

34246SG2-seq1-000001
SEQUENCE LISTING

<110> Chugai Seiyaku Kabushiki Kaisha
Agency for Science, Technology and Research

<120> Anti-Dengue Virus Antibodies, Polypeptides Containing Variant Fc
Regions, And Methods Of Use

<130> 34246SG1/MBR(JKN)/ndh

<160> 109

<170> PatentIn version 3.5

<210> 1
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1

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

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Thr Ala Ser Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Arg
100 105 110

34246SG2-seq1-000001

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
 115 120 125

Thr Val Ser Ser
 130

<210> 2
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH

<400> 2

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

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Ala Ser Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
 100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val

34246SG2-seq1-000001

115

120

125

Thr Val Ser Ser
130

<210> 3
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> VH

<400> 3

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

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
115 120 125

34246SG2-seq1-000001

Thr Val Ser Ser
130

<210> 4
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> VH

<400> 4

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

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Arg
100 105 110

Asp Asp Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
115 120 125

Thr Val Ser Ser

130

<210> 5
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH

<400> 5

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

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Arg
 100 105 110

Asp Leu Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
 115 120 125

Thr Val Ser Ser
 130

34246SG2-seq1-000001

<210> 6
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH

<400> 6

Gln Val Gln Leu Val Gln Ser Gly Pro Asp Val Glu 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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Gly Glu Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
 100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
 115 120 125

Thr Val Ser Ser
 130

<210> 7

34246SG2-seq1-000001

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

<400> 7

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

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

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

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

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

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

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

<210> 8
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL

<400> 8

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

34246SG2-seq1-000001

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

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

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

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

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

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

<210> 9
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL

<400> 9

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

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

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

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

34246SG2-seq1-000001

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

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

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

<210> 10
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL

<400> 10

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

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

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

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

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

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

34246SG2-seq1-000001

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

<210> 11
<211> 5
<212> PRT
<213> Homo sapiens

<400> 11

Ser Asn Tyr Ile His
1 5

<210> 12
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-H1

<400> 12

Ser Tyr Tyr Met His
1 5

<210> 13
<211> 17
<212> PRT
<213> Homo sapiens

<400> 13

Val Ile Asn Pro Arg Gly Gly Ser Thr Ala Ser Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 14
<211> 17
<212> PRT
<213> Artificial Sequence

34246SG2-seq1-000001

<220>

<223> HVR-H2

<400> 14

Val	Ile	Asn	Pro	Arg	Gly	Gly	Ser	Arg	Ala	Ser	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 15

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HVR-H2

<400> 15

Val	Ile	Asn	Pro	Arg	Gly	Gly	Ser	Arg	Arg	Ser	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 16

<211> 23

<212> PRT

<213> Homo sapiens

<400> 16

Gly	Gly	Arg	Ala	Leu	Phe	Tyr	Asp	Ser	Tyr	Thr	Thr	Pro	Arg	Asp	Gly
1				5					10					15	

Gly	Ser	Trp	Trp	Phe	Asp	Pro
					20	

<210> 17

34246SG2-seq1-000001

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

<220>
<223> HVR-H3

<400> 17

Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe Asp Gly
1 5 10 15

Gly Ser Trp Trp Phe Asp Pro
20

<210> 18
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-H3

<400> 18

Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Arg Asp Asp
1 5 10 15

Gly Ser Trp Trp Phe Asp Pro
20

<210> 19
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-H3

<400> 19

Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Arg Asp Leu
1 5 10 15

34246SG2-seq1-000001

Gly Ser Trp Trp Phe Asp Pro
20

<210> 20
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-H3

<400> 20

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

Gly Ser Trp Trp Phe Asp Pro
20

<210> 21
<211> 11
<212> PRT
<213> Homo sapiens

<400> 21

Gln Ala Ser Gln Asp Ile Arg Lys Tyr Leu Asn
1 5 10

<210> 22
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-L1

<400> 22

Gln Ala Ser Gln Asp Ile Arg Gln Tyr Leu Asn
1 5 10

34246SG2-seq1-000001

<210> 23
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVR-L1

<400> 23

Gln Ala Ser Gln Glu Ile Arg Lys Tyr Leu Asn
 1 5 10

<210> 24
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 24

Asp Ala Ser Asn Leu Lys Thr
 1 5

<210> 25
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVR-L2

<400> 25

Asp Ala Ser Asn Leu Lys Phe
 1 5

<210> 26
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVR-L2

<400> 26

Asp Ala Ser Glu Leu Lys Thr
1 5

<210> 27
<211> 9
<212> PRT
<213> Homo sapiens

<400> 27

Gln Gln Phe Asp Asp Leu Pro Ile Thr
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-L3

<400> 28

Gln Gln Phe Asp Ala Leu Pro Ile Thr
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-L3

<400> 29

Gln Gln Phe Ser Ala Leu Pro Ile Thr
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

34246SG2-seq1-000001

<220>

<223> HVR-L3

<400> 30

Gln Gln Phe Glu Asp Leu Pro Ile Thr
1 5

<210> 31

<211> 30

<212> PRT

<213> Homo sapiens

<400> 31

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

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

<210> 32

<211> 14

<212> PRT

<213> Homo sapiens

<400> 32

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 33

<211> 32

<212> PRT

<213> Homo sapiens

<400> 33

Arg Ile Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg

34246SG2-seq1-000001

20 25 30

<210> 34
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> FR-H3

<400> 34

Arg Ile Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

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

<210> 35
<211> 11
<212> PRT
<213> Homo sapiens

<400> 35

Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser
1 5 10

<210> 36
<211> 23
<212> PRT
<213> Homo sapiens

<400> 36

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

Asp Arg Val Thr Phe Thr Cys
20

<210> 37

34246SG2-seq1-000001

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

<400> 37

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 38
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 38

Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5					10					15	

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

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

<400> 39

Phe	Gly	Gln	Gly	Thr	Arg	Leu	Gln	Ile	Lys
1				5					10

<210> 40
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVR-H1

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)

<223> Xaa is Asn or Tyr

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa is Ile or Met

<400> 40

Ser Xaa Tyr Xaa His

1 5

<210> 41

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HVR-H2

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa is Thr or Arg

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa is Ala or Arg

<400> 41

Val Ile Asn Pro Arg Gly Gly Ser Xaa Xaa Ser Ala Gln Lys Phe Gln

1 5 10 15

Gly

<210> 42

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> HVR-H3

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa is Arg or Glu

<220>

<221> MISC_FEATURE

<222> (14)..(14)

<223> Xaa is Arg or Phe

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa is Gly, Asp or Leu

<400> 42

Gly	Gly	Xaa	Ala	Leu	Phe	Tyr	Asp	Ser	Tyr	Thr	Thr	Pro	Xaa	Asp	Xaa
1				5				10					15		

Gly	Ser	Trp	Trp	Phe	Asp	Pro
				20		

<210> 43

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> HVR-L1

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa is Asp or Glu

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa is Lys or Gln

<400> 43

Gln Ala Ser Gln Xaa Ile Arg Xaa Tyr Leu Asn
 1 5 10

<210> 44
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVR-L2

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa is Asn or Glu

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> Xaa is Thr or Phe

<400> 44

Asp Ala Ser Xaa Leu Lys Xaa
 1 5

<210> 45
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HVR-L3

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Xaa is Asp, Ser or Glu

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Xaa is Asp or Ala

34246SG2-seq1-000001

<400> 45

Gln Gln Phe Xaa Xaa Leu Pro Ile Thr
1 5

<210> 46

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> CH

<400> 46

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

Arg 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

34246SG2-seq1-000001

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 Glu Glu
225 230 235 240

Met 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

34246SG2-seq1-000001

Gln Lys Ser Leu Ser Leu Ser Pro
325

<210> 47
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

<400> 47

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

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

Pro Ala Pro Glu Ala Ala 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

34246SG2-seq1-000001

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 Glu Glu
 225 230 235 240

Met 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

325

<210> 48
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH

<400> 48

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

Arg 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

34246SG2-seq1-000001

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

Trp Ala Leu Pro Ala Pro Ile Ser 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 Glu Glu
225 230 235 240

Met 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
325

34246SG2-seq1-000001

<210> 49
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH

<400> 49

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

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

Pro Ala Pro Glu Leu Leu Ala 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 Glu Phe Glu Asp Pro Glu Val Lys Phe Asn Trp

34246SG2-seq1-000001

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 Thr Asn
 195 200 205
 Lys Ala Leu Pro Ala Pro Glu 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 Glu Glu
 225 230 235 240
 Met 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
 325

<210> 50

34246SG2-seq1-000001

<211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH

<400> 50

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

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

34246SG2-seql-000001

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 Thr 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 Glu Glu
225 230 235 240

Met 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
325

<210> 51
<211> 328
<212> PRT

<213> Artificial Sequence

<220>

<223> CH

<400> 51

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	

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

Pro	Ala	Pro	Glu	Ala	Ala	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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

34246SG2-seq1-000001

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

Trp Ala Leu Pro Ala Pro Ile Ser 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 Glu Glu
 225 230 235 240

Met 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
 325

<210> 52

<211> 328

<212> PRT

<213> Artificial Sequence

34246SG2-seq1-000001

<220>

<223> CH

<400> 52

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

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

Pro Ala Pro Glu Ala Ala Ala 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 Glu Phe 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

34246SG2-seq1-000001

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 Thr Asn
195 200 205

Lys Ala Leu Pro Ala Pro Glu 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 Glu Glu
225 230 235 240

Met 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
325

<210> 53
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

34246SG2-seq1-000001

<400> 53

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

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

Pro Ala Pro Glu Ala Ala 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 Glu Phe 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

34246SG2-seq1-000001

180

185

190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Thr 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 Glu Glu
225 230 235 240

Met 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
325

<210> 54
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

<400> 54

34246SG2-seq1-000001

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

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

Pro Ala Pro Glu Ala Ala 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

34246SG2-seq1-000001

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

Ala Ala Leu Pro Ala Pro Ile Ser 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 Glu Glu
225 230 235 240

Met 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
325

<210> 55
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

<400> 55

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

34246SG2-seq1-000001

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
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys	85	90	95
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys	100	105	110
Pro Ala Pro Glu Ala Ala 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
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			

34246SG2-seq1-000001

195

200

205

Asp Ala Leu Pro Ala Pro Ile Ser 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 Glu Glu
225 230 235 240

Met 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
325

<210> 56
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

<400> 56

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

34246SG2-seq1-000001

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

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

Pro Ala Pro Glu Ala Ala 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

34246SG2-seq1-000001

Glu Ala Leu Pro Ala Pro Ile Ser 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 Glu Glu
225 230 235 240

Met 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
325

<210> 57
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

<400> 57

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

34246SG2-seq1-000001

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

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

Pro Ala Pro Glu Ala Ala 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

Met Ala Leu Pro Ala Pro Ile Ser Lys Thr Ile Ser Lys Ala Lys Gly

34246SG2-seq1-000001

210

215

220

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

Met 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
325

<210> 58

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> CH

<400> 58

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

34246SG2-seq1-000001

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

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

Pro Ala Pro Glu Ala Ala 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

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

34246SG2-seq1-000001

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

Met 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 Leu His Glu Ala Leu His Ala His Thr Thr
305 310 315 320

Arg Lys Glu Leu Ser Leu Ser Pro
325

<210> 59
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

<400> 59

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

34246SG2-seq1-000001

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

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

Pro Ala Pro Glu Ala Ala 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

Ala Ala Leu Pro Ala Pro Ile Ser 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 Glu Glu

34246SG2-seq1-000001

225 230 235 240

Met	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	Leu	His	Glu	Ala	Leu	His	Ala	His	Tyr	Thr
305					310					315					320

Arg Lys Glu Leu Ser Leu Ser Pro
325

<210>	60
<211>	107
<212>	PRT
<213>	Artificial Sequence

$\langle 220 \rangle$
 $\langle 223 \rangle$ CL

<400> 60

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

34246SG2-seq1-000001

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> 61
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> DENV

<400> 61

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

Phe His Leu Thr Thr Arg Gly Gly Glu Pro His Met Ile Val Ser Lys
20 25 30

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

Met Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr
50 55 60

Met Thr Tyr Lys Cys Pro Arg Ile Thr Glu Ala Glu Pro Asp Asp Val
65 70 75 80

Asp Cys Trp Cys Asn Ala Thr Asp Thr Trp Val Thr Tyr Gly Thr Cys

34246SG2-seq1-000001

85

90

95

Ser Gln Thr Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala
 100 105 110

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

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

Arg His Pro Gly Phe Thr Val Ile Ala Leu Phe Leu Ala His Ala Ile
 145 150 155 160

Gly Thr Ser Ile Thr Gln Lys Gly Ile Ile Phe Ile Leu Leu Met Leu
 165 170 175

Val Thr Pro Ser Met Ala Met Arg Cys Val Gly Ile Gly Asn Arg Asp
 180 185 190

Phe Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu
 195 200 205

His Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp
 210 215 220

Ile Glu Leu Leu Lys Thr Glu Val Thr Asn Pro Ala Val Leu Arg Lys
 225 230 235 240

Leu Cys Ile Glu Ala Lys Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys
 245 250 255

Pro Thr Gln Gly Glu Ala Thr Leu Val Glu Glu Gln Asp Ala Asn Phe
 260 265 270

Val Cys Arg Arg Thr Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly

34246SG2-seq1-000001

275

280

285

Leu Phe Gly Lys Gly Ser Leu Leu Thr Cys Ala Lys Phe Lys Cys Val
 290 295 300

Thr Lys Leu Glu Gly Lys Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser
 305 310 315 320

Val Ile Val Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu
 325 330 335

Thr Thr Glu His Gly Thr Ile Ala Thr Ile Thr Pro Gln Ala Pro Thr
 340 345 350

Ser Glu Ile Gln Leu Thr Asp Tyr Gly Thr Leu Thr Leu Asp Cys Ser
 355 360 365

Pro Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Thr Met Lys
 370 375 380

Glu Lys Ser Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu
 385 390 395 400

Pro Trp Thr Ser Gly Ala Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln
 405 410 415

Asp Leu Leu Val Thr Phe Lys Thr Ala His Ala Lys Lys Gln Glu Val
 420 425 430

Val Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly
 435 440 445

Ala Thr Glu Ile Gln Thr Ser Gly Thr Thr Thr Ile Phe Ala Gly His
 450 455 460

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Thr Leu Lys Gly Met Ser

465 470 475 480

Tyr Val Met Cys Thr Gly Ser Phe Lys Leu Glu Lys Glu Val Ala Glu
485 490 495

Thr Gln His Gly Thr Val Leu Val Gln Val Lys Tyr Glu Gly Thr Asp
500 505 510

Ala Pro Cys Lys Ile Pro Phe Ser Thr Gln Asp Glu Lys Gly Val Thr
515 520 525

Gln Asn Gly Arg Leu Ile Thr Ala Asn Pro Ile Val Thr Asp Lys Glu
530 535 540

Lys Pro Val Asn Ile Glu Thr Glu Pro Pro Phe Gly Glu Ser Tyr Ile
545 550 555 560

Ile Val Gly Ala Gly Glu Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys
565 570 575

Gly His His His His His His His
580 585

$\langle 210 \rangle$	62
$\langle 211 \rangle$	585
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> DENV

<400> 62

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

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

34246SG2-seq1-000001

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

Met Cys Thr Leu Met Ala Met Asp Leu Gly Glu Leu Cys Glu Asp Thr
50 55 60

Ile Thr Tyr Lys Cys Pro Phe Leu Arg Gln Asn Glu Pro Glu Asp Ile
65 70 75 80

Asp Cys Trp Cys Asn Ser Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys
85 90 95

Thr Thr Thr Gly Glu His Arg Arg Glu Lys Arg Ser Val Ala Leu Val
100 105 110

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

Ser Glu Gly Ala Trp Lys His Ala Gln Arg Ile Glu Thr Trp Ile Leu
130 135 140

Arg His Pro Gly Phe Thr Ile Met Ala Ala Ile Leu Ala Tyr Thr Ile
145 150 155 160

Gly Thr Thr His Phe Gln Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala
165 170 175

Val Ala Pro Ser Met Thr Met Arg Cys Ile Gly Ile Ser Asn Arg Asp
180 185 190

Phe Val Glu Gly Val Ser Gly Gly Ser Trp Val Asp Ile Val Leu Glu
195 200 205

His Gly Ser Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp
210 215 220

34246SG2-seq1-000001

Phe Glu Leu Ile Lys Thr Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys
225 230 235 240

Tyr Cys Ile Glu Ala Lys Leu Thr Asn Thr Thr Thr Asp Ser Arg Cys
245 250 255

Pro Thr Gln Gly Glu Pro Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe
260 265 270

Val Cys Lys His Ser Met Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
275 280 285

Leu Phe Gly Lys Gly Gly Ile Val Thr Cys Ala Met Phe Thr Cys Lys
290 295 300

Lys Asn Met Lys Gly Lys Val Val Gln Pro Glu Asn Leu Glu Tyr Thr
305 310 315 320

Ile Val Ile Thr Pro His Ser Gly Glu Glu His Ala Val Gly Asn Asp
325 330 335

Thr Gly Lys His Gly Lys Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile
340 345 350

Thr Glu Ala Glu Leu Thr Gly Tyr Gly Thr Val Thr Met Glu Cys Ser
355 360 365

Pro Arg Thr Gly Leu Asp Phe Asn Glu Met Val Leu Leu Gln Met Glu
370 375 380

Asn Lys Ala Trp Leu Val His Arg Gln Trp Phe Leu Asp Leu Pro Leu
385 390 395 400

Pro Trp Leu Pro Gly Ala Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys
405 410 415

34246SG2-seq1-000001

Glu Thr Leu Val Thr Phe Lys Asn Pro His Ala Lys Lys Gln Asp Val
420 425 430

Val Val Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly
435 440 445

Ala Thr Glu Ile Gln Met Ser Ser Gly Asn Leu Leu Phe Thr Gly His
450 455 460

Leu Lys Cys Arg Leu Arg Met Asp Lys Leu Gln Leu Lys Gly Met Ser
465 470 475 480

Tyr Ser Met Cys Thr Gly Lys Phe Lys Val Val Lys Glu Ile Ala Glu
485 490 495

Thr Gln His Gly Thr Ile Val Ile Arg Val Gln Tyr Glu Gly Asp Gly
500 505 510

Ser Pro Cys Lys Ile Pro Phe Glu Ile Met Asp Leu Glu Lys Arg His
515 520 525

Val Leu Gly Arg Leu Ile Thr Val Asn Pro Ile Val Thr Glu Lys Asp
530 535 540

Ser Pro Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile
545 550 555 560

Ile Ile Gly Val Glu Pro Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys
565 570 575

Gly His His His His His His His
580 585

<210> 63
<211> 583
<212> PRT

<213> Artificial Sequence

<220>

<223> DENV

<400> 63

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
 1 5 10 15

Phe His Leu Thr Ser Arg Asp Gly Glu Pro Arg Met Ile Val Gly Lys
 20 25 30

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

Met Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Asp Asp Thr
 50 55 60

Val Thr Tyr Lys Cys Pro His Ile Thr Glu Val Glu Pro Glu Asp Ile
 65 70 75 80

Asp Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys
 85 90 95

Asn Gln Ala Gly Glu His Arg Arg Asp Lys Arg Ser Val Ala Leu Ala
 100 105 110

Pro His Val Gly Met Gly Leu Asp Thr Arg Thr Gln Thr Trp Met Ser
 115 120 125

Ala Glu Gly Ala Trp Arg Gln Val Glu Lys Val Glu Thr Trp Ala Leu
 130 135 140

Arg His Pro Gly Phe Thr Ile Leu Ala Leu Phe Leu Ala His Tyr Ile
 145 150 155 160

Gly Thr Ser Leu Thr Gln Lys Val Val Ile Phe Ile Leu Leu Met Leu

34246SG2-seq1-000001

165

170

175

Val Thr Pro Ser Met Thr Met Arg Cys Val Gly Val Gly Asn Arg Asp
 180 185 190

Phe Val Glu Gly Leu Ser Gly Ala Thr Trp Val Asp Val Val Leu Glu
 195 200 205

His Gly Gly Cys Val Thr Thr Met Ala Lys Asn Lys Pro Thr Leu Asp
 210 215 220

Ile Glu Leu Gln Lys Thr Glu Ala Thr Gln Leu Ala Thr Leu Arg Lys
 225 230 235 240

Leu Cys Ile Glu Gly Lys Ile Thr Asn Ile Thr Thr Asp Ser Arg Cys
 245 250 255

Pro Thr Gln Gly Glu Ala Ile Leu Pro Glu Glu Gln Asp Gln Asn Tyr
 260 265 270

Val Cys Lys His Thr Tyr Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
 275 280 285

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

Glu Ser Ile Glu Gly Lys Val Val Gln His Glu Asn Leu Lys Tyr Thr
 305 310 315 320

Val Ile Ile Thr Val His Thr Gly Asp Gln His Gln Val Gly Asn Glu
 325 330 335

Thr Gln Gly Val Thr Ala Glu Ile Thr Ser Gln Ala Ser Thr Ala Glu
 340 345 350

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

34246SG2-seq1-000001

355

360

365

Thr Gly Leu Asp Phe Asn Glu Met Ile Leu Leu Thr Met Lys Asn Lys
 370 375 380

Ala Trp Met Val His Arg Gln Trp Phe Phe Asp Leu Pro Leu Pro Trp
 385 390 395 400

Thr Ser Gly Ala Thr Thr Lys Thr Pro Thr Trp Asn Arg Lys Glu Leu
 405 410 415

Leu Val Thr Phe Lys Asn Ala His Ala Lys Lys Gln Glu Val Val Val
 420 425 430

Leu Gly Ser Gln Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr
 435 440 445

Glu Ile Gln Thr Ser Gly Gly Thr Ser Ile Phe Ala Gly His Leu Lys
 450 455 460

Cys Arg Leu Lys Met Asp Lys Leu Lys Leu Lys Gly Met Ser Tyr Ala
 465 470 475 480

Met Cys Leu Asn Thr Phe Val Leu Lys Lys Glu Val Ser Glu Thr Gln
 485 490 495

His Gly Thr Ile Leu Ile Lys Val Glu Tyr Lys Gly Glu Asp Ala Pro
 500 505 510

Cys Lys Ile Pro Phe Ser Thr Glu Asp Gly Gln Gly Lys Ala His Asn
 515 520 525

Gly Arg Leu Ile Thr Ala Asn Pro Val Val Thr Lys Lys Glu Glu Pro
 530 535 540

Val Asn Ile Glu Ala Glu Pro Pro Phe Gly Glu Ser Asn Ile Val Ile

34246SG2-seq1-000001

545 550 555 560

Gly Ile Gly Asp Lys Ala Leu Lys Ile Asn Trp Tyr Arg Lys Gly His
565 570 575

His His His His His His His
580

$\langle 210 \rangle$	64
$\langle 211 \rangle$	585
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> DENV

<400> 64

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

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

His Glu Arg Gly Arg Pro Leu Leu Phe Lys Thr Thr Glu Gly Ile Asn
35 40 45

Lys Cys Thr Leu Ile Ala Met Asp Leu Gly Glu Met Cys Glu Asp Thr
50 55 60

Val	Thr	Tyr	Lys	Cys	Pro	Leu	Leu	Val	Asn	Thr	Glu	Pro	Glu	Asp	Ile
65					70					75					80

Asp Cys Trp Cys Asn Leu Thr Ser Thr Trp Val Met Tyr Gly Thr Cys
85 90 95

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

34246SG2-seq1-000001

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

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

Arg Asn Pro Gly Phe Ala Leu Leu Ala Gly Phe Met Ala Tyr Met Ile
145 150 155 160

Gly Gln Thr Gly Ile Gln Arg Thr Val Phe Phe Val Leu Met Met Leu
165 170 175

Val Ala Pro Ser Tyr Gly Met Arg Cys Val Gly Val Gly Asn Arg Asp
180 185 190

Phe Val Glu Gly Val Ser Gly Gly Ala Trp Val Asp Leu Val Leu Glu
195 200 205

His Gly Gly Cys Val Thr Thr Met Ala Gln Gly Lys Pro Thr Leu Asp
210 215 220

Phe Glu Leu Thr Lys Thr Thr Ala Lys Glu Val Ala Leu Leu Arg Thr
225 230 235 240

Tyr Cys Ile Glu Ala Ser Ile Ser Asn Ile Thr Thr Ala Thr Arg Cys
245 250 255

Pro Thr Gln Gly Glu Pro Tyr Leu Lys Glu Glu Gln Asp Gln Gln Tyr
260 265 270

Ile Cys Arg Arg Asp Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
275 280 285

Leu Phe Gly Lys Gly Gly Val Val Thr Cys Ala Lys Phe Ser Cys Ser
290 295 300

34246SG2-seq1-000001

Gly Lys Ile Thr Gly Asn Leu Val Gln Ile Glu Asn Leu Glu Tyr Thr
305 310 315 320

Val Val Val Thr Val His Asn Gly Asp Thr His Ala Val Gly Asn Asp
325 330 335

Thr Ser Asn His Gly Val Thr Ala Met Ile Thr Pro Arg Ser Pro Ser
340 345 350

Val Glu Val Lys Leu Pro Asp Tyr Gly Glu Leu Thr Leu Asp Cys Glu
355 360 365

Pro Arg Ser Gly Ile Asp Phe Asn Glu Met Ile Leu Met Lys Met Lys
370 375 380

Lys Lys Thr Trp Leu Val His Lys Gln Trp Phe Leu Asp Leu Pro Leu
385 390 395 400

Pro Trp Thr Ala Gly Ala Asp Thr Ser Glu Val His Trp Asn Tyr Lys
405 410 415

Glu Arg Met Val Thr Phe Lys Val Pro His Ala Lys Arg Gln Asp Val
420 425 430

Thr Val Leu Gly Ser Gln Glu Gly Ala Met His Ser Ala Leu Ala Gly
435 440 445

Ala Thr Glu Val Asp Ser Gly Asp Gly Asn His Met Phe Ala Gly His
450 455 460

Leu Lys Cys Lys Val Arg Met Glu Lys Leu Arg Ile Lys Gly Met Ser
465 470 475 480

Tyr Thr Met Cys Ser Gly Lys Phe Ser Ile Asp Lys Glu Met Ala Glu
485 490 495

34246SG2-seq1-000001

Thr Gln His Gly Thr Thr Val Val Lys Val Lys Tyr Glu Gly Ala Gly
500 505 510

Ala Pro Cys Lys Val Pro Ile Glu Ile Arg Asp Val Asn Lys Glu Lys
515 520 525

Val Val Gly Arg Ile Ile Ser Ser Thr Pro Leu Ala Glu Asn Thr Asn
530 535 540

Ser Val Thr Asn Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile
545 550 555 560

Val Ile Gly Val Gly Asn Ser Ala Leu Thr Leu His Trp Phe Arg Lys
565 570 575

Gly His His His His His His His His
580 585

<210> 65
<211> 403
<212> PRT
<213> Artificial Sequence

<220>
<223> DENV

<400> 65

Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe Val Glu Gly Leu Ser
1 5 10 15

Gly Ala Thr Trp Val Asp Val Val Leu Glu His Gly Ser Cys Val Thr
20 25 30

Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Ile Glu Leu Leu Lys Thr
35 40 45

Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu Cys Ile Glu Ala Lys

34246SG2-seq1-000001

50

55

60

Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

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

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Leu Thr Cys Ala Lys Phe Lys Cys Val Thr Lys Leu Glu Gly Lys
115 120 125

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

Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr Thr Glu His Gly Thr
145 150 155 160

Ile Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser Glu Ile Gln Leu Thr
165 170 175

Asp Tyr Gly Thr Leu Thr Leu Asp Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

Phe Asn Glu Met Val Leu Leu Thr Met Lys Glu Lys Ser Trp Leu Val
195 200 205

His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Thr Ser Gly Ala
210 215 220

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

Lys Thr Ala His Ala Lys Lys Gln Glu Val Val Val Leu Gly Ser Gln

34246SG2-seq1-000001

245

250

255

Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Thr
260 265 270

Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu Lys Cys Arg Leu Lys
275 280 285

Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr Val Met Cys Thr Gly
290 295 300

Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr Gln His Gly Thr Val
305 310 315 320

Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala Pro Cys Lys Ile Pro
325 330 335

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

Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys Pro Val Asn Ile Glu
355 360 365

Thr Glu Pro Pro Phe Gly Glu Ser Tyr Ile Ile Val Gly Ala Gly Glu
370 375 380

Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly His His His His His
385 390 395 400

His His His

<210> 66

<211> 403

<212> PRT

<213> Artificial Sequence

34246SG2-seq1-000001

<220>

<223> DENV

<400> 66

Met Arg Cys Ile Gly Ile Ser Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

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

Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr
35 40 45

Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys
50 55 60

Leu Thr Asn Thr Thr Thr Asp Ser Arg Cys Pro Thr Gln Gly Glu Pro
65 70 75 80

Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly
100 105 110

Ile Val Thr Cys Ala Met Phe Thr Cys Lys Lys Asn Met Lys Gly Lys
115 120 125

Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His
130 135 140

Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys
145 150 155 160

Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr
165 170 175

34246SG2-seq1-000001

Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val
195 200 205

His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala
210 215 220

Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe
225 230 235 240

Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln
245 250 255

Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met
260 265 270

Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg
275 280 285

Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly
290 295 300

Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile
305 310 315 320

Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro
325 330 335

Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile
340 345 350

Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu
355 360 365

34246SG2-seq1-000001

Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro
370 375 380

Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly His His His His His
385 390 395 400

His His His

<210> 67
<211> 401
<212> PRT
<213> Artificial Sequence

<220>
<223> DENV

<400> 67

Met Arg Cys Val Gly Val Gly Asn Arg Asp Phe Val Glu Gly Leu Ser
1 5 10 15

Gly Ala Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Ile Glu Leu Gln Lys Thr
35 40 45

Glu Ala Thr Gln Leu Ala Thr Leu Arg Lys Leu Cys Ile Glu Gly Lys
50 55 60

Ile Thr Asn Ile Thr Thr Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Ile Leu Pro Glu Glu Gln Asp Gln Asn Tyr Val Cys Lys His Thr Tyr
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser

34246SG2-seq1-000001

100

105

110

Leu Val Thr Cys Ala Lys Phe Gln Cys Leu Glu Ser Ile Glu Gly Lys
 115 120 125

Val Val Gln His Glu Asn Leu Lys Tyr Thr Val Ile Ile Thr Val His
 130 135 140

Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr Gln Gly Val Thr Ala
 145 150 155 160

Glu Ile Thr Ser Gln Ala Ser Thr Ala Glu Ala Ile Leu Pro Glu Tyr
 165 170 175

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

Glu Met Ile Leu Leu Thr Met Lys Asn Lys Ala Trp Met Val His Arg
 195 200 205

Gln Trp Phe Phe Asp Leu Pro Leu Pro Trp Thr Ser Gly Ala Thr Thr
 210 215 220

Lys Thr Pro Thr Trp Asn Arg Lys Glu Leu Leu Val Thr Phe Lys Asn
 225 230 235 240

Ala His Ala Lys Lys Gln Glu Val Val Val Leu Gly Ser Gln Glu Gly
 245 250 255

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Thr Ser Gly
 260 265 270

Gly Thr Ser Ile Phe Ala Gly His Leu Lys Cys Arg Leu Lys Met Asp
 275 280 285

Lys Leu Lys Leu Lys Gly Met Ser Tyr Ala Met Cys Leu Asn Thr Phe

34246SG2-seq1-000001

290

295

300

Val Leu Lys Lys Glu Val Ser Glu Thr Gln His Gly Thr Ile Leu Ile
305 310 315 320

Lys Val Glu Tyr Lys Gly Glu Asp Ala Pro Cys Lys Ile Pro Phe Ser
325 330 335

Thr Glu Asp Gly Gln Gly Lys Ala His Asn Gly Arg Leu Ile Thr Ala
340 345 350

Asn Pro Val Val Thr Lys Lys Glu Glu Pro Val Asn Ile Glu Ala Glu
355 360 365

Pro Pro Phe Gly Glu Ser Asn Ile Val Ile Gly Ile Gly Asp Lys Ala
370 375 380

Leu Lys Ile Asn Trp Tyr Arg Lys Gly His His His His His His His
385 390 395 400

His

<210> 68

<211> 403

<212> PRT

<213> Artificial Sequence

<220>

<223> DENV

<400> 68

Met Arg Cys Val Gly Val Gly Asn Arg Asp Phe Val Glu Gly Val Ser
1 5 10 15

Gly Gly Ala Trp Val Asp Leu Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

34246SG2-seq1-000001

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

34246SG2-seq1-000001

Asp Thr Ser Glu Val His Trp Asn Tyr Lys Glu Arg Met Val Thr Phe
225 230 235 240

Lys Val Pro His Ala Lys Arg Gln Asp Val Thr Val Leu Gly Ser Gln
245 250 255

Glu Gly Ala Met His Ser Ala Leu Ala Gly Ala Thr Glu Val Asp Ser
260 265 270

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

Met Glu Lys Leu Arg Ile Lys Gly Met Ser Tyr Thr Met Cys Ser Gly
290 295 300

Lys Phe Ser Ile Asp Lys Glu Met Ala Glu Thr Gln His Gly Thr Thr
305 310 315 320

Val Val Lys Val Lys Tyr Glu Gly Ala Gly Ala Pro Cys Lys Val Pro
325 330 335

Ile Glu Ile Arg Asp Val Asn Lys Glu Lys Val Val Gly Arg Ile Ile
340 345 350

Ser Ser Thr Pro Leu Ala Glu Asn Thr Asn Ser Val Thr Asn Ile Glu
355 360 365

Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asn
370 375 380

Ser Ala Leu Thr Leu His Trp Phe Arg Lys Gly His His His His His
385 390 395 400

His His His

34246SG2-seq1-000001

<210> 69
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 69

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

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser
 20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
 35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
 50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
 65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
 85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
 100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
 115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
 130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
 145 150 155 160

34246SG2-seq1-000001

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
165 170 175

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

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
260 265 270

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

Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu
290 295 300

Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys
305 310 315 320

Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys
325 330 335

Val Ile Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys
340 345 350

34246SG2-seq1-000001

Cys Gln Glu Gln Lys Glu Glu Gln Leu Gln Glu Gly Val His Arg Lys
 355 360 365

Glu Pro Gln Gly Ala Thr
 370

<210> 70
 <211> 316
 <212> PRT
 <213> Homo sapiens
 <400> 70

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

Trp Leu Leu Gln Pro Leu Thr Val Leu Leu Leu Leu Ala Ser Ala Asp
 20 25 30

Ser Gln Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp
 35 40 45

Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala
 50 55 60

Arg Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu
 65 70 75 80

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn
 85 90 95

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp
 100 105 110

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro
 115 120 125

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser

34246SG2-seq1-000001

130

135

140

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys
 145 150 155 160

Ser Gln Lys Phe Ser His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala
 165 170 175

Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr
 180 185 190

Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser
 195 200 205

Met Gly Ser Ser Ser Pro Met Gly Val Ile Val Ala Val Val Ile Ala
 210 215 220

Thr Ala Val Ala Ala Ile Val Ala Ala Val Val Ala Leu Ile Tyr Cys
 225 230 235 240

Arg Lys Lys Arg Ile Ser Ala Asn Ser Thr Asp Pro Val Lys Ala Ala
 245 250 255

Gln Phe Glu Pro Pro Gly Arg Gln Met Ile Ala Ile Arg Lys Arg Gln
 260 265 270

Leu Glu Glu Thr Asn Asn Asp Tyr Glu Thr Ala Asp Gly Gly Tyr Met
 275 280 285

Thr Leu Asn Pro Arg Ala Pro Thr Asp Asp Asp Lys Asn Ile Tyr Leu
 290 295 300

Thr Leu Pro Pro Asn Asp His Val Asn Ser Asn Asn
 305 310 315

<210> 71

34246SG2-seq1-000001

<211> 316

<212> PRT

<213> Homo sapiens

<400> 71

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

Trp Leu Leu Gln Pro Leu Thr Val Leu Leu Leu Ala Ser Ala Asp
20 25 30

Ser Gln Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp
35 40 45

Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala
50 55 60

Arg Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu
65 70 75 80

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn
85 90 95

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp
100 105 110

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro
115 120 125

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser
130 135 140

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys
145 150 155 160

Ser Gln Lys Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala
165 170 175

34246SG2-seq1-000001

Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr
180 185 190

Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser
195 200 205

Met Gly Ser Ser Ser Pro Met Gly Val Ile Val Ala Val Val Ile Ala
210 215 220

Thr Ala Val Ala Ala Ile Val Ala Ala Val Val Ala Leu Ile Tyr Cys
225 230 235 240

Arg Lys Lys Arg Ile Ser Ala Asn Ser Thr Asp Pro Val Lys Ala Ala
245 250 255

Gln Phe Glu Pro Pro Gly Arg Gln Met Ile Ala Ile Arg Lys Arg Gln
260 265 270

Leu Glu Glu Thr Asn Asn Asp Tyr Glu Thr Ala Asp Gly Gly Tyr Met
275 280 285

Thr Leu Asn Pro Arg Ala Pro Thr Asp Asp Asp Lys Asn Ile Tyr Leu
290 295 300

Thr Leu Pro Pro Asn Asp His Val Asn Ser Asn Asn
305 310 315

<210> 72
<211> 291
<212> PRT
<213> Homo sapiens

<400> 72

Met Gly Ile Leu Ser Phe Leu Pro Val Leu Ala Thr Glu Ser Asp Trp
1 5 10 15

34246SG2-seq1-000001

Ala Asp Cys Lys Ser Pro Gln Pro Trp Gly His Met Leu Leu Trp Thr
20 25 30

Ala Val Leu Phe Leu Ala Pro Val Ala Gly Thr Pro Ala Ala Pro Pro
35 40 45

Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val Leu Gln Glu
50 55 60

Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro Glu Ser Asp
65 70 75 80

Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr His Thr Gln
85 90 95

Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly Glu Tyr Thr
100 105 110

Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His Leu Thr Val
115 120 125

Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln Glu
130 135 140

Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp Lys Pro Leu
145 150 155 160

Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys Phe Ser Arg
165 170 175

Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser His Ser Gly
180 185 190

Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr Ser Ser Lys
195 200 205

34246SG2-seq1-000001

Pro Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Gly Ile
210 215 220

Ile Val Ala Val Val Thr Gly Ile Ala Val Ala Ala Ile Val Ala Ala
225 230 235 240

Val Val Ala Leu Ile Tyr Cys Arg Lys Lys Arg Ile Ser Ala Asn Pro
245 250 255

Thr Asn Pro Asp Glu Ala Asp Lys Val Gly Ala Glu Asn Thr Ile Thr
260 265 270

Tyr Ser Leu Leu Met His Pro Asp Ala Leu Glu Glu Pro Asp Asp Gln
275 280 285

Asn Arg Ile
290

<210> 73
<211> 254
<212> PRT
<213> Homo sapiens

<400> 73

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

34246SG2-seq1-000001

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

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

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly Leu Ser Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
245 250

34246SG2-seq1-000001

<210> 74
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 74

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Val Ser Ala
 1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

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

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

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val

34246SG2-seq1-000001

165

170

175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly Leu Ser Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
245 250

<210> 75
<211> 233
<212> PRT
<213> Homo sapiens

<400> 75

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

Asn Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65 70 75 80

34246SG2-seql-000001

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

Ser Asp Pro Val Gln Leu Glu Val His Val Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Asp Arg Lys Tyr Phe His His Asn Ser Asp Phe His Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Ser Pro Pro Gly Tyr Gln
195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile
225 230

<210> 76
<211> 233
<212> PRT
<213> Homo sapiens

<400> 76

34246SG2-seq1-000001

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
20 25 30

Gln Trp Tyr Ser Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

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

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

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Asp Arg Lys Tyr Phe His His Asn Ser Asp Phe His Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

34246SG2-seq1-000001

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Ser Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
 210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile
 225 230

<210> 77
 <211> 404
 <212> PRT
 <213> Mus musculus

<400> 77

Met Ile Leu Thr Ser Phe Gly Asp Asp Met Trp Leu Leu Thr Thr Leu
 1 5 10 15

Leu Leu Trp Val Pro Val Gly Gly Glu Val Val Asn Ala Thr Lys Ala
 20 25 30

Val Ile Thr Leu Gln Pro Pro Trp Val Ser Ile Phe Gln Lys Glu Asn
 35 40 45

Val Thr Leu Trp Cys Glu Gly Pro His Leu Pro Gly Asp Ser Ser Thr
 50 55 60

Gln Trp Phe Ile Asn Gly Thr Ala Val Gln Ile Ser Thr Pro Ser Tyr
 65 70 75 80

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

Ile Gly Ser Ser Met Pro Ser Asp Pro Val Gln Leu Gln Ile His Asn
 100 105 110

34246SG2-seq1-000001

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

Pro Leu Ala Leu Arg Cys His Gly Trp Lys Asn Lys Leu Val Tyr Asn
130 135 140

Val Val Phe Tyr Arg Asn Gly Lys Ser Phe Gln Phe Ser Ser Asp Ser
145 150 155 160

Glu Val Ala Ile Leu Lys Thr Asn Leu Ser His Ser Gly Ile Tyr His
165 170 175

Cys Ser Gly Thr Gly Arg His Arg Tyr Thr Ser Ala Gly Val Ser Ile
180 185 190

Thr Val Lys Glu Leu Phe Thr Thr Pro Val Leu Arg Ala Ser Val Ser
195 200 205

Ser Pro Phe Pro Glu Gly Ser Leu Val Thr Leu Asn Cys Glu Thr Asn
210 215 220

Leu Leu Leu Gln Arg Pro Gly Leu Gln Leu His Phe Ser Phe Tyr Val
225 230 235 240

Gly Ser Lys Ile Leu Glu Tyr Arg Asn Thr Ser Ser Glu Tyr His Ile
245 250 255

Ala Arg Ala Glu Arg Glu Asp Ala Gly Phe Tyr Trp Cys Glu Val Ala
260 265 270

Thr Glu Asp Ser Ser Val Leu Lys Arg Ser Pro Glu Leu Glu Leu Gln
275 280 285

Val Leu Gly Pro Gln Ser Ser Ala Pro Val Trp Phe His Ile Leu Phe
290 295 300

34246SG2-seq1-000001

Tyr Leu Ser Val Gly Ile Met Phe Ser Leu Asn Thr Val Leu Tyr Val
305 310 315 320

Lys Ile His Arg Leu Gln Arg Glu Lys Lys Tyr Asn Leu Glu Val Pro
325 330 335

Leu Val Ser Glu Gln Gly Lys Lys Ala Asn Ser Phe Gln Gln Val Arg
340 345 350

Ser Asp Gly Val Tyr Glu Glu Val Thr Ala Thr Ala Ser Gln Thr Thr
355 360 365

Pro Lys Glu Ala Pro Asp Gly Pro Arg Ser Ser Val Gly Asp Cys Gly
370 375 380

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

Thr Ser Gln Ser

<210> 78
<211> 293
<212> PRT
<213> Mus musculus

<400> 78

Met Gly Ile Leu Pro Phe Leu Leu Ile Pro Met Glu Ser Asn Trp Thr
1 5 10 15

Val His Val Phe Ser Arg Thr Leu Cys His Met Leu Leu Trp Thr Ala
20 25 30

Val Leu Asn Leu Ala Ala Gly Thr His Asp Leu Pro Lys Ala Val Val
35 40 45

Lys Leu Glu Pro Pro Trp Ile Gln Val Leu Lys Glu Asp Thr Val Thr

34246SG2-seq1-000001

50

55

60

Leu Thr Cys Glu Gly Thr His Asn Pro Gly Asn Ser Ser Thr Gln Trp
 65 70 75 80

Phe His Asn Gly Arg Ser Ile Arg Ser Gln Val Gln Ala Ser Tyr Thr
 85 90 95

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

Gln Thr Arg Leu Ser Asp Pro Val Asp Leu Gly Val Ile Ser Asp Trp
 115 120 125

Leu Leu Leu Gln Thr Pro Gln Leu Val Phe Leu Glu Gly Glu Thr Ile
 130 135 140

Thr Leu Arg Cys His Ser Trp Arg Asn Lys Leu Leu Asn Arg Ile Ser
 145 150 155 160

Phe Phe His Asn Glu Lys Ser Val Arg Tyr His His Tyr Ser Ser Asn
 165 170 175

Phe Ser Ile Pro Lys Ala Asn His Ser His Ser Gly Asp Tyr Tyr Cys
 180 185 190

Lys Gly Ser Leu Gly Arg Thr Leu His Gln Ser Lys Pro Val Thr Ile
 195 200 205

Thr Val Gln Gly Pro Lys Ser Ser Arg Ser Leu Pro Val Leu Thr Ile
 210 215 220

Val Ala Ala Val Thr Gly Ile Ala Val Ala Ala Ile Val Ile Ile Leu
 225 230 235 240

Val Ser Leu Val Tyr Leu Lys Lys Lys Gln Val Pro Asp Asn Pro Pro

34246SG2-seq1-000001

245

250

255

Asp Leu Glu Glu Ala Ala Lys Thr Glu Ala Glu Asn Thr Ile Thr Tyr
 260 265 270

Ser Leu Leu Lys His Pro Glu Ala Leu Asp Glu Glu Thr Glu His Asp
 275 280 285

Tyr Gln Asn His Ile
 290

<210> 79
 <211> 267
 <212> PRT
 <213> Mus musculus

<400> 79

Met Thr Leu Asp Thr Gln Met Phe Gln Asn Ala His Ser Gly Ser Gln
 1 5 10 15

Trp Leu Leu Pro Pro Leu Thr Ile Leu Leu Leu Phe Ala Phe Ala Asp
 20 25 30

Arg Gln Ser Ala Ala Leu Pro Lys Ala Val Val Lys Leu Asp Pro Pro
 35 40 45

Trp Ile Gln Val Leu Lys Glu Asp Met Val Thr Leu Met Cys Glu Gly
 50 55 60

Thr His Asn Pro Gly Asn Ser Ser Thr Gln Trp Phe His Asn Trp Ser
 65 70 75 80

Ser Ile Arg Ser Gln Val Gln Ser Ser Tyr Thr Phe Lys Ala Thr Val
 85 90 95

Asn Asp Ser Gly Glu Tyr Arg Cys Gln Met Glu Gln Thr Arg Leu Ser
 100 105 110

34246SG2-seql-000001

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

Pro Gln Arg Val Phe Leu Glu Gly Glu Thr Ile Thr Leu Arg Cys His
 130 135 140

Ser Trp Arg Asn Lys Leu Leu Asn Arg Ile Ser Phe Phe His Asn Glu
 145 150 155 160

Lys Ser Val Arg Tyr His His Tyr Lys Ser Asn Phe Ser Ile Pro Lys
 165 170 175

Ala Asn His Ser His Ser Gly Asp Tyr Tyr Cys Lys Gly Ser Leu Gly
 180 185 190

Ser Thr Gln His Gln Ser Lys Pro Val Thr Ile Thr Val Gln Asp Pro
 195 200 205

Ala Thr Thr Ser Ser Ile Ser Leu Val Trp Tyr His Thr Ala Phe Ser
 210 215 220

Leu Val Met Cys Leu Leu Phe Ala Val Asp Thr Gly Leu Tyr Phe Tyr
 225 230 235 240

Val Arg Arg Asn Leu Gln Thr Pro Arg Asp Tyr Trp Arg Lys Ser Leu
 245 250 255

Ser Ile Arg Lys His Gln Ala Pro Gln Asp Lys
 260 265

<210> 80
 <211> 249
 <212> PRT
 <213> Mus musculus

<400> 80

34246SG2-seq1-000001

Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Val Leu Thr Ala Phe Ser
1 5 10 15

Gly Ile Gln Ala Gly Leu Gln Lys Ala Val Val Asn Leu Asp Pro Lys
20 25 30

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

Thr Phe Ser Pro Glu Asp Asn Ser Ile Lys Trp Phe His Asn Glu Ser
50 55 60

Leu Ile Pro His Gln Asp Ala Asn Tyr Val Ile Gln Ser Ala Arg Val
65 70 75 80

Lys Asp Ser Gly Met Tyr Arg Cys Gln Thr Ala Leu Ser Thr Ile Ser
85 90 95

Asp Pro Val Gln Leu Glu Val His Met Gly Trp Leu Leu Leu Gln Thr
100 105 110

Thr Lys Trp Leu Phe Gln Glu Gly Asp Pro Ile His Leu Arg Cys His
115 120 125

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

Lys Gly Lys Lys Tyr Phe His Glu Asn Ser Glu Leu Leu Ile Pro Lys
145 150 155 160

Ala Thr His Asn Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Ile Gly
165 170 175

His Asn Asn Lys Ser Ser Ala Ser Phe Arg Ile Ser Leu Gly Asp Pro
180 185 190

34246SG2-seq1-000001

Gly Ser Pro Ser Met Phe Pro Pro Trp His Gln Ile Thr Phe Cys Leu
195 200 205

Leu Ile Gly Leu Leu Phe Ala Ile Asp Thr Val Leu Tyr Phe Ser Val
210 215 220

Arg Arg Gly Leu Gln Ser Pro Val Ala Asp Tyr Glu Glu Pro Lys Ile
225 230 235 240

Gln Trp Ser Lys Glu Pro Gln Asp Lys
245

<210> 81
<211> 365
<212> PRT
<213> Homo sapiens

<400> 81

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

Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu Leu Tyr
20 25 30

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

Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Leu Ser Tyr Asn Ser Leu
50 55 60

Arg Gly Glu Ala Glu Pro Cys Gly Ala Trp Val Trp Glu Asn Gln Val
65 70 75 80

Ser Trp Tyr Trp Glu Lys Glu Thr Thr Asp Leu Arg Ile Lys Glu Lys
85 90 95

34246SG2-seq1-000001

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

Leu Gln Gly Leu Leu Gly Cys Glu Leu Gly Pro Asp Asn Thr Ser Val
115 120 125

Pro Thr Ala Lys Phe Ala Leu Asn Gly Glu Glu Phe Met Asn Phe Asp
130 135 140

Leu Lys Gln Gly Thr Trp Gly Gly Asp Trp Pro Glu Ala Leu Ala Ile
145 150 155 160

Ser Gln Arg Trp Gln Gln Gln Asp Lys Ala Ala Asn Lys Glu Leu Thr
165 170 175

Phe Leu Leu Phe Ser Cys Pro His Arg Leu Arg Glu His Leu Glu Arg
180 185 190

Gly Arg Gly Asn Leu Glu Trp Lys Glu Pro Pro Ser Met Arg Leu Lys
195 200 205

Ala Arg Pro Ser Ser Pro Gly Phe Ser Val Leu Thr Cys Ser Ala Phe
210 215 220

Ser Phe Tyr Pro Pro Glu Leu Gln Leu Arg Phe Leu Arg Asn Gly Leu
225 230 235 240

Ala Ala Gly Thr Gly Gln Gly Asp Phe Gly Pro Asn Ser Asp Gly Ser
245 250 255

Phe His Ala Ser Ser Ser Leu Thr Val Lys Ser Gly Asp Glu His His
260 265 270

Tyr Cys Cys Ile Val Gln His Ala Gly Leu Ala Gln Pro Leu Arg Val
275 280 285

34246SG2-seq1-000001

Glu Leu Glu Ser Pro Ala Lys Ser Ser Val Leu Val Val Gly Ile Val
290 295 300

Ile Gly Val Leu Leu Leu Thr Ala Ala Ala Val Gly Gly Ala Leu Leu
305 310 315 320

Trp Arg Arg Met Arg Ser Gly Leu Pro Ala Pro Trp Ile Ser Leu Arg
325 330 335

Gly Asp Asp Thr Gly Val Leu Leu Pro Thr Pro Gly Glu Ala Gln Asp
340 345 350

Ala Asp Leu Lys Asp Val Asn Val Ile Pro Ala Thr Ala
355 360 365

<210> 82
<211> 119
<212> PRT
<213> Homo sapiens

<400> 82

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser
1 5 10 15

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

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser
35 40 45

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

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp
65 70 75 80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp

34246SG2-seq1-000001

85

90

95

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

Val Lys Trp Asp Arg Asp Met
115

<210> 83
<211> 330
<212> PRT
<213> Homo sapiens

<400> 83

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

34246SG2-seq1-000001

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

34246SG2-seq1-000001

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

<210> 84
 <211> 326
 <212> PRT
 <213> Homo sapiens

<400> 84

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

Ser Thr Ser Glu Ser 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 Asn Phe Gly Thr Gln Thr
 65 70 75 80

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

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 115 120 125

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

34246SG2-seq1-000001

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

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

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

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

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

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

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

34246SG2-seq1-000001

<210> 85
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 85

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

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
 100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
 115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
 130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 145 150 155 160

34246SG2-seq1-000001

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

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

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

34246SG2-seq1-000001

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375

<210> 86
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <400> 86

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

Ser Thr Ser Glu Ser 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 Lys Thr
 65 70 75 80

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

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
 100 105 110

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

34246SG2-seq1-000001

130

135

140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys

325

<210> 87
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH

<400> 87

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

34246SG2-seq1-000001

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 Glu Glu
225 230 235 240

Met 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
325

34246SG2-seq1-000001

<210> 88
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH

<400> 88

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

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

Tyr Met Tyr Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

Ala Ile Ile Ser Gly Gly Gly Ser Tyr Thr Ser Tyr Pro Asp Ser Met
 50 55 60

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

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

Thr Arg Glu Ser Asn Gly Lys Pro Gly Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ala
 115

<210> 89
 <211> 111
 <212> PRT
 <213> Artificial Sequence

34246SG2-seq1-000001

<220>

<223> VL

<400> 89

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

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

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

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

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

<210> 90

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> VH

<400> 90

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

34246SG2-seq1-000001

20

25

30

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
 100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
 115 120 125

Thr Val Ser Ser
 130

<210> 91

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> VH

<400> 91

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 Asn
 20 25 30

34246SG2-seql-000001

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
 100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
 115 120 125

Thr Val Ser Ser
 130

<210> 92
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH

<400> 92

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

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

34246SG2-seq1-000001

35

40

45

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
115 120 125

Thr Val Ser Ser
130

<210> 93
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> VH

<400> 93

Gln Val Gln Leu Val Gln Ser Gly Pro Asp Val Glu 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

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

34246SG2-seq1-000001

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
115 120 125

Thr Val Ser Ser
130

<210> 94
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> VH

<400> 94

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe

34246SG2-seq1-000001

50

55

60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
115 120 125

Thr Val Ser Ser
130

<210> 95
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> VH

<400> 95

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Arg Arg Ser Ala Gln Lys Phe
50 55 60

34246SG2-seq1-000001

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

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

Ala Arg Gly Gly Glu Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Phe
100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
115 120 125

Thr Val Ser Ser
130

<210> 96
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL

<400> 96

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro

34246SG2-seq1-000001

65		70		75		80									
Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Phe	Glu	Asp	Leu	Pro	Ile
			85					90						95	
Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Gln	Ile	Lys					
			100					105							
<210> 97															
<211> 107															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> VL															
<400> 97															
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	
Asp	Arg	Val	Thr	Phe	Thr	Cys	Gln	Ala	Ser	Gln	Glu	Ile	Arg	Lys	Tyr
			20				25						30		
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Asp	Ala	Ser	Asn	Leu	Lys	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70				75						80	
Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Phe	Asp	Asp	Leu	Pro	Ile
			85					90						95	
Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Gln	Ile	Lys					
			100					105							

34246SG2-seq1-000001

<210> 98
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL

<400> 98

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

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

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

Tyr Asp Ala Ser Asn Leu Lys 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 Val Ala Thr Tyr Tyr Cys Gln Gln Phe Asp Asp Leu Pro Ile
 85 90 95

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

<210> 99
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL

<400> 99

34246SG2-seq1-000001

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

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

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

Tyr Asp Ala Ser Asn Leu Lys 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 Val Ala Thr Tyr Tyr Cys Gln Gln Phe Asp Asp Leu Pro Ile
85 90 95

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

<210> 100

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL

<400> 100

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

34246SG2-seq1-000001

35

40

45

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

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

<210> 101
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> HVR-H1

<400> 101

Ser Tyr Tyr Ile His
1 5

<210> 102
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> FR-H1

<400> 102

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

34246SG2-seq1-000001

20 25 30

<210> 103
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> FR-H3

<400> 103

Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
1 5 10 15

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

<210> 104
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> FR-L1

<400> 104

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

Asp Arg Val Thr Ile Thr Cys
20

<210> 105
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> FR-L3

<400> 105

34246SG2-seq1-000001

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 Val Ala Thr Tyr Tyr Cys
20 25 30

<210> 106
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> CD154

<400> 106

Asp Tyr Lys Asp Asp Asp Asp Lys Met Gln Lys Gly Asp Gln Asn Pro
1 5 10 15

Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser
20 25 30

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

Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu
50 55 60

Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser
65 70 75 80

Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg
85 90 95

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

Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln

34246SG2-seq1-000001

115

120

125

Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser
 130 135 140

His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
 145 150 155

<210> 107

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> CH

<400> 107

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

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

34246SG2-seq1-000001

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

Ala Ala Leu Pro Ala Pro Ile Ser 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 Glu Glu
225 230 235 240

Met 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

34246SG2-seq1-000001

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
325

<210> 108
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> CH

<400> 108

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

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

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

34246SG2-seq1-000001

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 Glu Glu
 225 230 235 240

Met 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 Leu His Glu Ala Leu His Ala His Thr Thr

305 310 315 320

<210>	109
<211>	328
<212>	PRT
<213>	Artificial Sequence

$$\begin{matrix} \langle 220 \rangle \\ \langle 223 \rangle \end{matrix} \quad \text{CH}$$

<400> 109

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

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

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

34246SG2-seq1-000001

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 Glu Glu
225 230 235 240

Met 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 Leu His Glu Ala Leu His Ala His Tyr Thr
305 310 315 320

34246SG2-seq1-000001

Arg Lys Glu Leu Ser Leu Ser Pro
325