val Ser Glu Ala Ile Glu Asp Tyr Phe Val Ser Glu Ile
85 90 95

Lys Gly Glu Lys His Asn Pro Arg Val Val Gln Tyr Phe Lys Asp Ala
100 105 110

His Ser Ser Trp Phe Thr Asp Asp Glu Thr Pro Trp Cys Ala Ala Ala
115 120 125

Val Ser Ser Trp Leu Glu Arg Ala Gly Ile Arg Ser Val Arg Ser Ala
130 135 140

Arg Ala Arg Asp His Ile Asn Phe Gly Thr Lys Leu Leu Glu Pro Arg
145 150 155 160

Phe Gly Ala Ile Val Val Leu Glu Arg Gly Ala Asn Ser Gly His Val
165 170 175

Gly Phe Val Asn Gly Val Thr Ala Asp Gly Lys Gln Ile Lys Val Leu
180 185 190

Gly Gly Asn Gln Ser Asp Ser Val Asn Glu Arg Met Phe Gln Val Thr
195 200 205

Arg Val Leu Gly Tyr Arg Gln Pro Glu Gly Phe Val Leu Pro Pro Cys
210 215 220

Pro Ile Val Gly Lys Gly Glu Leu Ser Lys Ser Glu Ala
225 230 235

<210> 28

<211> 4

<212> PRT

<213> artificial

<220>

<223> linker

<400> 28

Gly Ala Gly Ala

1

<210> 29

<211> 8

<212> PRT

<213> artificial

<220>

<223> linker

<400> 29

Gly Ala Gly Ala Gly Ala Gly Ala

1

5

<210> 30

<211> 12

<212> PRT

<213> artificial

<220>

<223> linker

<400> 30

Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala

1

5

10

<210> 31

<211> 6

<212> PRT

<213> artificial sequence

<220>

<223> His-Tag (6x)

<400> 31

His His His His His His

1

5

<210> 32
<211> 169
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from Cecropin A (*A. aegypti*) linked to
S394 endolysin

<400> 32

Met Gly Gly Leu Lys Lys Leu Gly Lys Lys Leu Lys Lys Ala Gly Lys
1 5 10 15

Arg Val Phe Lys Ala Ala Lys Lys Ala Leu Gly Gly Gly Ser Gly Ser
20 25 30

Met Ser Phe Lys Phe Gly Lys Asn Ser Glu Lys Gln Leu Ala Thr Val
35 40 45

Lys Pro Glu Leu Gln Lys Val Ala Arg Arg Ala Leu Glu Leu Ser Pro
50 55 60

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

Gln Asn Ile Ala Asn Gly Thr Ser Phe Leu Lys Asp Pro Ser Lys Ser
85 90 95

Lys His Val Thr Gly Asp Ala Ile Asp Phe Ala Pro Tyr Ile Asn Gly
100 105 110

Lys Ile Asp Trp Lys Asp Leu Glu Ala Phe Trp Ala Val Lys Lys Ala
115 120 125

Phe Glu Gln Ala Gly Lys Glu Leu Gly Ile Lys Leu Arg Phe Gly Ala
130 135 140

Asp Trp Asn Ser Ser Gly Asp Tyr His Asp Glu Ile Asp Arg Gly Thr
145 150 155 160

Tyr Asp Gly Gly His Val Glu Leu Val
165

<210> 33
<211> 355
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from Cecropin A (*A. aegypti*) linked to
OBPgpLys endolysin

<400> 33

Met Arg Gly Leu Lys Lys Leu Gly Arg Lys Leu Lys Lys Ala Gly Lys
1 5 10 15

Arg Val Phe Lys Ala Ala Lys Lys Ala Leu Gly Ser Lys Asn Ser Glu
20 25 30

Lys Asn Ala Ser Ile Ile Met Ser Ile Gln Arg Thr Leu Ala Ser Leu
35 40 45

Ser Leu Tyr Gly Gly Arg Ile Asp Gly Leu Phe Gly Glu Lys Cys Arg
50 55 60

Gly Ala Ile Ile Leu Met Leu Asn Lys Val Tyr Pro Asn Phe Ser Thr
65 70 75 80

Asn Lys Leu Pro Ser Asn Thr Tyr Glu Ala Glu Ser Val Phe Thr Phe
85 90 95

Leu Gln Thr Ala Leu Ala Gly Val Gly Leu Tyr Thr Ile Thr Ile Asp
100 105 110

Gly Lys Trp Gly Gly Thr Ser Gln Gly Ala Ile Asp Ala Leu Val Lys
115 120 125

Ser Tyr Arg Gln Ile Thr Glu Ala Glu Arg Ala Gly Ser Thr Leu Pro

130

135

140

Leu Gly Leu Ala Thr Val Met Ser Lys His Met Ser Ile Glu Gln Leu
 145 150 155 160

Arg Ala Met Leu Pro Thr Asp Arg Gln Gly Tyr Ala Glu Val Tyr Ile
 165 170 175

Asp Pro Leu Asn Glu Thr Met Asp Ile Phe Glu Ile Asn Thr Pro Leu
 180 185 190

Arg Ile Ala His Phe Met Ala Gln Ile Leu His Glu Thr Ala Cys Phe
 195 200 205

Lys Tyr Thr Glu Glu Leu Ala Ser Gly Lys Ala Tyr Glu Gly Arg Ala
 210 215 220

Asp Leu Gly Asn Thr Arg Pro Gly Asp Gly Pro Leu Phe Lys Gly Arg
 225 230 235 240

Gly Leu Leu Gln Ile Thr Gly Arg Leu Asn Tyr Val Lys Cys Gln Val
 245 250 255

Tyr Leu Arg Glu Lys Leu Lys Asp Pro Thr Phe Asp Ile Thr Ser Ser
 260 265 270

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

Ala Ser Gly Tyr Phe Trp Arg Phe Ile Lys Pro Lys Leu Asn Glu Thr
 290 295 300

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

Ala Lys Gln Ala Asn Pro Tyr Tyr Pro Asn Arg Asp Lys Glu Pro Asn
 325 330 335

His Met Lys Glu Arg Val Gln Met Leu Ala Val Thr Lys Lys Ala Leu
340 345 350

Gly Ile Val
355

<210> 34
<211> 290
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated peptide deriving from BMAP-28 linked to mutated KZ144
with C14S, C23S and C50S

<400> 34

Met Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Leu Arg Ala Trp Lys
1 5 10 15

Lys Tyr Gly Pro Ile Ile Val Pro Ile Ile Arg Ile Gly Gly Ser Lys
20 25 30

Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr
35 40 45

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

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

Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe
85 90 95

Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr
100 105 110

Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu
115 120 125

Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile
130 135 140

Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr
145 150 155 160

Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn
165 170 175

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

Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu
195 200 205

Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr
210 215 220

Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe
225 230 235 240

Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu
245 250 255

Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys
260 265 270

Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His
275 280 285

Arg Lys
290

<210> 35
<211> 162
<212> PRT
<213> Artificial sequence

<220>

<223> Mutated peptide deriving from MSI-78 (4-20) peptide linked to
S394 endolysin

<400> 35

Met Arg Phe Leu Arg Arg Ala Arg Arg Phe Gly Arg Ala Phe Val Arg
1 5 10 15

Ile Leu Gly Gly Gly Gly Ser Gly Ser Met Ser Phe Lys Phe Gly Lys
20 25 30

Asn Ser Glu Lys Gln Leu Ala Thr Val Lys Pro Glu Leu Gln Lys Val
35 40 45

Ala Arg Arg Ala Leu Glu Leu Ser Pro Tyr Asp Phe Thr Ile Val Gln
50 55 60

Gly Ile Arg Thr Val Ala Gln Ser Ala Gln Asn Ile Ala Asn Gly Thr
65 70 75 80

Ser Phe Leu Lys Asp Pro Ser Lys Ser Lys His Val Thr Gly Asp Ala
85 90 95

Ile Asp Phe Ala Pro Tyr Ile Asn Gly Lys Ile Asp Trp Lys Asp Leu
100 105 110

Glu Ala Phe Trp Ala Val Lys Lys Ala Phe Glu Gln Ala Gly Lys Glu
115 120 125

Leu Gly Ile Lys Leu Arg Phe Gly Ala Asp Trp Asn Ser Ser Gly Asp
130 135 140

Tyr His Asp Glu Ile Asp Arg Gly Thr Tyr Asp Gly Gly His Val Glu
145 150 155 160

Leu Val

<210> 36
<211> 166
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from magainin peptide linked to S394
endolysin

<400> 36

Met Gly Ile Lys Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala
1 5 10 15

Phe Lys Lys Val Ile Arg Gly Gly Gly Gly Ser Gly Ser Met Ser Phe
20 25 30

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

Leu Gln Lys Val Ala Arg Arg Ala Leu Glu Leu Ser Pro Tyr Asp Phe
50 55 60

Thr Ile Val Gln Gly Ile Arg Thr Val Ala Gln Ser Ala Gln Asn Ile
65 70 75 80

Ala Asn Gly Thr Ser Phe Leu Lys Asp Pro Ser Lys Ser Lys His Val
85 90 95

Thr Gly Asp Ala Ile Asp Phe Ala Pro Tyr Ile Asn Gly Lys Ile Asp
100 105 110

Trp Lys Asp Leu Glu Ala Phe Trp Ala Val Lys Lys Ala Phe Glu Gln
115 120 125

Ala Gly Lys Glu Leu Gly Ile Lys Leu Arg Phe Gly Ala Asp Trp Asn
130 135 140

Ser Ser Gly Asp Tyr His Asp Glu Ile Asp Arg Gly Thr Tyr Asp Gly
145 150 155 160

Gly His Val Glu Leu Val
165

<210> 37
<211> 282
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from HPA-NT3 peptide linked to mutated
KZ144 with C14S, C23S and C50S

<400> 37

Met Lys Arg Leu Lys Lys Leu Ala Lys Lys Ile Trp Lys Trp Gly Arg
1 5 10 15

Arg Gly Pro Gly Ser Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly
20 25 30

Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly Tyr Asp
35 40 45

Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val
50 55 60

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

Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro
85 90 95

Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala
100 105 110

Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln
115 120 125

Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile

130

135

140

Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly
 145 150 155 160

Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu
 165 170 175

Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu
 180 185 190

Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val
 195 200 205

Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe
 210 215 220

Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu
 225 230 235 240

Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe
 245 250 255

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

Met Asp Gly Lys Val Ala Ala His Arg Lys
 275 280

<210> 38

<211> 291

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 298-326 of the alpha subunit of stonustoxin linked to mutated KZ144 with C14S, C23S and C50S

<400> 38

Met Ile Lys Leu Ile Lys Arg Val Ile Lys Lys Phe Lys Lys Ile Phe
1 5 10 15

Arg Lys Tyr Pro Leu Thr Val Lys Lys Gly Ile Ala Val Gly Gly Ser
20 25 30

Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln
35 40 45

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

Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn
65 70 75 80

Ser Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu
85 90 95

Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro
100 105 110

Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val
115 120 125

Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser
130 135 140

Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala
145 150 155 160

Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu
165 170 175

Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu
180 185 190

Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys

195

200

205

Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp
 210 215 220

Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg
 225 230 235 240

Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys
 245 250 255

Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro
 260 265 270

Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala
 275 280 285

His Arg Lys
 290

<210> 39

<211> 289

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 26-48 of CagL protein
 linked to mutated KZ144 with C14S, C23S and C50S

<400> 39

Met Gly Leu Lys Lys Leu Lys Arg Val Tyr Arg Lys Trp Val Lys Ala
 1 5 10 15

Val Lys Lys Val Leu Lys Leu Gly Gly Gly Gly Ser Gly Ser Lys Val
 20 25 30

Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu
 35 40 45

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

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

Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser
85 90 95

Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala
100 105 110

Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn
115 120 125

Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu
130 135 140

Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly
145 150 155 160

Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr
165 170 175

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

Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn
195 200 205

Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp
210 215 220

Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu
225 230 235 240

Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala
245 250 255

Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr
260 265 270

Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg
275 280 285

Lys

<210> 40

<211> 284

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 26-48 of CagL protein
linked to mutated KZ144 with C14S, C23S and C50S

<400> 40

Met Gly Leu Lys Val Leu Lys Lys Ala Tyr Arg Arg Ile Arg Lys Ala
1 5 10 15

Val Arg Lys Ile Leu Lys Ala Gly Ser Lys Val Leu Arg Lys Gly Asp
20 25 30

Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly
35 40 45

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

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

Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro
85 90 95

Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala

100

105

110

Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg
115 120 125

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

Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu
145 150 155 160

Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly
165 170 175

Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser
180 185 190

Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg
195 200 205

Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His
210 215 220

Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn
225 230 235 240

Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser
245 250 255

Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr
260 265 270

Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
275 280

<210> 41

<211> 281

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from amino acids 178-198 of IE1 protein
linked to mutated KZ144 with C14S, C23S and C50S

<400> 41

Met Tyr Lys Arg Ala Phe Lys Lys Val Leu Lys Arg Ile Arg Arg Tyr
1 5 10 15

Ala Lys Arg Ser Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp
20 25 30

Glu Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly Tyr Asp Val
35 40 45

Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val
50 55 60

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

Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr
85 90 95

Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr
100 105 110

Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu
115 120 125

Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys
130 135 140

Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr
145 150 155 160

Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr
165 170 175

Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met
180 185 190

Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu
195 200 205

Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly
210 215 220

Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala
225 230 235 240

Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr
245 250 255

Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met
260 265 270

Asp Gly Lys Val Ala Ala His Arg Lys
275 280

<210> 42
<211> 168
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 42

Met Gly Phe Phe Lys Lys Ala Trp Arg Lys Val Lys His Ala Gly Arg
1 5 10 15

Arg Val Leu Lys Thr Ala Lys Gly Val Gly Gly Gly Ser Gly Ser Met
20 25 30

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

Pro Glu Leu Gln Lys Val Ala Arg Arg Ala Leu Glu Leu Ser Pro Tyr
50 55 60

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

Asn Ile Ala Asn Gly Thr Ser Phe Leu Lys Asp Pro Ser Lys Ser Lys
85 90 95

His Val Thr Gly Asp Ala Ile Asp Phe Ala Pro Tyr Ile Asn Gly Lys
100 105 110

Ile Asp Trp Lys Asp Leu Glu Ala Phe Trp Ala Val Lys Lys Ala Phe
115 120 125

Glu Gln Ala Gly Lys Glu Leu Gly Ile Lys Leu Arg Phe Gly Ala Asp
130 135 140

Trp Asn Ser Ser Gly Asp Tyr His Asp Glu Ile Asp Arg Gly Thr Tyr
145 150 155 160

Asp Gly Gly His Val Glu Leu Val
165

<210> 43

<211> 267

<212> PRT

<213> artificial sequence

<220>

<223> Mutated peptide deriving from magainin peptide linked to tail
baseplate protein of Vibrio phage ICP1

<400> 43

Met Gly Ile Lys Lys Phe Leu Lys Ser Ala Lys Lys Phe Gly Lys Ala
1 5 10 15

Phe Lys Lys Val Ile Arg Gly Gly Gly Gly Ser Gly Ser Met Ile Leu

20

25

30

Lys Arg Gly Ser Ser Gly Ala Asp Val Lys Asn Met Gln Glu Tyr Leu
 35 40 45

Thr Ala Leu Gly Tyr Asp Thr Lys Gly Val Glu Gly Thr Phe Glu Gly
 50 55 60

Gly Thr Glu Ser Ala Val Lys Ala Phe Gln Lys Asp Met Ser Phe Thr
 65 70 75 80

Val Val Asp Gly Ile Ile Gly Asn Gln Thr Ala Lys His Leu Val Asp
 85 90 95

Met Tyr Tyr Gly Lys Val Val Pro Phe Gly Tyr Val Thr Asn Thr Pro
 100 105 110

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

Glu Lys His Asn Pro Arg Val Val Gln Tyr Phe Lys Asp Ala His Ser
 130 135 140

Ser Trp Phe Thr Asp Asp Glu Thr Pro Trp Cys Ala Ala Ala Val Ser
 145 150 155 160

Ser Trp Leu Glu Arg Ala Gly Ile Arg Ser Val Arg Ser Ala Arg Ala
 165 170 175

Arg Asp His Ile Asn Phe Gly Thr Lys Leu Leu Glu Pro Arg Phe Gly
 180 185 190

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

Val Asn Gly Val Thr Ala Asp Gly Lys Gln Ile Lys Val Leu Gly Gly
 210 215 220

Asn Gln Ser Asp Ser Val Asn Glu Arg Met Phe Gln Val Thr Arg Val
225 230 235 240

Leu Gly Tyr Arg Gln Pro Glu Gly Phe Val Leu Pro Pro Cys Pro Ile
245 250 255

Val Gly Lys Gly Glu Leu Ser Lys Ser Glu Ala
260 265

<210> 44
<211> 36
<212> PRT
<213> Aedes aegypti

<400> 44

Gly Gly Leu Lys Lys Leu Gly Lys Lys Leu Glu Gly Ala Gly Lys Arg
1 5 10 15

Val Phe Asn Ala Ala Glu Lys Ala Leu Pro Val Val Ala Gly Ala Lys
20 25 30

Ala Leu Arg Lys
35

<210> 45
<211> 184
<212> PRT
<213> Artificial sequence

<220>
<223> Cecropin A (A. aegypti) linked to S394 endolysin

<400> 45

Met Gly Gly Leu Lys Lys Leu Gly Lys Lys Leu Glu Gly Ala Gly Lys
1 5 10 15

Arg Val Phe Asn Ala Ala Glu Lys Ala Leu Pro Val Val Ala Gly Ala
20 25 30

Lys Ala Leu Arg Lys Gly Ala Gly Ala Gly Ala Gly Ser Met
35 40 45

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

Pro Glu Leu Gln Lys Val Ala Arg Arg Ala Leu Glu Leu Ser Pro Tyr
65 70 75 80

Asp Phe Thr Ile Val Gln Gly Ile Arg Thr Val Ala Gln Ser Ala Gln
85 90 95

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

His Val Thr Gly Asp Ala Ile Asp Phe Ala Pro Tyr Ile Asn Gly Lys
115 120 125

Ile Asp Trp Lys Asp Leu Glu Ala Phe Trp Ala Val Lys Lys Ala Phe
130 135 140

Glu Gln Ala Gly Lys Glu Leu Gly Ile Lys Leu Arg Phe Gly Ala Asp
145 150 155 160

Trp Asn Ser Ser Gly Asp Tyr His Asp Glu Ile Asp Arg Gly Thr Tyr
165 170 175

Asp Gly Gly His Val Glu Leu Val
180

<210> 46

<211> 366

<212> PRT

<213> Artificial sequence

<220>

<223> Cecropin A (*A. aegypti*) linked to OBPgpLys endolysin

<400> 46

Met Gly Gly Leu Lys Lys Leu Gly Lys Lys Leu Glu Gly Ala Gly Lys
1 5 10 15

Arg Val Phe Asn Ala Ala Glu Lys Ala Leu Pro Val Val Ala Gly Ala
20 25 30

Lys Ala Leu Arg Lys Gly Ser Lys Asn Ser Glu Lys Asn Ala Ser Ile
35 40 45

Ile Met Ser Ile Gln Arg Thr Leu Ala Ser Leu Ser Leu Tyr Gly Gly
50 55 60

Arg Ile Asp Gly Leu Phe Gly Glu Lys Cys Arg Gly Ala Ile Ile Leu
65 70 75 80

Met Leu Asn Lys Val Tyr Pro Asn Phe Ser Thr Asn Lys Leu Pro Ser
85 90 95

Asn Thr Tyr Glu Ala Glu Ser Val Phe Thr Phe Leu Gln Thr Ala Leu
100 105 110

Ala Gly Val Gly Leu Tyr Thr Ile Thr Ile Asp Gly Lys Trp Gly Gly
115 120 125

Thr Ser Gln Gly Ala Ile Asp Ala Leu Val Lys Ser Tyr Arg Gln Ile
130 135 140

Thr Glu Ala Glu Arg Ala Gly Ser Thr Leu Pro Leu Gly Leu Ala Thr
145 150 155 160

Val Met Ser Lys His Met Ser Ile Glu Gln Leu Arg Ala Met Leu Pro
165 170 175

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

Thr Met Asp Ile Phe Glu Ile Asn Thr Pro Leu Arg Ile Ala His Phe
195 200 205

Met Ala Gln Ile Leu His Glu Thr Ala Cys Phe Lys Tyr Thr Glu Glu
210 215 220

Leu Ala Ser Gly Lys Ala Tyr Glu Gly Arg Ala Asp Leu Gly Asn Thr
225 230 235 240

Arg Pro Gly Asp Gly Pro Leu Phe Lys Gly Arg Gly Leu Leu Gln Ile
245 250 255

Thr Gly Arg Leu Asn Tyr Val Lys Cys Gln Val Tyr Leu Arg Glu Lys
260 265 270

Leu Lys Asp Pro Thr Phe Asp Ile Thr Ser Ser Val Thr Cys Ala Gln
275 280 285

Gln Leu Ser Glu Ser Pro Leu Leu Ala Ala Leu Ala Ser Gly Tyr Phe
290 295 300

Trp Arg Phe Ile Lys Pro Lys Leu Asn Glu Thr Ala Asp Lys Asp Asp
305 310 315 320

Ile Tyr Trp Val Ser Val Tyr Val Asn Gly Tyr Ala Lys Gln Ala Asn
325 330 335

Pro Tyr Tyr Pro Asn Arg Asp Lys Glu Pro Asn His Met Lys Glu Arg
340 345 350

Val Gln Met Leu Ala Val Thr Lys Lys Ala Leu Gly Ile Val
355 360 365

<210> 47

<211> 28

<212> PRT

<213> Unknown

<220>

<223> BMAP-28, bovines

<400> 47

Gly Gly Leu Arg Ser Leu Gly Arg Lys Ile Leu Arg Ala Trp Lys Lys
1 5 10 15

Tyr Gly Pro Ile Ile Val Pro Ile Ile Arg Ile Gly
20 25

<210> 48

<211> 290

<212> PRT

<213> Artificial sequence

<220>

<223> BMAP-28 linked to mutated KZ144 with C14S, C23S and C50S

<400> 48

Met Gly Gly Leu Arg Ser Leu Gly Arg Lys Ile Leu Arg Ala Trp Lys
1 5 10 15

Lys Tyr Gly Pro Ile Ile Val Pro Ile Ile Arg Ile Gly Gly Ser Lys
20 25 30

Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr
35 40 45

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

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

Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe
85 90 95

Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr
100 105 110

Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu
115 120 125

Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile
130 135 140

Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr
145 150 155 160

Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn
165 170 175

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

Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu
195 200 205

Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr
210 215 220

Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe
225 230 235 240

Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu
245 250 255

Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys
260 265 270

Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His
275 280 285

Arg Lys
290

<210> 49

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MSI-78 (4-20) peptide

<400> 49

Lys Phe Leu Lys Lys Ala Lys Lys Phe Gly Lys Ala Phe Val Lys Ile
1 5 10 15

Leu

<210> 50

<211> 162

<212> PRT

<213> Artificial sequence

<220>

<223> MSI-78 (4-20) peptide linked to S394 endolysin

<400> 50

Met Lys Phe Leu Lys Lys Ala Lys Lys Phe Gly Lys Ala Phe Val Lys
1 5 10 15

Ile Leu Gly Gly Gly Gly Ser Gly Ser Met Ser Phe Lys Phe Gly Lys
20 25 30

Asn Ser Glu Lys Gln Leu Ala Thr Val Lys Pro Glu Leu Gln Lys Val
35 40 45

Ala Arg Arg Ala Leu Glu Leu Ser Pro Tyr Asp Phe Thr Ile Val Gln
50 55 60

Gly Ile Arg Thr Val Ala Gln Ser Ala Gln Asn Ile Ala Asn Gly Thr
65 70 75 80

Ser Phe Leu Lys Asp Pro Ser Lys Ser Lys His Val Thr Gly Asp Ala
85 90 95

Ile Asp Phe Ala Pro Tyr Ile Asn Gly Lys Ile Asp Trp Lys Asp Leu
100 105 110

Glu Ala Phe Trp Ala Val Lys Lys Ala Phe Glu Gln Ala Gly Lys Glu
115 120 125

Leu Gly Ile Lys Leu Arg Phe Gly Ala Asp Trp Asn Ser Ser Gly Asp
130 135 140

Tyr His Asp Glu Ile Asp Arg Gly Thr Tyr Asp Gly Gly His Val Glu
145 150 155 160

Leu Val

<210> 51
<211> 23
<212> PRT
<213> *Xenopus laevis*

<400> 51

Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
1 5 10 15

Val Gly Glu Ile Met Asn Ser
20

<210> 52
<211> 163
<212> PRT
<213> Artificial sequence

<220>
<223> Magainin peptide linked to S394 endolysin

<400> 52

Met Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala
1 5 10 15

Phe Val Gly Glu Ile Met Asn Ser Gly Ser Met Ser Phe Lys Phe Gly
20 25 30

Lys Asn Ser Glu Lys Gln Leu Ala Thr Val Lys Pro Glu Leu Gln Lys
35 40 45

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

Gln Gly Ile Arg Thr Val Ala Gln Ser Ala Gln Asn Ile Ala Asn Gly
65 70 75 80

Thr Ser Phe Leu Lys Asp Pro Ser Lys Ser Lys His Val Thr Gly Asp
85 90 95

Ala Ile Asp Phe Ala Pro Tyr Ile Asn Gly Lys Ile Asp Trp Lys Asp
100 105 110

Leu Glu Ala Phe Trp Ala Val Lys Lys Ala Phe Glu Gln Ala Gly Lys
115 120 125

Glu Leu Gly Ile Lys Leu Arg Phe Gly Ala Asp Trp Asn Ser Ser Gly
130 135 140

Asp Tyr His Asp Glu Ile Asp Arg Gly Thr Tyr Asp Gly Gly His Val
145 150 155 160

Glu Leu Val

<210> 53
<211> 15
<212> PRT
<213> Helicobacter pylori

<400> 53

Phe Lys Arg Leu Lys Lys Leu Phe Lys Lys Ile Trp Asn Trp Lys
1 5 10 15

<210> 54
<211> 277

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acids XXX of HPA-NT3 peptide linked to mutated KZ144 with C14S, C23S and C50S

<400> 54

Met Phe Lys Arg Leu Lys Lys Leu Phe Lys Lys Ile Trp Asn Trp Lys
1 5 10 15

Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Ser Gln
20 25 30

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

Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys
50 55 60

Asp Asn Ser Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala
65 70 75 80

Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro
85 90 95

Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn
100 105 110

Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe
115 120 125

Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser
130 135 140

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

Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly

165

170

175

Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu
 180 185 190

Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro
 195 200 205

Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala
 210 215 220

Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe
 225 230 235 240

Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly
 245 250 255

Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val
 260 265 270

Ala Ala His Arg Lys
 275

<210> 55
 <211> 29
 <212> PRT
 <213> Synanceia verrucosa

<400> 55

Ile Pro Leu Ile His Asp Lys Ile Ser Asn Phe Gln Gln Ile Phe Gln
 1 5 10 15

Asp Tyr Met Leu Thr Val Gln Lys Lys Ile Ala Glu Lys
 20 25

<210> 56
 <211> 291
 <212> PRT
 <213> Artificial sequence

<220>

<223> Amino acids 298-326 of the alpha subunit of stonustoxin linked to mutated KZ144 with C14S, C23S and C50S

<400> 56

Met	Ile	Pro	Leu	Ile	His	Asp	Lys	Ile	Ser	Asn	Phe	Gln	Gln	Ile	Phe
1				5					10					15	

Gln	Asp	Tyr	Met	Leu	Thr	Val	Gln	Lys	Lys	Ile	Ala	Glu	Lys	Gly	Ser
			20					25					30		

Lys	Val	Leu	Arg	Lys	Gly	Asp	Arg	Gly	Asp	Glu	Val	Ser	Gln	Leu	Gln
		35					40					45			

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

Phe	Gly	Asn	Asn	Thr	Phe	Asn	Gln	Val	Val	Lys	Phe	Gln	Lys	Asp	Asn
65					70					75					80

Ser	Leu	Asp	Ser	Asp	Gly	Ile	Val	Gly	Lys	Asn	Thr	Trp	Ala	Glu	Leu
				85					90					95	

Phe	Ser	Lys	Tyr	Ser	Pro	Pro	Ile	Pro	Tyr	Lys	Thr	Ile	Pro	Met	Pro
			100					105					110		

Thr	Ala	Asn	Lys	Ser	Arg	Ala	Ala	Ala	Thr	Pro	Val	Met	Asn	Ala	Val
		115					120					125			

Glu	Asn	Ala	Thr	Gly	Val	Arg	Ser	Gln	Leu	Leu	Leu	Thr	Phe	Ala	Ser
	130					135					140				

Ile	Glu	Ser	Ala	Phe	Asp	Tyr	Glu	Ile	Lys	Ala	Lys	Thr	Ser	Ser	Ala
145					150					155					160

Thr	Gly	Trp	Phe	Gln	Phe	Leu	Thr	Gly	Thr	Trp	Lys	Thr	Met	Ile	Glu
				165					170					175	

Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu
180 185 190

Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys
195 200 205

Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp
210 215 220

Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg
225 230 235 240

Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys
245 250 255

Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro
260 265 270

Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala
275 280 285

His Arg Lys
290

<210> 57
<211> 22
<212> PRT
<213> Helicobacter pylori

<400> 57

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

Leu Lys Asn Leu Asp Glu
20

<210> 58
<211> 284

<212> PRT

<213> Artificial sequence

<220>

<223> Amino acids 26-48 of CagL protein linked to mutated KZ144 with
C14S, C23S and C50S

<400> 58

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

Val Leu Lys Asn Leu Asp Glu Gly Ser Lys Val Leu Arg Lys Gly Asp
20 25 30

Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly
35 40 45

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

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

Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro
85 90 95

Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala
100 105 110

Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg
115 120 125

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

Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu
145 150 155 160

Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly

165

170

175

Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser
 180 185 190

Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg
 195 200 205

Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His
 210 215 220

Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn
 225 230 235 240

Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser
 245 250 255

Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr
 260 265 270

Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
 275 280

<210> 59
 <211> 19
 <212> PRT
 <213> Human cytomegalovirus

<400> 59

Tyr Lys Glu Lys Phe Met Val Cys Leu Lys Gln Ile Val Gln Tyr Ala
 1 5 10 15

Val Asn Ser

<210> 60
 <211> 281
 <212> PRT
 <213> Artificial sequence

<220>

<223> Amino acids 178-198 of IE1 protein linked to mutated KZ144 with C14S, C23S and C50S

<400> 60

Met Tyr Lys Glu Lys Phe Met Val Cys Leu Lys Gln Ile Val Gln Tyr
1 5 10 15

Ala Val Asn Ser Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp
20 25 30

Glu Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly Tyr Asp Val
35 40 45

Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val
50 55 60

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

Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr
85 90 95

Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr
100 105 110

Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu
115 120 125

Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys
130 135 140

Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr
145 150 155 160

Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr
165 170 175

Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met
180 185 190

Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu
195 200 205

Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly
210 215 220

Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala
225 230 235 240

Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr
245 250 255

Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met
260 265 270

Asp Gly Lys Val Ala Ala His Arg Lys
275 280

<210> 61
<211> 278
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 61

Met Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys
1 5 10 15

Lys Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Ser
20 25 30

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

Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln
50 55 60

Lys Asp Asn Ser Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp
65 70 75 80

Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile
85 90 95

Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met
100 105 110

Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr
115 120 125

Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr
130 135 140

Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr
145 150 155 160

Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr
165 170 175

Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu
180 185 190

Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu
195 200 205

Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala
210 215 220

Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His
225 230 235 240

Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp

245

250

255

Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys
 260 265 270

Val Ala Ala His Arg Lys
 275

<210> 62
 <211> 286
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic sequence

<400> 62

Met Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys
 1 5 10 15

Lys Gly Ala Gly Ala Gly Ala Gly Ala Gly Ser Lys Val Leu Arg Lys
 20 25 30

Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn Leu
 35 40 45

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

Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Ser Leu Asp Ser Asp
 65 70 75 80

Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser
 85 90 95

Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser
 100 105 110

Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly

115

120

125

Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe
130 135 140

Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln
145 150 155 160

Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys
165 170 175

Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg
180 185 190

Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile
195 200 205

Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu
210 215 220

Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly
225 230 235 240

Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn
245 250 255

Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu
260 265 270

Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
275 280 285

<210> 63

<211> 279

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence

<400> 63

Met Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys
1 5 10 15

Lys Tyr Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val
20 25 30

Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly Tyr Asp Val Gly Lys
35 40 45

Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe
50 55 60

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

Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr
85 90 95

Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val
100 105 110

Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu
115 120 125

Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys
130 135 140

Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys
145 150 155 160

Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro
165 170 175

Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala
180 185 190

Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg
195 200 205

Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly
210 215 220

Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr
225 230 235 240

His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys
245 250 255

Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly
260 265 270

Lys Val Ala Ala His Arg Lys
275

<210> 64
<211> 285
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 64

Met Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys
1 5 10 15

Lys Tyr Lys Pro Lys Pro Lys Pro Gly Ser Lys Val Leu Arg Lys Gly
20 25 30

Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser
35 40 45

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

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

Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro
85 90 95

Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg
100 105 110

Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val
115 120 125

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

Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe
145 150 155 160

Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr
165 170 175

Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile
180 185 190

Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu
195 200 205

Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala
210 215 220

His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln
225 230 235 240

Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro
245 250 255

Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val

260

265

270

Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
 275 280 285

<210> 65

<211> 280

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence

<400> 65

Met Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys
 1 5 10 15

Lys Tyr Gly Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu
 20 25 30

Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly Tyr Asp Val Gly
 35 40 45

Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys
 50 55 60

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

Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys
 85 90 95

Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro
 100 105 110

Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu
 115 120 125

Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala

130

135

140

Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp
 145 150 155 160

Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp
 165 170 175

Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly
 180 185 190

Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys
 195 200 205

Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro
 210 215 220

Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala
 225 230 235 240

Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn
 245 250 255

Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp
 260 265 270

Gly Lys Val Ala Ala His Arg Lys
 275 280

<210> 66

<211> 284

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence

<400> 66

Met Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys

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

Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His
210 215 220

Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn
225 230 235 240

Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser
245 250 255

Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr
260 265 270

Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
275 280

<210> 67
<211> 280
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 67

Met Gly Arg Lys Ile Ala His Gly Val Lys Lys Tyr Gly Arg Gly Leu
1 5 10 15

Arg Arg Leu Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu
20 25 30

Val Ser Gln Leu Gln Thr Leu Leu Asn Leu Ser Gly Tyr Asp Val Gly
35 40 45

Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys
50 55 60

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

Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys
85 90 95

Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro
100 105 110

Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu
115 120 125

Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala
130 135 140

Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp
145 150 155 160

Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp
165 170 175

Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly
180 185 190

Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys
195 200 205

Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro
210 215 220

Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala
225 230 235 240

Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn
245 250 255

Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp
260 265 270

Gly Lys Val Ala Ala His Arg Lys

275

280

<210> 68
 <211> 291
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic sequence

<400> 68

Met Gly Arg Lys Ile Ala His Gly Val Lys Lys Tyr Gly Arg Gly Leu
 1 5 10 15

Arg Arg Leu Pro Thr Val Leu Arg Ile Ile Arg Ile Ala Gly Gly Ser
 20 25 30

Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln
 35 40 45

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

Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn
 65 70 75 80

Ser Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu
 85 90 95

Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro
 100 105 110

Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val
 115 120 125

Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser
 130 135 140

Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala

1 5 10 15

Ile Arg Arg Pro Leu Lys Arg Leu Ala
20 25

<210> 70

<211> 295

<212> PRT

<213> artificial sequence

<220>

<223> MW2 peptide linked to mutated KZ144 with C14S, C23S and C50S

<400> 70

Met Gly Lys Pro Gly Trp Leu Ile Lys Val Ala Leu Lys Phe Lys Lys
1 5 10 15

Leu Ile Arg Arg Pro Leu Lys Arg Leu Ala Gly Ser Lys Val Leu Arg
20 25 30

Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn
35 40 45

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

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

Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr
85 90 95

Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys
100 105 110

Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr
115 120 125

Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala

130

135

140

Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe
 145 150 155 160

Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met
 165 170 175

Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro
 180 185 190

Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn
 195 200 205

Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr
 210 215 220

Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr
 225 230 235 240

Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala
 245 250 255

Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln
 260 265 270

Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu
 275 280 285

Glu His His His His His
 290 295

<210> 71

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence; MW2 mut (I7R;L11R;P20G)

<400> 71

Gly Lys Pro Gly Trp Leu Arg Lys Val Ala Arg Lys Phe Lys Lys Leu
1 5 10 15

Ile Arg Arg Gly Leu Lys Arg Leu Ala
20 25

<210> 72

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence; MW2 mut (P3V;I7R;L11R)

<400> 72

Gly Lys Val Gly Trp Leu Arg Lys Val Ala Arg Lys Phe Lys Lys Leu
1 5 10 15

Ile Arg Arg Pro Leu Lys Arg Leu Ala
20 25

<210> 73

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence; MW2 mut (I7R)

<400> 73

Gly Lys Pro Gly Trp Leu Arg Lys Val Ala Leu Lys Phe Lys Lys Leu
1 5 10 15

Ile Arg Arg Pro Leu Lys Arg Leu Ala
20 25

<210> 74

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence; MW2 mut (L11R)

<400> 74

Gly Lys Pro Gly Trp Leu Ile Lys Val Ala Arg Lys Phe Lys Lys Leu
1 5 10 15

Ile Arg Arg Pro Leu Lys Arg Leu Ala
20 25

<210> 75

<211> 295

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from MW2 peptide linked to mutated KZ144
with C14S, C23S and C50S

<400> 75

Met Gly Lys Pro Gly Trp Leu Arg Lys Val Ala Arg Lys Phe Lys Lys
1 5 10 15

Leu Ile Arg Arg Gly Leu Lys Arg Leu Ala Gly Ser Lys Val Leu Arg
20 25 30

Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn
35 40 45

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

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

Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr
85 90 95

Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys
100 105 110

Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr
115 120 125

Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala
130 135 140

Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe
145 150 155 160

Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met
165 170 175

Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro
180 185 190

Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn
195 200 205

Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr
210 215 220

Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr
225 230 235 240

Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala
245 250 255

Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln
260 265 270

Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu
275 280 285

Glu His His His His His His
290 295

<210> 76
<211> 295
<212> PRT
<213> Artificial sequence

<220>
<223> Mutated peptide deriving from MW2 peptide linked to mutated KZ144
with C14S, C23S and C50S

<400> 76

Met Gly Lys Val Gly Trp Leu Arg Lys Val Ala Arg Lys Phe Lys Lys
1 5 10 15

Leu Ile Arg Arg Pro Leu Lys Arg Leu Ala Gly Ser Lys Val Leu Arg
20 25 30

Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn
35 40 45

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

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

Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr
85 90 95

Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys
100 105 110

Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr
115 120 125

Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala
130 135 140

Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe

145 150 155 160

Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro
180 185 190

Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr
210 215 220

Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala
245 250 255

Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu
275 280 285

<210> 77

Met Gly Lys Pro Gly Trp Leu Arg Lys Val Ala Leu Lys Phe Lys Lys
1 5 10 15

Leu Ile Arg Arg Pro Leu Lys Arg Leu Ala Gly Ser Lys Val Leu Arg
20 25 30

Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn
35 40 45

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

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

Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr
85 90 95

Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys
100 105 110

Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr
115 120 125

Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala
130 135 140

Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe
145 150 155 160

Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met
165 170 175

Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro
180 185 190

Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn
195 200 205

Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr
210 215 220

Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr
225 230 235 240

Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala
245 250 255

Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln
260 265 270

Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu
275 280 285

Glu His His His His His His
290 295

<210> 78

<211> 295

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated peptide deriving from MW2 peptide linked to mutated KZ144
with C14S, C23S and C50S

<400> 78

Met Gly Lys Pro Gly Trp Leu Ile Lys Val Ala Arg Lys Phe Lys Lys
1 5 10 15

Leu Ile Arg Arg Pro Leu Lys Arg Leu Ala Gly Ser Lys Val Leu Arg
20 25 30

Lys Gly Asp Arg Gly Asp Glu Val Ser Gln Leu Gln Thr Leu Leu Asn
35 40 45

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

50

55

60

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

Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr
 85 90 95

Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys
 100 105 110

Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr
 115 120 125

Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala
 130 135 140

Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe
 145 150 155 160

Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met
 165 170 175

Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro
 180 185 190

Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn
 195 200 205

Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr
 210 215 220

Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr
 225 230 235 240

Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala
 245 250 255

Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln
260 265 270

Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu
275 280 285

Glu His His His His His
290 295

<210> 79

<211> 264

<212> PRT

<213> Artificial sequence

<220>

<223> Magainin peptide linked to tail baseplate protein of Vibrio phage
ICP1

<400> 79

Met Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala
1 5 10 15

Phe Val Gly Glu Ile Met Asn Ser Gly Ser Met Ile Leu Lys Arg Gly
20 25 30

Ser Ser Gly Ala Asp Val Lys Asn Met Gln Glu Tyr Leu Thr Ala Leu
35 40 45

Gly Tyr Asp Thr Lys Gly Val Glu Gly Thr Phe Glu Gly Gly Thr Glu
50 55 60

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

Gly Ile Ile Gly Asn Gln Thr Ala Lys His Leu Val Asp Met Tyr Tyr
85 90 95

Gly Lys Val Val Pro Phe Gly Tyr Val Thr Asn Thr Pro Trp Val Ser
100 105 110

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

Asn Pro Arg Val Val Gln Tyr Phe Lys Asp Ala His Ser Ser Trp Phe
130 135 140

Thr Asp Asp Glu Thr Pro Trp Cys Ala Ala Ala Val Ser Ser Trp Leu
145 150 155 160

Glu Arg Ala Gly Ile Arg Ser Val Arg Ser Ala Arg Ala Arg Asp His
165 170 175

Ile Asn Phe Gly Thr Lys Leu Leu Glu Pro Arg Phe Gly Ala Ile Val
180 185 190

Val Leu Glu Arg Gly Ala Asn Ser Gly His Val Gly Phe Val Asn Gly
195 200 205

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

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

Arg Gln Pro Glu Gly Phe Val Leu Pro Pro Cys Pro Ile Val Gly Lys
245 250 255

Gly Glu Leu Ser Lys Ser Glu Ala
260