

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG
 <120> Bispecific antibodies specific for a costimulatory TNF receptor
 <130> P33116-W0
 <150> EP15188095.2
 <151> 2015-10-02
 <150> EP16170363.2
 <151> 2016-05-19
 <160> 347
 <170> PatentIn version 3.5
 <210> 1
 <211> 186
 <212> PRT
 <213> Homo sapiens
 <400> 1

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
 1 5 10 15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
 20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
 35 40 45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
 50 55 60

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

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
 85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala

100

105

110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
 115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
 130 135 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
 145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
 165 170 175

Arg Pro Val Glu Val Pro Gly Gly Arg Ala
 180 185

<210> 2
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<220>
 <223> OX40(8H9,49B4,1G4, 20B7) CDR-H1

<400> 2

Ser Tyr Ala Ile Ser
 1 5

<210> 3
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<220>
 <223> OX40(CLC-563, CLC-564, 17A9) CDR-H1

<400> 3

Ser Tyr Ala Met Ser
 1 5

<210> 4
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<220>
 <223> OX40(8H9,49B4,1G4, 20B7) CDR-H2

<400> 4

Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 5
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<220>
 <223> OX40(CLC-563, CLC-564, 17A9) CDR-H2

<400> 5

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

Gly

<210> 6
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(8H9) CDR-H3

<400> 6

Glu	Tyr	Gly	Trp	Met	Asp	Tyr
1				5		

<210> 7
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(49B4) CDR-H3

<400> 7

Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr
 1 5

<210> 8
 <211> 7
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 <213> Artificial sequence

<220>
 <223> OX40(1G4) CDR-H3

<400> 8

Glu Tyr Gly Ser Met Asp Tyr
 1 5

<210> 9
 <211> 13
 <212> PRT
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<220>
 <223> OX40(20B7) CDR-H3

<400> 9

Val Asn Tyr Pro Tyr Ser Tyr Trp Gly Asp Phe Asp Tyr
 1 5 10

<210> 10
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 <212> PRT
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<220>
 <223> OX40(CLC-563) CDR-H3

<400> 10

Asp Val Gly Ala Phe Asp Tyr
1 5

<210> 11

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(CLC-564) CDR-H3

<400> 11

Asp Val Gly Pro Phe Asp Tyr
1 5

<210> 12

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(17A9)-CDR-H3

<400> 12

Val Phe Tyr Arg Gly Gly Val Ser Met Asp Tyr
1 5 10

<210> 13

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(8H9,49B4,1G4, 20B7) CDR-L1

<400> 13

Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 14

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

<220>
 <223> OX40(CLC-563, CLC564) CDR-L1

<400> 14

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	Tyr	Leu	Ala
1				5					10		

<210> 15
 <211> 11
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(17A9) CDR-L1

<400> 15

Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser
1				5					10	

<210> 16
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(8H9,49B4,1G4, 20B7) CDR-L2

<400> 16

Asp	Ala	Ser	Ser	Leu	Glu	Ser
1				5		

<210> 17
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(CLC-563, CLC564) CDR-L2

<400> 17

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 18
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> OX40(17A9) CDR-L2

<400> 18

Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 19
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> OX40(8H9) CDR-L3

<400> 19

Gln Gln Tyr Leu Thr Tyr Ser Arg Phe Thr
1 5 10

<210> 20
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> OX40(49B4) CDR-L3

<400> 20

Gln Gln Tyr Ser Ser Gln Pro Tyr Thr
1 5

<210> 21
<211> 10
<212> PRT

<213> Artificial sequence

<220>

<223> OX40(1G4) CDR-L3

<400> 21

Gln	Gln	Tyr	Ile	Ser	Tyr	Ser	Met	Leu	Thr
1				5					10

<210> 22

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(20B7) CDR-L3

<400> 22

Gln	Gln	Tyr	Gln	Ala	Phe	Ser	Leu	Thr
1				5				

<210> 23

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(CLC-563, CLC-164) CDR-L3

<400> 23

Gln	Gln	Tyr	Gly	Ser	Ser	Pro	Leu	Thr
1				5				

<210> 24

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(17A9) CDR-L3

<400> 24

Asn Ser Arg Val Met Pro His Asn Arg Val

1 5 10

<210> 25
 <211> 116
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(8H9) VH

<400> 25

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Trp Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

Thr Val Ser Ser
 115

<210> 26
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>

<223> OX40(8H9) VL

<400> 26

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

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

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

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

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

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

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

<210> 27

<211> 118

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(49B4) VH

<400> 27

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser
 115

<210> 28
 <211> 107
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(49B4) VL

<400> 28

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

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

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

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

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

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

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

<210> 29

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(1G4) VH

<400> 29

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

Thr Val Ser Ser
115

<210> 30
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> OX40(1G4) VL

<400> 30

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

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

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

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

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Met
85 90 95

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

<210> 31
<211> 122
<212> PRT
<213> Artificial sequence

<220>
<223> OX40(20B7) VH

<400> 31

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Val Asn Tyr Pro Tyr Ser Tyr Trp Gly Asp Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 32

<211> 107

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(20B7) VL

<400> 32

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp

20

25

30

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

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

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

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

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

<210> 33
 <211> 116
 <212> PRT
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<220>
 <223> OX40(CLC-563) VH

<400> 33

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Leu Asp Val Gly Ala Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 34
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(CLC-563) VL

<400> 34

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

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

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

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

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

Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100

105

<210> 35
 <211> 116
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(CLC-564) VH

<400> 35

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Phe Asp Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 36
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>

<223> OX40(CLC-564) VL

<400> 36

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

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

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

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

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

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

<210> 37

<211> 120

<212> PRT

<213> Artificial sequence

<220>

<223> OX40(17A9) VH

<400> 37

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Val Phe Tyr Arg Gly Gly Val Ser Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 106
 <212> PRT
 <213> Artificial sequence

<220>
 <223> OX40(17A9) VL

<400> 38

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

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

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

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

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Val Met Pro His Asn Arg
85 90 95

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

<210> 39

<211> 163

<212> PRT

<213> Homo sapiens

<400> 39

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

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

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
 130 135 140

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
 145 150 155 160

Ser Pro Gln

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

<220>
 <223> 4-1BB(12B3,11D5, 9B11, 20G2) CDR-H1

<400> 40

Ser Tyr Ala Ile Ser
 1 5

<210> 41
 <211> 5
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 <213> Artificial Sequence

<220>
 <223> 4-1BB(25G7) CDR-H1

<400> 41

Ser Tyr Ala Met Ser
 1 5

<210> 42
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4-1BB(12B3,11D5, 9B11, 20G2) CDR-H2

<400> 42

Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 43

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(25G7) CDR-H2

<400> 43

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

Gly

<210> 44

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(12B3) CDR-H3

<400> 44

Ser	Glu	Phe	Arg	Phe	Tyr	Ala	Asp	Phe	Asp	Tyr
1				5				10		

<210> 45

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(25G7) CDR-H3

<400> 45

Asp Asp Pro Trp Pro Pro Phe Asp Tyr
1 5

<210> 46

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(11D5) CDR-H3

<400> 46

Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr
1 5 10

<210> 47

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(9B11) CDR-H3

<400> 47

Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr
1 5 10

<210> 48

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(20G2) CDR-H3

<400> 48

Ser Tyr Tyr Trp Glu Ser Tyr Pro Phe Asp Tyr
1 5 10

<210> 49

<211> 11

<212> PRT
 <213> Artificial Sequence

<220>
 <223> 4-1BB(12B3,11D5, 9B11, 20G2) CDR-L1

<400> 49

Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Trp	Leu	Ala
1				5					10	

<210> 50
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4-1BB(25G7) CDR-L1

<400> 50

Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser
1				5					10	

<210> 51
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4-1BB(12B3,11D5, 9B11, 20G2) CDR-L2

<400> 51

Asp	Ala	Ser	Ser	Leu	Glu	Ser
1				5		

<210> 52
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4-1BB(25G7) CDR-L2

<400> 52

Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB(12B3) CDR-L3

<400> 53

Gln Gln Tyr His Ser Tyr Pro Gln Thr
1 5

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB(25G7) CDR-L3

<400> 54

Asn Ser Leu Asp Arg Arg Gly Met Trp Val
1 5 10

<210> 55
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB(11D5) CDR-L3

<400> 55

Gln Gln Leu Asn Ser Tyr Pro Gln Thr
1 5

<210> 56
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> 4-1BB(9B11) CDR-L3

<400> 56

Gln Gln Val Asn Ser Tyr Pro Gln Thr
 1 5

<210> 57

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(20G2) CDR-L3

<400> 57

Gln Gln Gln His Ser Tyr Tyr Thr
 1 5

<210> 58

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(12B3) VH

<400> 58

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 59

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(12B3) VL

<400> 59

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

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

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

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

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

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

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

<210> 60
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4-1BB(25G7) VH

<400> 60

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 61
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 4-1BB(25G7) VL

<400> 61

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

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

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

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

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Asp Arg Arg Gly Met Trp
 85 90 95

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

<210> 62

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(11D5) VH

<400> 62

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Thr Thr Val Thr Val Ser Ser
 115

<210> 63

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(11D5) VL

<400> 63

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

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

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

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

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

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

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

<210> 64

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(9B11) VH

<400> 64

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 65
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4-1BB(9B11) VL

<400> 65

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

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

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

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

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

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

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

<210> 66
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 4-1BB(20G2) VH

<400> 66

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Tyr Tyr Trp Glu Ser Tyr Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 67

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB(20G2) VL

<400> 67

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

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

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

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

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

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

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

<210> 68
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(28H1) CDR-H1

<400> 68

Ser His Ala Met Ser
 1 5

<210> 69
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) CDR-H1

<400> 69

Ser Tyr Ala Met Ser
 1 5

<210> 70
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(28H1) CDR-H2

<400> 70

Ala	Ile	Trp	Ala	Ser	Gly	Glu	Gln	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
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<210> 71
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) CDR-H2

<400> 71

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

Gly

<210> 72
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(28H1) CDR-H3

<400> 72

Gly	Trp	Leu	Gly	Asn	Phe	Asp	Tyr
1			5				

<210> 73
 <211> 8

<212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) CDR-H3

<400> 73

Gly Trp Phe Gly Gly Phe Asn Tyr
 1 5

<210> 74
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(28H1) CDR-L1

<400> 74

Arg Ala Ser Gln Ser Val Ser Arg Ser Tyr Leu Ala
 1 5 10

<210> 75
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) CDR-L1

<400> 75

Arg Ala Ser Gln Ser Val Thr Ser Ser Tyr Leu Ala
 1 5 10

<210> 76
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(28H1) CDR-L2

<400> 76

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 77
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-L2

<400> 77

Val Gly Ser Arg Arg Ala Thr
1 5

<210> 78
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(28H1) CDR-L3

<400> 78

Gln Gln Gly Gln Val Ile Pro Pro Thr
1 5

<210> 79
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-L3

<400> 79

Gln Gln Gly Ile Met Leu Pro Pro Thr
1 5

<210> 80
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> FAP(28H1) VH

<400> 80

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
 20 25 30

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

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

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

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 81

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> FAP(28H1) VL

<400> 81

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Ser
 20 25 30

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

Ile Ile Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

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

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

<210> 82

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> FAP(4B9) VH

<400> 82

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 83
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) VL

<400> 83

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Ser Ser
 20 25 30

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

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

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

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

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

<210> 84
 <211> 760
 <212> PRT
 <213> Homo sapiens

<400> 84

Met Lys Thr Trp Val Lys Ile Val Phe Gly Val Ala Thr Ser Ala Val
 1 5 10 15

Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
 20 25 30

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

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

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

Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
 85 90 95

Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
 100 105 110

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

Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly Glu Phe Val Arg Gly Asn
 130 135 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser

145		150		155		160									
Lys	Leu	Ala	Tyr	Val	Tyr	Gln	Asn	Asn	Ile	Tyr	Leu	Lys	Gln	Arg	Pro
				165					170					175	
Gly	Asp	Pro	Pro	Phe	Gln	Ile	Thr	Phe	Asn	Gly	Arg	Glu	Asn	Lys	Ile
			180					185					190		
Phe	Asn	Gly	Ile	Pro	Asp	Trp	Val	Tyr	Glu	Glu	Glu	Met	Leu	Ala	Thr
		195					200					205			
Lys	Tyr	Ala	Leu	Trp	Trp	Ser	Pro	Asn	Gly	Lys	Phe	Leu	Ala	Tyr	Ala
	210					215					220				
Glu	Phe	Asn	Asp	Thr	Asp	Ile	Pro	Val	Ile	Ala	Tyr	Ser	Tyr	Tyr	Gly
225					230					235					240
Asp	Glu	Gln	Tyr	Pro	Arg	Thr	Ile	Asn	Ile	Pro	Tyr	Pro	Lys	Ala	Gly
				245					250					255	
Ala	Lys	Asn	Pro	Val	Val	Arg	Ile	Phe	Ile	Ile	Asp	Thr	Thr	Tyr	Pro
			260					265					270		
Ala	Tyr	Val	Gly	Pro	Gln	Glu	Val	Pro	Val	Pro	Ala	Met	Ile	Ala	Ser
		275					280					285			
Ser	Asp	Tyr	Tyr	Phe	Ser	Trp	Leu	Thr	Trp	Val	Thr	Asp	Glu	Arg	Val
	290					295					300				
Cys	Leu	Gln	Trp	Leu	Lys	Arg	Val	Gln	Asn	Val	Ser	Val	Leu	Ser	Ile
305					310					315					320
Cys	Asp	Phe	Arg	Glu	Asp	Trp	Gln	Thr	Trp	Asp	Cys	Pro	Lys	Thr	Gln
				325					330					335	
Glu	His	Ile	Glu	Glu	Ser	Arg	Thr	Gly	Trp	Ala	Gly	Gly	Phe	Phe	Val
			340					345					350		

Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe
 355 360 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
 370 375 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile
 385 390 395 400

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
 405 410 415

Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
 420 425 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
 435 440 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
 450 455 460

Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
 465 470 475 480

Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
 485 490 495

Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
 500 505 510

Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
 515 520 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
 530 535 540

Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr

545		550		555		560									
Leu	Ala	Ser	Lys	Glu	Gly	Met	Val	Ile	Ala	Leu	Val	Asp	Gly	Arg	Gly
				565					570					575	
Thr	Ala	Phe	Gln	Gly	Asp	Lys	Leu	Leu	Tyr	Ala	Val	Tyr	Arg	Lys	Leu
			580					585					590		
Gly	Val	Tyr	Glu	Val	Glu	Asp	Gln	Ile	Thr	Ala	Val	Arg	Lys	Phe	Ile
		595					600					605			
Glu	Met	Gly	Phe	Ile	Asp	Glu	Lys	Arg	Ile	Ala	Ile	Trp	Gly	Trp	Ser
	610					615					620				
Tyr	Gly	Gly	Tyr	Val	Ser	Ser	Leu	Ala	Leu	Ala	Ser	Gly	Thr	Gly	Leu
625					630					635					640
Phe	Lys	Cys	Gly	Ile	Ala	Val	Ala	Pro	Val	Ser	Ser	Trp	Glu	Tyr	Tyr
				645					650					655	
Ala	Ser	Val	Tyr	Thr	Glu	Arg	Phe	Met	Gly	Leu	Pro	Thr	Lys	Asp	Asp
			660					665					670		
Asn	Leu	Glu	His	Tyr	Lys	Asn	Ser	Thr	Val	Met	Ala	Arg	Ala	Glu	Tyr
		675					680					685			
Phe	Arg	Asn	Val	Asp	Tyr	Leu	Leu	Ile	His	Gly	Thr	Ala	Asp	Asp	Asn
	690					695					700				
Val	His	Phe	Gln	Asn	Ser	Ala	Gln	Ile	Ala	Lys	Ala	Leu	Val	Asn	Ala
705					710					715					720
Gln	Val	Asp	Phe	Gln	Ala	Met	Trp	Tyr	Ser	Asp	Gln	Asn	His	Gly	Leu
				725					730					735	
Ser	Gly	Leu	Ser	Thr	Asn	His	Leu	Tyr	Thr	His	Met	Thr	His	Phe	Leu
			740					745					750		

Lys Gln Cys Phe Ser Leu Ser Asp
 755 760

<210> 85
 <211> 748
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu FAP ectodomain+poly-lys-tag+his6-tag

<400> 85

Arg Pro Ser Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
 1 5 10 15

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

Pro Asn Trp Ile Ser Gly Gln Glu Tyr Leu His Gln Ser Ala Asp Asn
 35 40 45

Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
 50 55 60

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

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
 85 90 95

Arg Tyr Ser Tyr Thr Ala Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly
 100 105 110

Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
 115 120 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
 130 135 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
 145 150 155 160

Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
 165 170 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
 180 185 190

Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
 195 200 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
 210 215 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val Arg Ile Phe Ile
 225 230 235 240

Ile Asp Thr Thr Tyr Pro Ala Tyr Val Gly Pro Gln Glu Val Pro Val
 245 250 255

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
 260 265 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
 275 280 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
 290 295 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
 305 310 315 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
 325 330 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His

340

345

350

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

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
 370 375 380

Ser Ser Asn Glu Phe Glu Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
 385 390 395 400

Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
 405 410 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
 420 425 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
 435 440 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
 450 455 460

Asn Lys Glu Leu Glu Asn Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu
 465 470 475 480

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
 485 490 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
 500 505 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
 515 520 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
 530 535 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
 545 550 555 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
 565 570 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
 580 585 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
 595 600 605

Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
 610 615 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu Arg Phe Met Gly
 625 630 635 640

Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
 645 650 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
 660 665 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
 675 680 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
 690 695 700

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
 705 710 715 720

His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly Lys
 725 730 735

Lys Lys Lys Lys Lys Gly His His His His His His

740

745

<210> 86
 <211> 2244
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hu FAP ectodomain+poly-lys-tag+his6-tag

<400> 86
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 tatcttcac aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180
 tataaccattt tgagtaatag aaccatgaaa agtgtgaatg cttcaaatta cggcttatca 240
 cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac 300
 acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360
 cctcgtccaa ttcagtattt atgctggctg cctgttggga gtaaattagc atatgtctat 420
 caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaa ataacattta 480
 ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540
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 tggcagacat gggattgtcc aaagaccag gagcatatag aagaaagcag aactggatgg 960
 gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc gtactacaaa 1020
 atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat 1080
 gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat 1140

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tcactgtttt attctagcaa tgaatttgaa gaataccctg gaagaagaaa catctacaga      1200
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tacggcccag gcatcccat ttccaccctt catgatggac gcactgatca agaaattaa      1380
atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag      1440
gaaattaaga aacttgaagt agatgaaatt actttatggg acaagatgat tcttcctcct      1500
caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatgggtg tccctgcagt      1560
cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg      1620
atggtcattg ccttggtgga tggtcgagga acagctttcc aaggtgacaa actcctctat      1680
gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa      1740
ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga      1800
ggatacgttt catcactggc ccttgcatct ggaactggtc ttttcaaatg tggtatagca      1860
gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt      1920
ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca      1980
gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac      2040
tttcaaaact cagcacagat tgctaaagct ctggttaatg cacaagtgga tttccaggca      2100
atgtgggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc      2160
cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa      2220
aagggccacc accatcacca tcac                                          2244

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<210> 87
<211> 761
<212> PRT
<213> Mus musculus

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<400> 87

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

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Leu Ala Leu Val Val Ile Cys Ile Val Leu Arg Pro Ser Arg Val Tyr
 20 25 30

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

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

Gln Glu Tyr Leu His Gln Ser Glu Asp Asp Asn Ile Val Phe Tyr Asn
 65 70 75 80

Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu Ser Asn Ser Thr Met Lys
 85 90 95

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

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

Thr Tyr Tyr Ile Tyr Asp Leu Gln Asn Gly Glu Phe Val Arg Gly Tyr
 130 135 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
 145 150 155 160

Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
 165 170 175

Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr Gly Arg Glu Asn Arg Ile
 180 185 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
 195 200 205

Lys Tyr Ala Leu Trp Trp Ser Pro Asp Gly Lys Phe Leu Ala Tyr Val
 210 215 220

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

Asp Gly Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
 245 250 255

Ala Lys Asn Pro Val Val Arg Val Phe Ile Val Asp Thr Thr Tyr Pro
 260 265 270

His His Val Gly Pro Met Glu Val Pro Val Pro Glu Met Ile Ala Ser
 275 280 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Ser Ser Glu Arg Val
 290 295 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
 305 310 315 320

Cys Asp Phe Arg Glu Asp Trp His Ala Trp Glu Cys Pro Lys Asn Gln
 325 330 335

Glu His Val Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
 340 345 350

Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr Ser Tyr Tyr Lys Ile Phe
 355 360 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
 370 375 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Tyr Ile
 385 390 395 400

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
 405 410 415

Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Asn Ser
 420 425 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
 435 440 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys Ala Lys Tyr Tyr Ala Leu
 450 455 460

Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser Thr Leu His Asp Gly Arg
 465 470 475 480

Thr Asp Gln Glu Ile Gln Val Leu Glu Glu Asn Lys Glu Leu Glu Asn
 485 490 495

Ser Leu Arg Asn Ile Gln Leu Pro Lys Val Glu Ile Lys Lys Leu Lys
 500 505 510

Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
 515 520 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
 530 535 540

Cys Ser Gln Ser Val Lys Ser Val Phe Ala Val Asn Trp Ile Thr Tyr
 545 550 555 560

Leu Ala Ser Lys Glu Gly Ile Val Ile Ala Leu Val Asp Gly Arg Gly
 565 570 575

Thr Ala Phe Gln Gly Asp Lys Phe Leu His Ala Val Tyr Arg Lys Leu
 580 585 590

Gly Val Tyr Glu Val Glu Asp Gln Leu Thr Ala Val Arg Lys Phe Ile
 595 600 605

Glu Met Gly Phe Ile Asp Glu Glu Arg Ile Ala Ile Trp Gly Trp Ser
 610 615 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625 630 635 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
645 650 655

Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
660 665 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
675 680 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
690 695 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705 710 715 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Ile
725 730 735

Ser Ser Gly Arg Ser Gln Asn His Leu Tyr Thr His Met Thr His Phe
740 745 750

Leu Lys Gln Cys Phe Ser Leu Ser Asp
755 760

<210> 88

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine FAP ectodomain+poly-lys-tag+his6-tag

<400> 88

Arg Pro Ser Arg Val Tyr Lys Pro Glu Gly Asn Thr Lys Arg Ala Leu
1 5 10 15

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

Pro Asn Trp Ile Ser Glu Gln Glu Tyr Leu His Gln Ser Glu Asp Asp
 35 40 45

Asn Ile Val Phe Tyr Asn Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu
 50 55 60

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

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
 85 90 95

Arg Tyr Ser Tyr Thr Ala Thr Tyr Tyr Ile Tyr Asp Leu Gln Asn Gly
 100 105 110

Glu Phe Val Arg Gly Tyr Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
 115 120 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
 130 135 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr
 145 150 155 160

Gly Arg Glu Asn Arg Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
 165 170 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asp Gly
 180 185 190

Lys Phe Leu Ala Tyr Val Glu Phe Asn Asp Ser Asp Ile Pro Ile Ile
 195 200 205

Ala Tyr Ser Tyr Tyr Gly Asp Gly Gln Tyr Pro Arg Thr Ile Asn Ile
 210 215 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val Arg Val Phe Ile
 225 230 235 240

Val Asp Thr Thr Tyr Pro His His Val Gly Pro Met Glu Val Pro Val
 245 250 255

Pro Glu Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
 260 265 270

Val Ser Ser Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
 275 280 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp His Ala Trp
 290 295 300

Glu Cys Pro Lys Asn Gln Glu His Val Glu Glu Ser Arg Thr Gly Trp
 305 310 315 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr
 325 330 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
 340 345 350

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

Trp Glu Ala Ile Tyr Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
 370 375 380

Ser Ser Asn Glu Phe Glu Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
 385 390 395 400

Ile Ser Ile Gly Asn Ser Pro Pro Ser Lys Lys Cys Val Thr Cys His
 405 410 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys
 420 425 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser
 435 440 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Gln Val Leu Glu Glu
 450 455 460

Asn Lys Glu Leu Glu Asn Ser Leu Arg Asn Ile Gln Leu Pro Lys Val
 465 470 475 480

Glu Ile Lys Lys Leu Lys Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met
 485 490 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
 500 505 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Lys Ser Val Phe Ala
 515 520 525

Val Asn Trp Ile Thr Tyr Leu Ala Ser Lys Glu Gly Ile Val Ile Ala
 530 535 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Phe Leu His
 545 550 555 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Leu Thr
 565 570 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Glu Arg Ile
 580 585 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
 595 600 605

Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
 610 615 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly
 625 630 635 640

Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
 645 650 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
 660 665 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
 675 680 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
 690 695 700

Asp Gln Asn His Gly Ile Leu Ser Gly Arg Ser Gln Asn His Leu Tyr
 705 710 715 720

Thr His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly
 725 730 735

Lys Lys Lys Lys Lys Lys Gly His His His His His His
 740 745

<210> 89

<211> 2247

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine FAP ectodomain+poly-lys-tag+his6-tag

<400> 89

cgtccctcaa gagtttacaac acctgaagga aacacaaaaga gagctcttac cttgaaggat 60

attttaaatg gaacattctc atataaaaca tattttccca actggatttc agaacaagaa 120

tatcttcac aatctgagga tgataacata gtattttata atattgaaac aagagaatca 180

tatatcattt tgagtaatag caccatgaaa agtgtgaatg ctacagatta tggtttgtca	240
cctgatcggc aatttgtgta tctagaaagt gattattcaa agctctggcg atattcatac	300
acagcgacat actacatcta cgaccttcag aatggggaat ttgtaagagg atacgagctc	360
cctcgtccaa ttcagtatct atgctggtcg cctgttggga gtaaattagc atatgtatat	420
caaaacaata tttatttgaa acaaagacca ggagatccac cttttcaa at aacttatact	480
ggaagagaaa atagaatatt taatggaata ccagactggg tttatgaaga ggaaatgctt	540
gccacaaaat atgctctttg gtggtctcca gatggaaaat ttttggcata tgtagaattt	600
aatgattcag atataccaat tattgcctat tcttattatg gtgatggaca gtatcctaga	660
actataaata ttccatatcc aaaggctggg gctaagaatc cggttggttcg tgtttttatt	720
gttgacacca cctaccctca ccacgtgggc ccaatggaag tgccagttcc agaaatgata	780
gcctcaagtg actattatct cagctggctc acatgggtgt ccagtgaacg agtatgcttg	840
cagtggctaa aaagagtgca gaatgtctca gtcctgtcta tatgtgattt cagggaagac	900
tggcatgcat gggaatgtcc aaagaaccag gagcatgtag aagaaagcag aacaggatgg	960
gctggtggat tctttgtttc gacaccagct tttagccagg atgccacttc ttactacaaa	1020
atatttagcg acaaggatgg ttacaaacat attcactaca tcaaagacac tgttgaaaat	1080
gctattcaaa ttacaagtgg caagtgggag gccatatata tattccgcgt aacacaggat	1140
tcactgtttt attctagcaa tgaatttgaa gggtaccctg gaagaagaaa catctacaga	1200
attagcattg gaaactctcc tccgagcaag aagtgtgtta cttgccatct aaggaaagaa	1260
aggtgccaat attacacagc aagtttcagc taaaaagcca agtactatgc actcgtctgc	1320
tatggccctg gcctccccat ttccaccctc catgatggcc gcacagacca agaaatacaa	1380
gtattagaag aaaacaaaga actggaaaat tctctgagaa atatccagct gcctaaagtg	1440
gagattaaga agctcaaaga cgggggactg actttctggt acaagatgat tctgcctcct	1500
cagtttgaca gatcaaagaa gtaccctttg ctaattcaag tgtatggtgg tcctttagc	1560
cagagtgtta agtctgtgtt tgctgttaat tggataactt atctcgcaag taaggagggg	1620
atagtcattg ccctggtaga tggtcggggc actgctttcc aaggtagcaa attcctgcat	1680

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gccgtgtatc gaaaactggg tgtatatgaa gttgaggacc agctcacagc tgtcagaaaa 1740
ttcatagaaa tgggtttcat tgatgaagaa agaatagcc a tatggggctg gtcctacgga 1800
ggttatgttt catccctggc ccttgcatct ggaactggtc ttttcaa atg tggcatagca 1860
gtggctccag tctccagctg ggaatattac gcatctatct actcagagag attcatgggc 1920
ctcccaacaa aggacgacaa tctcgaacac tataaaaaatt caactgtgat ggcaagagca 1980
gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040
tttcagaact cagcacagat tgctaaagct ttggttaatg cacaagtgga tttccaggcg 2100
atgtgggtact ctgaccagaa ccatgggtata ttatctgggc gctcccagaa tcatttatat 2160
acccacatga cgcacttcct caagcaatgc ttttctttat cagacggcaa aaagaaaaaag 2220
aaaaagggcc accaccatca ccatcac 2247

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<210> 90
<211> 748
<212> PRT
<213> Artificial Sequence

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<220>
<223> Cynomolgus FAP ectodomain+poly-lys-tag+his6-tag

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<400> 90

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Arg Pro Pro Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
1           5           10           15

```

```

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

```

```

Pro Asn Trp Ile Ser Gly Gln Glu Tyr Leu His Gln Ser Ala Asp Asn
          35           40           45

```

```

Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
          50           55           60

```

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

```

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
 85 90 95

Arg Tyr Ser Tyr Thr Ala Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly
 100 105 110

Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
 115 120 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
 130 135 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
 145 150 155 160

Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
 165 170 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
 180 185 190

Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
 195 200 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
 210 215 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Phe Val Arg Ile Phe Ile
 225 230 235 240

Ile Asp Thr Thr Tyr Pro Ala Tyr Val Gly Pro Gln Glu Val Pro Val
 245 250 255

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
 260 265 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
 275 280 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
 290 295 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
 305 310 315 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
 325 330 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
 340 345 350

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

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
 370 375 380

Ser Ser Asn Glu Phe Glu Asp Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
 385 390 395 400

Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
 405 410 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
 420 425 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
 435 440 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
 450 455 460

Asn Lys Glu Leu Glu Asn Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu
 465 470 475 480

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
 485 490 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
 500 505 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
 515 520 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
 530 535 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
 545 550 555 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
 565 570 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
 580 585 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
 595 600 605

Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
 610 615 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu Arg Phe Met Gly
 625 630 635 640

Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
 645 650 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
 660 665 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
 675 680 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
 690 695 700

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
 705 710 715 720

His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly Lys
 725 730 735

Lys Lys Lys Lys Lys Gly His His His His His His
 740 745

<210> 91
 <211> 2244
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Cynomolgus FAP ectodomain+poly-lys-tag+his6-tag

<400> 91
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 attttaaatg ggacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa 120
 tatcttcatc aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180
 tataccattt tgagtaacag aaccatgaaa agtgtgaatg cttcaaatta tggcttatca 240
 cctgatcggc aatttgata tctagaaagt gattattcaa agctttggag atactcttac 300
 acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360
 cctcgtccaa ttcagtatct atgctggctg cctgttggga gtaaattagc atatgtctat 420
 caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaa ataacattta 480
 ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540
 gctacaaaat atgctctctg gtgggtctcct aatggaaaat ttttggcata tgcggaattt 600
 aatgatacag atataccagt tattgcctat tcctattatg gcgatgaaca atatcccaga 660

acaataaata ttccataccc aaaggccgga gctaagaatc cttttgttcg gatattttatt	720
atcgatacca cttaccctgc gtatgtaggt ccccaggaag tgcctgttcc agcaatgata	780
gcctcaagtg attattatatt cagttggctc acgtgggtta ctgatgaacg agtatgtttg	840
cagtggtctaa aaagagtcca gaatgtttcg gtcttgtcta tatgtgattt cagggaagac	900
tggcagacat gggattgtcc aaagaccag gagcatatag aagaaagcag aactggatgg	960
gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc atactacaaa	1020
atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat	1080
gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat	1140
tcactgtttt attctagcaa tgaatttgaa gattaccctg gaagaagaaa catctacaga	1200
attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa	1260
aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc	1320
tatggcccag gcatccccat ttccaccctt catgacggac gcactgatca agaaattaaa	1380
atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag	1440
gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct	1500
caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt	1560
cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taagggaagg	1620
atgggtcattg ccttgggtgga tggtcgggga acagctttcc aagggtgaca actcctgtat	1680
gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa	1740
ttcatagaaa tgggtttcat tgatgaaaaa agaatagccca tatggggctg gtcctatgga	1800
ggatatgttt catcactggc ccttgcatct ggaactggtc ttttcaaagtg tgggatagca	1860
gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt	1920
ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca	1980
gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac	2040
tttcaaaact cagcacagat tgctaaagct ctgggttaatg cacaagtgga tttccaggca	2100
atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc	2160

cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa 2220

aagggccacc accatcacca tcac 2244

<210> 92

<211> 702

<212> PRT

<213> Homo sapiens

<400> 92

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

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

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125

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

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys

145		150		155		160									
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
			165						170					175	
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln
			180					185					190		
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn
		195					200					205			
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg
	210					215					220				
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
225					230					235					240
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn
				245					250					255	
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe
			260					265					270		
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
		275					280					285			
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser
	290					295					300				
Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala
305					310					315					320
Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu
				325					330					335	
Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr
			340					345					350		

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Lys Leu Ser
 385 390 395 400

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510

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

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn

545 550 555 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
565 570 575

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
580 585 590

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
595 600 605

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
610 615 620

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625 630 635 640

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
645 650 655

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
660 665 670

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
675 680 685

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
690 695 700

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<212> PRT
<213> Homo sapiens
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<400> 93

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Ala Leu Thr Leu Thr Met Leu Ala Arg Leu Ala Ser Ala Ala Ser Phe
 20 25 30

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

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

Leu Leu Ala Ala Gly Pro Ala Asp His Leu Leu Leu Gln Leu Tyr Ser
 65 70 75 80

Gly Arg Leu Gln Val Arg Leu Val Leu Gly Gln Glu Glu Leu Arg Leu
 85 90 95

Gln Thr Pro Ala Glu Thr Leu Leu Ser Asp Ser Ile Pro His Thr Val
 100 105 110

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

Leu Asn Ala Ser Ser Ala Val Pro Gly Ala Pro Leu Glu Val Pro Tyr
 130 135 140

Gly Leu Phe Val Gly Gly Thr Gly Thr Leu Gly Leu Pro Tyr Leu Arg
 145 150 155 160

Gly Thr Ser Arg Pro Leu Arg Gly Cys Leu His Ala Ala Thr Leu Asn
 165 170 175

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

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

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

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

Phe Gln Ala Gly Gly Arg Arg Gly Asp Phe Ile Tyr Val Asp Ile Phe
 245 250 255

Glu Gly His Leu Arg Ala Val Val Glu Lys Gly Gln Gly Thr Val Leu
 260 265 270

Leu His Asn Ser Val Pro Val Ala Asp Gly Gln Pro His Glu Val Ser
 275 280 285

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

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

Ser Leu Leu Leu Gly Gly Leu Asp Ala Glu Ala Ser Arg His Leu Gln
 325 330 335

Glu His Arg Leu Gly Leu Thr Pro Glu Ala Thr Asn Ala Ser Leu Leu
 340 345 350

Gly Cys Met Glu Asp Leu Ser Val Asn Gly Gln Arg Arg Gly Leu Arg
 355 360 365

Glu Ala Leu Leu Thr Arg Asn Met Ala Ala Gly Cys Arg Leu Glu Glu
 370 375 380

Glu Glu Tyr Glu Asp Asp Ala Tyr Gly His Tyr Glu Ala Phe Ser Thr
 385 390 395 400

Leu Ala Pro Glu Ala Trp Pro Ala Met Glu Leu Pro Glu Pro Cys Val
 405 410 415

Pro Glu Pro Gly Leu Pro Pro Val Phe Ala Asn Phe Thr Gln Leu Leu
 420 425 430

Thr Ile Ser Pro Leu Val Val Ala Glu Gly Gly Thr Ala Trp Leu Glu
 435 440 445

Trp Arg His Val Gln Pro Thr Leu Asp Leu Met Glu Ala Glu Leu Arg
 450 455 460

Lys Ser Gln Val Leu Phe Ser Val Thr Arg Gly Ala Arg His Gly Glu
 465 470 475 480

Leu Glu Leu Asp Ile Pro Gly Ala Gln Ala Arg Lys Met Phe Thr Leu
 485 490 495

Leu Asp Val Val Asn Arg Lys Ala Arg Phe Ile His Asp Gly Ser Glu
 500 505 510

Asp Thr Ser Asp Gln Leu Val Leu Glu Val Ser Val Thr Ala Arg Val
 515 520 525

Pro Met Pro Ser Cys Leu Arg Arg Gly Gln Thr Tyr Leu Leu Pro Ile
 530 535 540

Gln Val Asn Pro Val Asn Asp Pro Pro His Ile Ile Phe Pro His Gly
 545 550 555 560

Ser Leu Met Val Ile Leu Glu His Thr Gln Lys Pro Leu Gly Pro Glu
 565 570 575

Val Phe Gln Ala Tyr Asp Pro Asp Ser Ala Cys Glu Gly Leu Thr Phe
 580 585 590

Gln Val Leu Gly Thr Ser Ser Gly Leu Pro Val Glu Arg Arg Asp Gln
 595 600 605

Pro Gly Glu Pro Ala Thr Glu Phe Ser Cys Arg Glu Leu Glu Ala Gly
 610 615 620

Ser Leu Val Tyr Val His Arg Gly Gly Pro Ala Gln Asp Leu Thr Phe
625 630 635 640

Arg Val Ser Asp Gly Leu Gln Ala Ser Pro Pro Ala Thr Leu Lys Val
645 650 655

Val Ala Ile Arg Pro Ala Ile Gln Ile His Arg Ser Thr Gly Leu Arg
660 665 670

Leu Ala Gln Gly Ser Ala Met Pro Ile Leu Pro Ala Asn Leu Ser Val
675 680 685

Glu Thr Asn Ala Val Gly Gln Asp Val Ser Val Leu Phe Arg Val Thr
690 695 700

Gly Ala Leu Gln Phe Gly Glu Leu Gln Lys Gln Gly Ala Gly Gly Val
705 710 715 720

Glu Gly Ala Glu Trp Trp Ala Thr Gln Ala Phe His Gln Arg Asp Val
725 730 735

Glu Gln Gly Arg Val Arg Tyr Leu Ser Thr Asp Pro Gln His His Ala
740 745 750

Tyr Asp Thr Val Glu Asn Leu Ala Leu Glu Val Gln Val Gly Gln Glu
755 760 765

Ile Leu Ser Asn Leu Ser Phe Pro Val Thr Ile Gln Arg Ala Thr Val
770 775 780

Trp Met Leu Arg Leu Glu Pro Leu His Thr Gln Asn Thr Gln Gln Glu
785 790 795 800

Thr Leu Thr Thr Ala His Leu Glu Ala Thr Leu Glu Glu Ala Gly Pro
805 810 815

Ser Pro Pro Thr Phe His Tyr Glu Val Val Gln Ala Pro Arg Lys Gly
 820 825 830

Asn Leu Gln Leu Gln Gly Thr Arg Leu Ser Asp Gly Gln Gly Phe Thr
 835 840 845

Gln Asp Asp Ile Gln Ala Gly Arg Val Thr Tyr Gly Ala Thr Ala Arg
 850 855 860

Ala Ser Glu Ala Val Glu Asp Thr Phe Arg Phe Arg Val Thr Ala Pro
 865 870 875 880

Pro Tyr Phe Ser Pro Leu Tyr Thr Phe Pro Ile His Ile Gly Gly Asp
 885 890 895

Pro Asp Ala Pro Val Leu Thr Asn Val Leu Leu Val Val Pro Glu Gly
 900 905 910

Gly Glu Gly Val Leu Ser Ala Asp His Leu Phe Val Lys Ser Leu Asn
 915 920 925

Ser Ala Ser Tyr Leu Tyr Glu Val Met Glu Arg Pro Arg His Gly Arg
 930 935 940

Leu Ala Trp Arg Gly Thr Gln Asp Lys Thr Thr Met Val Thr Ser Phe
 945 950 955 960

Thr Asn Glu Asp Leu Leu Arg Gly Arg Leu Val Tyr Gln His Asp Asp
 965 970 975

Ser Glu Thr Thr Glu Asp Asp Ile Pro Phe Val Ala Thr Arg Gln Gly
 980 985 990

Glu Ser Ser Gly Asp Met Ala Trp Glu Glu Val Arg Gly Val Phe Arg
 995 1000 1005

Val Ala Ile Gln Pro Val Asn Asp His Ala Pro Val Gln Thr Ile
 1010 1015 1020

Ser Arg Ile Phe His Val Ala Arg Gly Gly Arg Arg Leu Leu Thr
 1025 1030 1035

Thr Asp Asp Val Ala Phe Ser Asp Ala Asp Ser Gly Phe Ala Asp
 1040 1045 1050

Ala Gln Leu Val Leu Thr Arg Lys Asp Leu Leu Phe Gly Ser Ile
 1055 1060 1065

Val Ala Val Asp Glu Pro Thr Arg Pro Ile Tyr Arg Phe Thr Gln
 1070 1075 1080

Glu Asp Leu Arg Lys Arg Arg Val Leu Phe Val His Ser Gly Ala
 1085 1090 1095

Asp Arg Gly Trp Ile Gln Leu Gln Val Ser Asp Gly Gln His Gln
 1100 1105 1110

Ala Thr Ala Leu Leu Glu Val Gln Ala Ser Glu Pro Tyr Leu Arg
 1115 1120 1125

Val Ala Asn Gly Ser Ser Leu Val Val Pro Gln Gly Gly Gln Gly
 1130 1135 1140

Thr Ile Asp Thr Ala Val Leu His Leu Asp Thr Asn Leu Asp Ile
 1145 1150 1155

Arg Ser Gly Asp Glu Val His Tyr His Val Thr Ala Gly Pro Arg
 1160 1165 1170

Trp Gly Gln Leu Val Arg Ala Gly Gln Pro Ala Thr Ala Phe Ser
 1175 1180 1185

Gln Gln Asp Leu Leu Asp Gly Ala Val Leu Tyr Ser His Asn Gly
 1190 1195 1200

Ser	Leu	Ser	Pro	Arg	Asp	Thr	Met	Ala	Phe	Ser	Val	Glu	Ala	Gly
1205						1210					1215			
Pro	Val	His	Thr	Asp	Ala	Thr	Leu	Gln	Val	Thr	Ile	Ala	Leu	Glu
1220						1225					1230			
Gly	Pro	Leu	Ala	Pro	Leu	Lys	Leu	Val	Arg	His	Lys	Lys	Ile	Tyr
1235						1240					1245			
Val	Phe	Gln	Gly	Glu	Ala	Ala	Glu	Ile	Arg	Arg	Asp	Gln	Leu	Glu
1250						1255					1260			
Ala	Ala	Gln	Glu	Ala	Val	Pro	Pro	Ala	Asp	Ile	Val	Phe	Ser	Val
1265						1270					1275			
Lys	Ser	Pro	Pro	Ser	Ala	Gly	Tyr	Leu	Val	Met	Val	Ser	Arg	Gly
1280						1285					1290			
Ala	Leu	Ala	Asp	Glu	Pro	Pro	Ser	Leu	Asp	Pro	Val	Gln	Ser	Phe
1295						1300					1305			
Ser	Gln	Glu	Ala	Val	Asp	Thr	Gly	Arg	Val	Leu	Tyr	Leu	His	Ser
1310						1315					1320			
Arg	Pro	Glu	Ala	Trp	Ser	Asp	Ala	Phe	Ser	Leu	Asp	Val	Ala	Ser
1325						1330					1335			
Gly	Leu	Gly	Ala	Pro	Leu	Glu	Gly	Val	Leu	Val	Glu	Leu	Glu	Val
1340						1345					1350			
Leu	Pro	Ala	Ala	Ile	Pro	Leu	Glu	Ala	Gln	Asn	Phe	Ser	Val	Pro
1355						1360					1365			
Glu	Gly	Gly	Ser	Leu	Thr	Leu	Ala	Pro	Pro	Leu	Leu	Arg	Val	Ser
1370						1375					1380			
Gly	Pro	Tyr	Phe	Pro	Thr	Leu	Leu	Gly	Leu	Ser	Leu	Gln	Val	Leu
1385						1390					1395			

Glu Pro Pro Gln His Gly Ala Leu Gln Lys Glu Asp Gly Pro Gln
 1400 1405 1410

Ala Arg Thr Leu Ser Ala Phe Ser Trp Arg Met Val Glu Glu Gln
 1415 1420 1425

Leu Ile Arg Tyr Val His Asp Gly Ser Glu Thr Leu Thr Asp Ser
 1430 1435 1440

Phe Val Leu Met Ala Asn Ala Ser Glu Met Asp Arg Gln Ser His
 1445 1450 1455

Pro Val Ala Phe Thr Val Thr Val Leu Pro Val Asn Asp Gln Pro
 1460 1465 1470

Pro Ile Leu Thr Thr Asn Thr Gly Leu Gln Met Trp Glu Gly Ala
 1475 1480 1485

Thr Ala Pro Ile Pro Ala Glu Ala Leu Arg Ser Thr Asp Gly Asp
 1490 1495 1500

Ser Gly Ser Glu Asp Leu Val Tyr Thr Ile Glu Gln Pro Ser Asn
 1505 1510 1515

Gly Arg Val Val Leu Arg Gly Ala Pro Gly Thr Glu Val Arg Ser
 1520 1525 1530

Phe Thr Gln Ala Gln Leu Asp Gly Gly Leu Val Leu Phe Ser His
 1535 1540 1545

Arg Gly Thr Leu Asp Gly Gly Phe Arg Phe Arg Leu Ser Asp Gly
 1550 1555 1560

Glu His Thr Ser Pro Gly His Phe Phe Arg Val Thr Ala Gln Lys
 1565 1570 1575

Gln Val 1580	Leu Leu Ser Leu Lys 1585	Gly Ser Gln Thr Leu Thr Val Cys 1590
Pro Gly 1595	Ser Val Gln Pro Leu Ser Ser Gln Thr Leu Arg Ala Ser 1600 1605	
Ser Ser 1610	Ala Gly Thr Asp Pro Gln Leu Leu Leu Tyr Arg Val Val 1615 1620	
Arg Gly 1625	Pro Gln Leu Gly Arg Leu Phe His Ala Gln Gln Asp Ser 1630 1635	
Thr Gly 1640	Glu Ala Leu Val Asn Phe Thr Gln Ala Glu Val Tyr Ala 1645 1650	
Gly Asn 1655	Ile Leu Tyr Glu His Glu Met Pro Pro Glu Pro Phe Trp 1660 1665	
Glu Ala 1670	His Asp Thr Leu Glu Leu Gln Leu Ser Ser Pro Pro Ala 1675 1680	
Arg Asp 1685	Val Ala Ala Thr Leu Ala Val Ala Val Ser Phe Glu Ala 1690 1695	
Ala Cys 1700	Pro Gln Arg Pro Ser His Leu Trp Lys Asn Lys Gly Leu 1705 1710	
Trp Val 1715	Pro Glu Gly Gln Arg Ala Arg Ile Thr Val Ala Ala Leu 1720 1725	
Asp Ala 1730	Ser Asn Leu Leu Ala Ser Val Pro Ser Pro Gln Arg Ser 1735 1740	
Glu His 1745	Asp Val Leu Phe Gln Val Thr Gln Phe Pro Ser Arg Gly 1750 1755	
Gln Leu 1760	Leu Val Ser Glu Glu Pro Leu His Ala Gly Gln Pro His 1765 1770	

Phe Leu Gln Ser Gln Leu Ala Ala Gly Gln Leu Val Tyr Ala His
 1775 1780 1785

Gly Gly Gly Gly Thr Gln Gln Asp Gly Phe His Phe Arg Ala His
 1790 1795 1800

Leu Gln Gly Pro Ala Gly Ala Ser Val Ala Gly Pro Gln Thr Ser
 1805 1810 1815

Glu Ala Phe Ala Ile Thr Val Arg Asp Val Asn Glu Arg Pro Pro
 1820 1825 1830

Gln Pro Gln Ala Ser Val Pro Leu Arg Leu Thr Arg Gly Ser Arg
 1835 1840 1845

Ala Pro Ile Ser Arg Ala Gln Leu Ser Val Val Asp Pro Asp Ser
 1850 1855 1860

Ala Pro Gly Glu Ile Glu Tyr Glu Val Gln Arg Ala Pro His Asn
 1865 1870 1875

Gly Phe Leu Ser Leu Val Gly Gly Gly Leu Gly Pro Val Thr Arg
 1880 1885 1890

Phe Thr Gln Ala Asp Val Asp Ser Gly Arg Leu Ala Phe Val Ala
 1895 1900 1905

Asn Gly Ser Ser Val Ala Gly Ile Phe Gln Leu Ser Met Ser Asp
 1910 1915 1920

Gly Ala Ser Pro Pro Leu Pro Met Ser Leu Ala Val Asp Ile Leu
 1925 1930 1935

Pro Ser Ala Ile Glu Val Gln Leu Arg Ala Pro Leu Glu Val Pro
 1940 1945 1950

Gln Ala Leu Gly Arg Ser Ser Leu Ser Gln Gln Gln Leu Arg Val
 1955 1960 1965

Val Ser Asp Arg Glu Glu Pro Glu Ala Ala Tyr Arg Leu Ile Gln
 1970 1975 1980

Gly Pro Gln Tyr Gly His Leu Leu Val Gly Gly Arg Pro Thr Ser
 1985 1990 1995

Ala Phe Ser Gln Phe Gln Ile Asp Gln Gly Glu Val Val Phe Ala
 2000 2005 2010

Phe Thr Asn Phe Ser Ser Ser His Asp His Phe Arg Val Leu Ala
 2015 2020 2025

Leu Ala Arg Gly Val Asn Ala Ser Ala Val Val Asn Val Thr Val
 2030 2035 2040

Arg Ala Leu Leu His Val Trp Ala Gly Gly Pro Trp Pro Gln Gly
 2045 2050 2055

Ala Thr Leu Arg Leu Asp Pro Thr Val Leu Asp Ala Gly Glu Leu
 2060 2065 2070

Ala Asn Arg Thr Gly Ser Val Pro Arg Phe Arg Leu Leu Glu Gly
 2075 2080 2085

Pro Arg His Gly Arg Val Val Arg Val Pro Arg Ala Arg Thr Glu
 2090 2095 2100

Pro Gly Gly Ser Gln Leu Val Glu Gln Phe Thr Gln Gln Asp Leu
 2105 2110 2115

Glu Asp Gly Arg Leu Gly Leu Glu Val Gly Arg Pro Glu Gly Arg
 2120 2125 2130

Ala Pro Gly Pro Ala Gly Asp Ser Leu Thr Leu Glu Leu Trp Ala
 2135 2140 2145

Gln Gly 2150	Val Pro Pro Ala Val 2155	Ala Ser Leu Asp Phe 2160	Ala Thr Glu
Pro Tyr 2165	Asn Ala Ala Arg Pro 2170	Tyr Ser Val Ala Leu 2175	Leu Ser Val
Pro Glu 2180	Ala Ala Arg Thr Glu 2185	Ala Gly Lys Pro Glu 2190	Ser Ser Thr
Pro Thr 2195	Gly Glu Pro Gly Pro 2200	Met Ala Ser Ser Pro 2205	Glu Pro Ala
Val Ala 2210	Lys Gly Gly Phe Leu 2215	Ser Phe Leu Glu Ala 2220	Asn Met Phe
Ser Val 2225	Ile Ile Pro Met Cys 2230	Leu Val Leu Leu Leu 2235	Leu Ala Leu
Ile Leu 2240	Pro Leu Leu Phe Tyr 2245	Leu Arg Lys Arg Asn 2250	Lys Thr Gly
Lys His 2255	Asp Val Gln Val Leu 2260	Thr Ala Lys Pro Arg 2265	Asn Gly Leu
Ala Gly 2270	Asp Thr Glu Thr Phe 2275	Arg Lys Val Glu Pro 2280	Gly Gln Ala
Ile Pro 2285	Leu Thr Ala Val Pro 2290	Gly Gln Gly Pro Pro 2295	Pro Gly Gly
Gln Pro 2300	Asp Pro Glu Leu Leu 2305	Gln Phe Cys Arg Thr 2310	Pro Asn Pro
Ala Leu 2315	Lys Asn Gly Gln Tyr 2320	Trp Val	

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 <212> PRT
 <213> Homo sapiens

<400> 94

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
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Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
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Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
 35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
 50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
 65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
 85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
 100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
 115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
 130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
 145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
 165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
 180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
 195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
 210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
 225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
 245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
 260 265 270

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

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
 290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
 305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
 325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
 340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
 355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr

370

375

380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
 580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
 595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
 610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
 625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
 645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
 660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
 675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
 690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
 705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
 725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
 740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
 755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser

770

775

780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
 785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
 805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
 820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
 835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
 850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
 865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
 885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
 900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
 915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
 930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
 945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
 965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
 980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
 995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
 1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
 1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
 1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
 1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
 1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
 1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
 1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
 1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
 1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
 1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln

1160

1165

1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
 1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
 1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
 1205 1210

<210> 95

<211> 556

<212> PRT

<213> Homo sapiens

<400> 95

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

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

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
 50 55 60

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
 65 70 75 80

Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
 85 90 95

Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
 100 105 110

Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
 115 120 125

Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
 130 135 140

Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
 145 150 155 160

Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro
 165 170 175

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
 180 185 190

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
 195 200 205

Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser
 210 215 220

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
 225 230 235 240

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
 245 250 255

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
 260 265 270

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
 275 280 285

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

Cys Ser Leu Val Gly Ile Leu His Leu Gln Arg Ala Leu Val Leu Arg
 305 310 315 320

Arg Lys Arg Lys Arg Met Thr Asp Pro Thr Arg Arg Phe Phe Lys Val
 325 330 335

Thr Pro Pro Pro Gly Ser Gly Pro Gln Asn Gln Tyr Gly Asn Val Leu
 340 345 350

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
 355 360 365

Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
 370 375 380

Val Gln Ala Asp Gly Ala Leu Gly Ser Arg Ser Pro Pro Gly Val Gly
 385 390 395 400

Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
 405 410 415

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
 420 425 430

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
 435 440 445

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
 450 455 460

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
 465 470 475 480

Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
 485 490 495

Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
 500 505 510

Leu Arg Ser Ile Arg Gly Gln Pro Gly Pro Asn His Glu Glu Asp Ala
 515 520 525

Asp Ser Tyr Glu Asn Met Asp Asn Pro Asp Gly Pro Asp Pro Ala Trp
 530 535 540

Gly Gly Gly Gly Arg Met Gly Thr Trp Ser Thr Arg
 545 550 555

<210> 96

<211> 297

<212> PRT

<213> Homo sapiens

<400> 96

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
 1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
 20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
 35 40 45

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

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
 65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
 85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
 100 105 110

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

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
 130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
 145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
 165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
 180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
 195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
 210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
 225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
 245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu
 260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
 275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
 290 295

<210> 97
 <211> 364
 <212> PRT
 <213> Homo sapiens

<400> 97

Met Pro Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
 1 5 10 15

Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln
 20 25 30

Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro
 35 40 45

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

Ala Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln
 65 70 75 80

Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro
 85 90 95

Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp
 100 105 110

Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser
 115 120 125

Tyr Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg
 130 135 140

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

Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile
 165 170 175

Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr
 180 185 190

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

Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu
 210 215 220

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr
 225 230 235 240

Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly
 245 250 255

Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala
 260 265 270

Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys
 275 280 285

Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly
 290 295 300

Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr
 305 310 315 320

Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu
 325 330 335

Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys
 340 345 350

Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
 355 360

<210> 98

<211> 277

<212> PRT

<213> Homo sapiens

<400> 98

Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro Cys Ala Ala Leu
 1 5 10 15

Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val
 20 25 30

Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
 35 40 45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
 50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
 65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
 85 90 95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
 100 105 110

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
 115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
 130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
 145 150 155 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
 165 170 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
 180 185 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu

195

200

205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
 210 215 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
 225 230 235 240

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

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
 260 265 270

Thr Leu Ala Lys Ile
 275

<210> 99
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 99

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
 1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
 20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
 35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
 50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
 65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
85 90 95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
180 185 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
245 250 255

<210> 100

<211> 260

<212> PRT

<213> Homo sapiens

<400> 100

Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val
 1 5 10 15

Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
 20 25 30

Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
 35 40 45

Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
 50 55 60

Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
 65 70 75 80

Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
 85 90 95

Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
 100 105 110

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

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
 130 135 140

Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
 145 150 155 160

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

His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
 180 185 190

Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala

195

200

205

Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
 210 215 220

Pro Val Glu Pro Ala Glu Pro Cys His Tyr Ser Cys Pro Arg Glu Glu
 225 230 235 240

Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
 245 250 255

Ala Cys Ser Pro
 260

<210> 101
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 101

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1 5 10 15

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

Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
 35 40 45

Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 50 55 60

Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
 65 70 75 80

Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
 85 90 95

Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 100 105 110

Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 115 120 125

Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 130 135 140

Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 145 150 155 160

Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
 165 170 175

Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
 180 185 190

Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
 195 200 205

Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
 210 215 220

Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
 225 230 235 240

Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
 245 250 255

Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
 260 265 270

Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
 275 280

<210> 102

<211> 595

<212> PRT

<213> Homo sapiens

<400> 102

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

Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn
 20 25 30

Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys
 35 40 45

Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp
 50 55 60

Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg
 65 70 75 80

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

Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met
 100 105 110

Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His
 115 120 125

Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln
 130 135 140

Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys
 145 150 155 160

Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln
 165 170 175

Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met

180

185

190

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

Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp
 210 215 220

Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys
 225 230 235 240

Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys
 245 250 255

Thr Ala Cys Val Ser Cys Ser Arg Asp Asp Leu Val Glu Lys Thr Pro
 260 265 270

Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile
 275 280 285

Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro
 290 295 300

Ile Cys Ala Ala Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys
 305 310 315 320

Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn
 325 330 335

Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln
 340 345 350

Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr
 355 360 365

Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala
 370 375 380

Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Val Gly
 385 390 395 400

Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
 405 410 415

Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
 420 425 430

Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
 435 440 445

Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
 450 455 460

Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
 465 470 475 480

Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
 485 490 495

Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
 500 505 510

Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
 515 520 525

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

Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
 545 550 555 560

Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
 565 570 575

Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala

580

585

590

Ser Gly Lys
595

<210> 103
<211> 241
<212> PRT
<213> Homo sapiens

<400> 103

Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15

Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30

Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 40 45

Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60

Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65 70 75 80

Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
85 90 95

Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
100 105 110

Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
115 120 125

Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
130 135 140

Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
 145 150 155 160

Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
 165 170 175

Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
 180 185 190

Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
 195 200 205

Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
 210 215 220

Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
 225 230 235 240

Val

<210> 104
 <211> 272
 <212> PRT
 <213> Mus musculus

<400> 104

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

Thr Leu Gly Val Thr Ala Arg Arg Leu Asn Cys Val Lys His Thr Tyr
 20 25 30

Pro Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met
 35 40 45

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

Thr Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys
65 70 75 80

Thr Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr
85 90 95

Pro Thr Gln Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg
100 105 110

Gln Asp Ser Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro
115 120 125

Gly His Phe Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn
130 135 140

Cys Thr Leu Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu
145 150 155 160

Asp Ala Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu
165 170 175

Thr Gln Arg Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val
180 185 190

Trp Pro Arg Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro
195 200 205

Glu Gly Pro Ala Phe Ala Val Leu Leu Gly Leu Gly Leu Gly Leu Leu
210 215 220

Ala Pro Leu Thr Val Leu Leu Ala Leu Tyr Leu Leu Arg Lys Ala Trp
225 230 235 240

Arg Leu Pro Asn Thr Pro Lys Pro Cys Trp Gly Asn Ser Phe Arg Thr
245 250 255

Pro Ile Gln Glu Glu His Thr Asp Ala His Phe Thr Leu Ala Lys Ile

260

265

270

<210> 105

<211> 256

<212> PRT

<213> Mus musculus

<400> 105

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

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
 20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
 35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
 50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
 65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
 85 90 95

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

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
 115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
 130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
 145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
 165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala
 180 185 190

Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
 195 200 205

Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
 210 215 220

Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
 225 230 235 240

Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu
 245 250 255

<210> 106
 <211> 254
 <212> PRT
 <213> cynomolgus

<400> 106

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
 1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Leu Cys Ser Asn Cys Pro
 20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Ser Gln Ile Cys Ser Pro Cys
 35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
 50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Lys Thr Arg Lys Glu Cys Ser Ser
 65 70 75 80

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

Ala Glu Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Ala Thr Pro Pro Ala
165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Phe Phe Leu Ala
180 185 190

Leu Thr Ser Thr Val Val Leu Phe Leu Leu Phe Phe Leu Val Leu Arg
195 200 205

Phe Ser Val Val Lys Arg Ser Arg Lys Lys Leu Leu Tyr Ile Phe Lys
210 215 220

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
225 230 235 240

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
245 250

<210> 107

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 107

Gly Gly Gly Gly Ser

1 5

<210> 108

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 108

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10

<210> 109

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 109

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

1 5 10

<210> 110

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

1 5 10

<210> 111
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 111

Gly Ser Pro Gly Ser Ser Ser Ser Gly Ser
 1 5 10

<210> 112
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 112

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 113
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 113

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser
 20

<210> 114
 <211> 8
 <212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 114

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 115

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 115

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

<210> 116

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 116

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 117

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide linker

<400> 117

Gly Gly Ser Gly Ser Gly

1 5

<210> 118
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 118

Gly Gly Ser Gly
 1

<210> 119
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 119

Gly Gly Ser Gly Asn Gly Ser Gly
 1 5

<210> 120
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Peptide linker

<400> 120

Gly Gly Asn Gly Ser Gly Ser Gly
 1 5

<210> 121
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>

<223> Peptide linker

<400> 121

Gly Gly Asn Gly Ser Gly
 1 5

<210> 122

<211> 186

<212> PRT

<213> cynomolgus

<400> 122

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

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Asn Arg Ser Gln
 20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
 35 40 45

Ser Ala Lys Pro Cys Lys Ala Cys Thr Trp Cys Asn Leu Arg Ser Gly
 50 55 60

Ser Glu Arg Lys Gln Pro Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
 65 70 75 80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
 85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
 100 105 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
 115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
 130 135 140

Pro Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Thr Thr
 145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Arg Pro Ser Thr
 165 170 175

Arg Pro Val Glu Val Pro Arg Gly Pro Ala
 180 185

<210> 123
 <211> 192
 <212> PRT
 <213> Mus musculus

<400> 123

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

His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg
 20 25 30

Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu Thr Gly Phe
 35 40 45

Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr Gln Cys
 50 55 60

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

Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg Gln Asp Ser
 85 90 95

Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly His Phe
 100 105 110

Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu

115

120

125

Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu Asp Ala Val
 130 135 140

Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg
 145 150 155 160

Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val Trp Pro Arg
 165 170 175

Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro Glu Gly Pro
 180 185 190

<210> 124
 <211> 681
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence Fc hole chain

<400> 124
 gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc 60
 ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120
 tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 180
 ggcgtggagg tgcataatgc caagacaaag ccgcggggagg agcagtacaa cagcacgtac 240
 cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300
 tgcaagggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360
 gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 420
 aaccagggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 480
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540
 gacggctcct tcttctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 600
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggtaa a 681

<210> 125

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence human OX40 antigen Fc knob chain

<400> 125

ctgcactgcg tgggcgacac ctaccccagc aacgaccggt gctgccacga gtgcagaccc	60
ggcaacggca tgggtgtcccg gtgcagccgg tcccagaaca ccgtgtgcag accttgccggc	120
cctggcttct acaacgacgt ggtgtccagc aagccctgca agccttgtag ctggtgcaac	180
ctgcggagcg gcagcgagcg gaagcagctg tgtaccgcca cccaggatac cgtgtgccgg	240
tgtagagccg gcacccagcc cctggacagc taaaaacccg gcgtggactg cgccccttgc	300
cctcctggcc acttcagccc tggcgacaac caggcctgca agccttggac caactgcacc	360
ctggccggca agcacaccct gcagcccgcc agcaatagca gcgacgccat ctgcgaggac	420
cgggatcctc ctgccaccca gcctcaggaa acccagggcc ctcccgccag acccatcacc	480
gtgcagccta cagaggcctg gccagaacc agccaggggc ctagcaccag acccgtggaa	540
gtgcctggcg gcagagccgt cgacgaacag ttatatatttc agggcggctc acccaaactct	600
gcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	660
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	720
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	780
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	840
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	900
aagtgcagg tctccaacaa agccctcca gccccatcg agaaaaccat ctcaaagcc	960
aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc	1020
aagaaccagg tcagcctgtg gtgcctggtc aaaggcttct atcccagcga catcgccgtg	1080
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1140

tccgacggct ccttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag	1200
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1260
agcctctccc tgtctccggg taaatccgga ggccctgaacg acatcttcga ggcccagaag	1320
attgaatggc acgag	1335

<210> 126

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence cynomolgus OX40 antigen Fc knob chain

<400> 126

ctccactgtg tcggggacac ctaccccagc aacgaccggg gctgtcagga gtgcaggcca	60
ggcaacggga tgggtgagccg ctgcaaccgc tcccagaaca cggtgtgccg tccgtgcggg	120
cccggcttct acaacgacgt ggtcagcgcc aagccctgca aggcctgcac atggtgcaac	180
ctcagaagtg ggagtgagcg gaaacagccg tgcacggcca cacaggacac agtctgccgc	240
tgccggggcgg gcacccagcc cctggacagc tacaagcctg gagttgactg tgccccctgc	300
cctccagggc acttctcccc gggcgacaac caggcctgca agccctggac caactgcacc	360
ttggccggga agcacaccct gcagccagcc agcaatagct cggacgccat ctgtgaggac	420
agggaccccc cacccacaca gccccaggag acccagggcc ccccgccag gcccaccact	480
gtccagccca ctgaagcctg gcccagaacc tcacagagac cctccacccg gcccgtggag	540
gtccccaggg gccctgcggt cgacgaacag ttatatatttc agggcggctc acccaaattct	600
gcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca	660
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	720
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	780
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	840
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	900
aagtgcagg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc	960

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aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc      1020
aagaaccagg tcagcctgtg gtgcctggtc aaaggcttct atcccagcga catcgccgtg      1080
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac      1140
tccgacggct ctttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag      1200
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag      1260
agcctctccc tgtctccggg taaatccgga ggcctgaacg acatcttcga ggcccagaag      1320
attgaatggc acgag                                                                1335

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<210> 127
<211> 1353
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Nucleotide sequence murine OX40 antigen Fc knob chain

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<400> 127
gtgaccgcca gacggctgaa ctgctgaag cacacctacc ccagcggcca caagtgtgc      60
agagagtgcc agcccgcca cgcatgggtg tccagatgcg accacacacg ggacaccctg      120
tgccaccctt gcgagacagg cttctacaac gaggccgtga actacgatac ctgcaagcag      180
tgcaccaggt gcaaccacag aagcggcagc gagctgaagc agaactgcac cccacccag      240
gataccgtgt gcagatgcag acccggcacc cagcccagac aggacagcgg ctacaagctg      300
ggcgtggact gcgtgccctg ccctcctggc cacttcagcc ccggcaacaa ccaggcctgc      360
aagccctgga ccaactgcac cctgagcggc aagcagacca gacaccccg cagcgacagc      420
ctggatgccg tgtgcgagga cagaagcctg ctggccaccc tgctgtggga gacacagcgg      480
cccaccttca gaccaccac cgtgcagagc accaccgtgt ggcccagaac cagcgagctg      540
cccagtcctc ctaccctcgt gacacctgag ggccccgtcg acgaacagtt atattttcag      600
ggcggctcac ccaaactctg agacaaaact cacacatgcc caccgtgccc agcacctgaa      660
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc      720
tcccggaacc ctgaggtcac atgcgtgggtg gtggacgtga gccacgaaga ccctgaggtc      780

```

```

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag      840
gagcagtaca acagcacgta ccgtgtgggtc agcgtcctca ccgtcctgca ccaggactgg      900
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag      960
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca     1020
tgccgggatg agctgaccaa gaaccagggtc agcctgtggt gcctgggtcaa aggcttctat     1080
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc     1140
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac     1200
aagagcagggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac     1260
aaccactaca cgcagaagag cctctccctg tctccgggta aatccggagg cctgaacgac     1320
atcttcgagg cccagaagat tgaatggcac gag                                  1353

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```

<210> 128
<211> 227
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> Fc hole chain

```

```

<400> 128

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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1           5           10           15

```

```

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
          20           25           30

```

```

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
          35           40           45

```

```

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

```

```

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65           70           75           80

```


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 85 90 95

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

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 115 120 125

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

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
 180 185 190

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro Gly Lys
 225

<210> 129
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human OX40 antigen Fc knob chain

<400> 129

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
 1 5 10 15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
 20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
 35 40 45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
 50 55 60

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

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
 85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
 100 105 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
 115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
 130 135 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
 145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
 165 170 175

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

Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro

195

200

205

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 210 215 220

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 225 230 235 240

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 245 250 255

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 260 265 270

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 275 280 285

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 290 295 300

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 305 310 315 320

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
 325 330 335

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
 340 345 350

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 355 360 365

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 370 375 380

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 385 390 395 400

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 405 410 415

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu
 420 425 430

Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
 435 440 445

<210> 130

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> cynomolgus OX40 antigen

Fc knob chain

<400> 130

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

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Asn Arg Ser Gln
 20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
 35 40 45

Ser Ala Lys Pro Cys Lys Ala Cys Thr Trp Cys Asn Leu Arg Ser Gly
 50 55 60

Ser Glu Arg Lys Gln Pro Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
 65 70 75 80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
 85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala

100

105

110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
 115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
 130 135 140

Pro Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Thr Thr
 145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Arg Pro Ser Thr
 165 170 175

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

Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
 195 200 205

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 210 215 220

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 225 230 235 240

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 245 250 255

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 260 265 270

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 275 280 285

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 290 295 300

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 305 310 315 320

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
 325 330 335

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
 340 345 350

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 355 360 365

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 370 375 380

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 385 390 395 400

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 405 410 415

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu
 420 425 430

Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
 435 440 445

<210> 131

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> murine OX40 antigen Fc knob chain

<400> 131

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

His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg
 20 25 30

Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu Thr Gly Phe
 35 40 45

Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr Gln Cys
 50 55 60

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

Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg Gln Asp Ser
 85 90 95

Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly His Phe
 100 105 110

Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu
 115 120 125

Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu Asp Ala Val
 130 135 140

Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg
 145 150 155 160

Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val Trp Pro Arg
 165 170 175

Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro Glu Gly Pro
 180 185 190

Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp
 195 200 205

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

210

215

220

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 225 230 235 240

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 245 250 255

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 260 265 270

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 275 280 285

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 305 310 315 320

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 325 330 335

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 340 345 350

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 355 360 365

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 370 375 380

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 385 390 395 400

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 405 410 415

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 420 425 430

Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
 435 440 445

Trp His Glu
 450

<210> 132
 <211> 1613
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence of library DP88-4

<400> 132
 tgaaataacct attgcctacg gcagccgctg gattgttatt actcgcggcc cagccggcca 60
 tggccgacat ccagatgacc cagtctcctt ccaccctgtc tgcattctgta ggagaccgtg 120
 tcaccatcac ttgccgtgcc agtcagagta ttagtagctg gttggcctgg tatcagcaga 180
 aaccagggaa agcccctaag ctctgatct atgatgcctc cagtttggaa agtgggggtcc 240
 catcacgttt cagcggcagt ggatccggga cagaattcac tctcaccatc agcagcttgc 300
 agcctgatga ttttgcaact tattactgcc aacagtataa tagttattct acgtttggcc 360
 agggcaccaa agtcgagatc aagcgtacgg tggctgcacc atctgtcttc atcttcccgc 420
 catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg aataacttct 480
 atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg ggtaactccc 540
 aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc agcaccctga 600
 cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc acccatcagg 660
 gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgtggagcc gcagaacaaa 720
 aactcatctc agaagaggat ctgaatggag ccgcagacta caaggacgac gacgacaagg 780
 gtgccgcata ataaggcgcg ccaattctat ttcaaggaga cagtcatatg aaatacctgc 840

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tgccgaccgc tgctgctggc ctgctgctcc tcgctgccc gccggcgatg gcccagggtgc      900
aattgggtgca gtctggggct gaggtgaaga agcctgggtc ctcggtgaaag gtctcctgca      960
aggcctccgg aggcacattc agcagctacg ctataagctg ggtgacgacag gcccctggac     1020
aagggtctga gtggatggga gggatcatcc ctatctttgg tacagcaaac tacgcacaga     1080
agttccaggc cagggtcacc attactgcag acaaatccac gagcacagcc tacatggagc     1140
tgagcagcct gagatctgag gacaccgccg tgtattactg tgcgagacta tccccaggcg     1200
gttactatgt tatggatgcc tggggccaag ggaccaccgt gaccgtctcc tcagctagca     1260
ccaaaggccc atcggctctc cccctggcac cctcctcaa gagcacctct gggggcacag     1320
cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg tcgtggaact     1380
caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc tcaggactct     1440
actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccagc acctacatct     1500
gcaacgtgaa tcacaagccc agcaacacca aagtggacaa gaaagttgag cccaaatctt     1560
gtgacgcggc cgcaagcact agtgcccatc accatcacca tcacgccgcg gca             1613

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<210> 133
<211> 723
<212> DNA
<213> Artificial Sequence

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<220>
<223> nucleotide sequence of Fab light chain Vk1_5

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<400> 133
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gtgccagtca gagtattagt agctgggttg cctggatatca gcagaaacca     120
gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca     180
cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct     240
gatgattttg caacttatta ctgccaacag tataatagtt attctacgtt tggccagggc     300
accaaagtcg agatcaagcg tacggtggct gcaccatctg tcttcacatt cccgccatct     360
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc     420

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agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag      480
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg      540
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg      600
agctcgccccg tcacaaagag cttcaacagg ggagagtgtg gagccgcaga acaaaaaactc      660
atctcagaag aggatctgaa tggagccgca gactacaagg acgacgacga caagggtgcc      720
gca                                                                    723

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<210> 134
<211> 241
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fab light chain Vk1_5

```

```

<400> 134

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100          105          110

```

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 210 215 220

Asp Leu Asn Gly Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala
 225 230 235 240

Ala

<210> 135

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of Fab heavy chain VH1_69

<400> 135

cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

```

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactatcc      300
ccaggcgggtt actatgttat ggatgcctgg ggccaaggga ccaccgtgac cgtctcctca      360
gctagcacca aaggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg      480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc      600
tacatctgca acgtgaatca caagcccagc aacaccaaag tggacaagaa agttgagccc      660
aaatcttggt acgcggccgc aagcactagt gcccatacacc atcaccatca cgccgcggca      720

```

```

<210> 136
<211> 240
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fab heavy chain VH1_69

```

```

<400> 136

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60

```

```

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

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Ala Ala Ala Ser Thr Ser Ala His His His His His His Ala Ala Ala
 225 230 235 240

<210> 137

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> LMB3 Primer

<400> 137

caggaaacag ctatgaccat gattac 26

<210> 138
 <211> 71
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vk1_5_L3r_S Primer

<400> 138
 ctcgactttg gtgccctggc caaacgtsba atacgaatta tactgttggc agtaataagt 60
 tgcaaaatca t 71

<210> 139
 <211> 74
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vk1_5_L3r_SY Primer

<400> 139
 ctcgactttg gtgccctggc caaacgtmhr sgratacgaa ttatactgtt ggcagtaata 60
 agttgcaaaa tcat 74

<210> 140
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vk1_5_L3r_SPY

<400> 140
 ctcgactttg gtgccctggc caaacgtmhh msssgratac gaattatact gttggcagta 60
 ataagttgca aaatcat 77

<210> 141
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> RJH31 Primer

<400> 141

acgttttgcc agggcaccaa agtcgag

27

<210> 142

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> RJH32 Primer

<400> 142

tctcgcacag taatacacgg cggtgtcc

28

<210> 143

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> DP88-v4-4

<400> 143

ggacaccgcc gtgtattact gtgcgagaga ctactggggc caagggacca ccgtgaccgt

60

ctcc

64

<210> 144

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> DP88-v4-6

<400> 144

ggacaccgcc gtgtattact gtgcgagaga ctactggggc caagggacca ccgtgaccgt

60

ctcc

64

<210> 145

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> DP88-v4-8

<400> 145

ggacaccgcc gtgtattact gtgcgagaga ctactggggc caagggacca ccgtgaccgt 60

ctcc 64

<210> 146

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> fdseqlong Primer

<400> 146

gacgttagta aatgaatttt ctgtatgagg 30

<210> 147

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> (Vk3_20/VH3_23) template

<400> 147

atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60

atggccgaaa tcgtgttaac gcagtctcca ggcaccctgt ctttgtctcc aggggaaaga 120

gccaccctct cttgcagggc cagtcagagt gttagcagca gctacttagc ctggtaccag 180

cagaaacctg gccaggctcc caggctcctc atctatggag catccagcag ggccactggc 240

atcccagaca ggttcagtgg cagtggatcc gggacagact tcactctcac catcagcaga 300

ctggagcctg aagattttgc agtgtattac tgtcagcagt atggtagctc accgctgacg 360

ttcggccagg ggaccaaagt ggaaatcaaa cgtacgggtg ctgcaccatc tgtcttcac 420

ttcccgcctat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaagggtg ataacgccct ccaatcgggt 540

```

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc      600
accctgacgc tgagcaaagc agactacgag aaacacaaaag tctacgcctg cgaagtcacc      660
catcagggcc tgagctcgcc cgtcacaaaag agcttcaaca ggggagagtg tggagccgca      720
catcaccatc accatcacgg agccgcagac tacaaggacg acgacgacaa gggtgccgca      780
taataaggcg cgccaattct atttcaagga gacagtcata tgaaatacct gctgccgacc      840
gctgctgctg gtctgctgct cctcgctgcc cagccggcga tggccgaggt gcaattgctg      900
gagtctgggg gaggcttggt acagcctggg ggggtccctga gactctcctg tgcagcctcc      960
ggattcacct ttagcagtta tgccatgagc tgggtccgcc aggctccagg gaaggggctg     1020
gagtgggtct cagctattag tggtagtggg ggtagcacat actacgcaga ctccgtgaag     1080
ggccgggttca ccatctccag agacaattcc aagaacacgc tgtatctgca gatgaacagc     1140
ctgagagccg aggacacggc cgtatattac tgtgcgaaac cgtttccgta ttttgactac     1200
tggggccaag gaaccctggg caccgtctcg agtgctagca ccaaaggccc atcgggtcttc     1260
cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc     1320
aaggactact tccccgaacc ggtgacgggtg tcgtggaact caggcgccct gaccagcggc     1380
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtgggtg     1440
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc     1500
agcaacacca aagtggacaa gaaagttgag cccaaatctt gtgacgcggc cgcagaacaa     1560
aaactcatct cagaagagga tctgaatgcc gcggca                                1596

```

<210> 148

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<223> Fab light chain Vk3_20

<400> 148

```

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa     120

```

```

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgct gacgttcggc      300
cagggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg      360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420
tatcccagag aggccaaaagt acagtggaag gtggataacg cctccaatc gggtaactcc      480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600
ggcctgagct cgcccgtcac aaagagcttc aacagggggag agtgtggagc cgcacatcac      660
catcaccatc acggagccgc agactacaag gacgacgacg acaagggtgc cgca          714

```

```

<210> 149
<211> 238
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Fab light chain Vk3_20

```

```

<400> 149

```

```

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

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20          25          30

```

```

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

```

```

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

```

```

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

```

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

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

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205

Ser Phe Asn Arg Gly Glu Cys Gly Ala Ala His His His His His His
 210 215 220

Gly Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala
 225 230 235

<210> 150

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> Fab heavy chain VH3_23

<400> 150

```

gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc      60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct      120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt      300
ccgtattttg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaaa      360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc      420
ctgggctgcc tggtaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc      480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc      540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac      600
gtgaatcaca agcccagcaa caccaaagtg gacaagaaag ttgagcccaa atcttgtgac      660
gcggccgcag aacaaaaaact catctcagaa gaggatctga atgccgcggc a              711

```

<210> 151

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<223> Fab heavy chain VH3_23 (DP47)

<400> 151

```

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

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20           25           30

```

```

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

```

```

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50           55           60

```

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

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

Ala Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Ala Ala Ala Glu
 210 215 220

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Ala Ala
 225 230 235

<210> 152

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> MS64 Primer

<400> 152

acgttcggcc aggggaccaa agtgg

25

<210> 153

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> DP47CDR3_ba Primer

<400> 153

cgcacagtaa tatacggccg tgtcc

25

<210> 154

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> DP47-v4-4

<400> 154

cgaggacacg gccgtatatt actgtgcgga ctactggggc caaggaaccc tggtcaccgt

60

ctcg

64

<210> 155

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> DP47-v4-6

<400> 155

cgaggacacg gccgtatatt actgtgcgga ctactggggc caaggaaccc tggtcaccgt

60

ctcg

64

<210> 156

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> DP47-v4-8

<400> 156

cgaggacacg gccgtatatt actgtgcgga ctactggggc caaggaaccc tggtcaccgt 60

ctcg 64

<210> 157

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> fdseqlong

<400> 157

gacgttagta aatgaatttt ctgtatgagg 30

<210> 158

<211> 1605

<212> DNA

<213> Artificial Sequence

<220>

<223> V13_19/VH3_23 library template

<400> 158

atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60

atggcctcgt ctgagctgac tcaggaccct gctgtgtctg tggccttggg acagacagtc 120

aggatcacat gccaaaggaga cagcctcaga agttattatg caagctggta ccagcagaag 180

ccaggacagg cccctgtact tgtcatctat ggtaaaaaaca accggccctc agggatccca 240

gaccgattct ctggctccag ctgaggaaac acagcttcct tgaccatcac tggggctcag 300

gcggaagatg aggctgacta ttactgtaac tcccgtgata gtagcggtaa tcatgtggta 360

ttcggcggag ggaccaagct gaccgtccta ggacaacca aggctgcccc cagcgtgacc 420

ctgttcccc ccagcagcga ggaattgcag gccacaagg ccaccctggg ctgcctgatc 480

agcgacttct acccaggcgc cgtgaccgtg gcctggaagg ccgacagcag ccccgatgaag 540


```

gccggcgtgg agaccaccac ccccgcaag cagagcaaca acaagtacgc cgccagcagc      600
tacctgagcc tgacccccga gcagtgggaag agccacaggt cctacagctg ccagggtgacc      660
cacgaggggca gcaccgtgga gaaaaccgtg gccccaccg agtgcagcgg agccgcagaa      720
caaaaactca tctcagaaga ggatctgaat ggagccgcag actacaagga cgacgacgac      780
aagggtgccg cataataagg cgcgccaatt ctatttcaag gagacagtca tatgaaatac      840
ctgctgccga ccgctgctgc tggctgctg ctctcgctg cccagccggc gatggccgag      900
gtgcaattgc tggagtctgg gggaggcttg gtacagcctg gggggtcctt gagactctcc      960
tgtgcagcct ccggattcac ctttagcagt tatgccatga gctgggtccg ccaggctcca     1020
gggaaggggc tggagtgggt ctgagctatt agtggtagt gtggtagcac atactacgca     1080
gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg     1140
cagatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgaa accgtttccg     1200
tattttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaaaggc     1260
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg     1320
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc     1380
ctgaccagcg gcgtgcacac cttcccggt gtcctacagt cctcaggact ctactccctc     1440
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg     1500
aatcacaagc ccagcaacac caaagtggac aagaaaagtt agcccaaatac ttgtgacgcg     1560
gccgcaagca ctagtgccca tcaccatcac catcacgccg cggca                      1605

```

<210> 159

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Fab light chain V13_19

<400> 159

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tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc      60
acatgccaaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga     120

```

```

caggccccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga      180
ttctctgggt ccagctcagg aaacacagct tccttgacca tctctggggc tcaggcggaa      240
gatgaggctg actattactg taactcccgt gatagtagcg gtaatcatgt ggtattcggc      300
ggagggacca agctgaccgt cctaggacaa cccaaggctg ccccagcgt gaccctgttc      360
ccccccagca gcgaggaatt gcaggccaac aaggccaccc tggctctgcct gatcagcgac      420
ttctacccag gcgccgtgac cgtggcctgg aaggccgaca gcagccccgt gaaggccggc      480
gtggagacca ccacccccag caagcagagc aacaacaagt acgccgccag cagctacctg      540
agcctgaccc ccgagcagtg gaagagccac aggtcctaca gctgccaggt gaccacagag      600
ggcagcaccg tggagaaaac cgtggcccc accgagtgca gcggagccgc agaacaaaaa      660
ctcatctcag aagaggatct gaatggagcc gcagactaca aggacgacga cgacaagggt      720
gccgca                                          726

```

```

<210> 160
<211> 242
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Fab light chain V13_19

```

```

<400> 160

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

```

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

Ala Ala

<210> 161

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> LMB3 lambda-DP47 library

<400> 161

caggaaacag ctatgaccat gattac 26

<210> 162

<211> 85

<212> DNA

<213> Artificial Sequence

<220>

<223> V1_3_19_L3r_V lambda-DP47 library

<400> 162

ggacgggtcag cttgggtccct ccgccgaata cvhvattacc gctactatca cgggaggttac 60

agtaatagtc agcctcatct tccgc 85

<210> 163

<211> 88

<212> DNA

<213> Artificial Sequence

<220>

<223> V1_3_19_L3r_HV lambda-DP47

<400> 163

ggacgggtcag cttgggtccct ccgccgaata ccmmtgatt accgctacta tcacgggagt 60

tacagtaata gtcagcctca tcttccgc 88

<210> 164

<211> 91

<212> DNA

<213> Artificial Sequence

<220>

<223> V1_3_19_L3r_HLV lambda-DP47

<400> 164

ggacgggtcag cttgggtccct ccgccgaata crhmvwgatg attaccgcta ctatcacggg 60

agttacagta atagtcagcc tcatcttccg c 91

<210> 165
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> RJH80 lambda-DP47

<400> 165
 ttcggcggag ggaccaagct gaccgtcc 28

<210> 166
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (8H9) VL

<400> 166
 tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60
 acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120
 caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180
 ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240
 gatgaggctg actattactg taactcccgt gttatgcctc ataatcgcgt attcggcgga 300
 gggaccaagc tgaccgtc 318

<210> 167
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (8H9) VH

<400> 167
 gaggtgcaat tgttgagtc tgggggaggc ttgttacagc ctggggggc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagt ggtctcagct attagtggta gtgggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttttc 300
 taccgtgggtg gtgttttctat ggactactgg ggccaaggaa ccctgggtcac cgtctcgagt 360

<210> 168
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (49B4) VL

<400> 168
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctgggttg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag tatagtctgc agccgtatac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 169
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (49B4) VH

<400> 169
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300
 taccgtgggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctca 354

<210> 170
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (1G4) VL

<400> 170
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag tatatttcgt attccatgtt gacgtttggc 300
 cagggcacca aagtcgagat caag 324

<210> 171
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (1G4) VH

<400> 171
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300
 ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctca 348

<210> 172
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>

<223> DNA (20B7) VL

<400> 172

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gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gtgccagtca gagtattagt agctggttgg cctgggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca      180
cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct      240
gatgattttg caacttatta ctgccaacag tatcaggcctt tttcgcttac gtttggccag      300
ggcaccaaag tcgagatcaa g                                              321

```

<210> 173

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (20B7) VH

<400> 173

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caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac      300
taccctgact cttactgggg tgacttcgac tactggggcc aagggaccac cgtgaccgtc      360
tcctca                                              366

```

<210> 174

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (CLC-563) VL

<400> 174


```

gagatcgtgc tgaccagag ccccggcaca ctctccctgt ctctgggga aaggccacc      60
ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag    120
ccaggacaag cccccgcct cctgatttac ggcgcttcct ctcgggcaac tggtatccct    180
gacaggttct caggagcgg aagcggaaca gattttacct tgactatttc tagactggag    240
ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagccccct cacctttggc    300
caggggacaa aagtcgaaat caag                                           324

```

```

<210> 175
<211> 348
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> DNA (CLC-563) VH

```

```

<400> 175
gaggtgcaat tgttgagtc tgggggaggc ttgttacagc ctggggggtc cctgagactc      60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct    120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac    180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat     240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcttgacgtt    300
ggtgctttcg actactgggg ccaaggagcc ctggtcaccg tctcgagt                 348

```

```

<210> 176
<211> 324
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> DNA (CLC-564) VL

```

```

<400> 176
gagatcgtgc tgaccagag ccccggcaca ctctccctgt ctctgggga aaggccacc      60
ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag    120
ccaggacaag cccccgcct cctgatttac ggcgcttcct ctcgggcaac tggtatccct    180

```

gacaggttct cagggagcgg aagcggaaca gattttacct tgactatttc tagactggag 240
ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagccccct cacctttggc 300
caggggacaa aagtcgaaat caag 324

<210> 177
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA (CLC-564) VH

<400> 177
gaggtgcaat tgttggagtc tgggggaggc ttgttacagc ctgggggggc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gttcgacgtt 300
gggccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagt 348

<210> 178
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA (17A9) VL

<400> 178
tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60
acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120
caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat ccagaccga 180
ttctctggct ccagctcagg aaacacagct tccttgacca tcaactggggc tcaggcggaa 240
gatgaggctg actattactg taactcccgt gttatgcctc ataatcgctg attcggcgga 300
gggaccaagc tgaccgtc 318

<210> 179
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (17A9) VH

<400> 179
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttttc 300
 taccgtgggtg gtgtttctat ggactactgg ggccaaggaa ccctgggtcac cgtctcgagt 360

<210> 180
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 8H9 P329GLALA IgG1 light chain

<400> 180
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag tatttgacgt attcgcggtt tacgtttggc 300
 cagggcacca aagtcgagat caagcgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
 ggccctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 181
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 8H9 P329GLALA IgG1 heavy chain

<400> 181
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300
 ggttgatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360
 ggcccatcgg tcttccccct ggacacctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgtcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggagggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac 1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tccctgtctc cgggtaaa 1338

<210> 182
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> 8H9 P329GLALA IgG1 light chain

<400> 182

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

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

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

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

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

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

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser

115

120

125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 183
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 8H9 P329GLALA IgG1 Heavy chain

<400> 183

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

50

55

60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Trp Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 184

<211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 49B4 P329GLALA IgG1 light chain

<400> 184
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag tatagttcgc agccgtatac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 185
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 49B4 P329GLALA IgG1 heavy chain

<400> 185
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

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taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc      360
accaagggcc catcgggtctt ccccttggca ccctcctcca agagcacctc tgggggcaca      420
gcggcccttg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac      480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc      540
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc      600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagtga gcccaaattc      660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca      720
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgga ccttgaggtc      780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg      840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg      900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac      960
aagtgcaagg tctccaacaa agccctcggc gccccatcg agaaaacat ctccaaagcc     1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc     1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg     1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac     1200
tccgacggct ctttcttct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag     1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag     1320
agcctctccc tgtctccggg taaa                                             1344

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<210> 186

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 49B4 P329GLALA IgG1 light chain

<400> 186

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys

210

<210> 187
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 49B4 heavy chain

<400> 187

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145					150					155					160
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
				165					170					175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
				180					185					190	
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
				195					200					205	
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
				210					215					220	
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser
				225					230					235	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
				260					265					270	
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				275					280					285	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
				290					295					300	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
				305					310					315	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
				340					345					350	

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 188

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA 1G4 P329GLALA IgG1 light chain

<400> 188

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggatatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatatttcgt attccatggt gacgtttggc 300

cagggcacca aagtcgagat caagcgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
 ggcttgagct cgcccgtcac aaagagcttc aacagggggag agtgt 645

<210> 189
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 1G4 P329GLALA IgG1 heavy chain

<400> 189
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 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatggggagg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300
 ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cggtgtcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggctctca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020

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cagccccgag aaccacaggt gtacaccctg ccccatcccc gggatgagct gaccaagaac      1080
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg      1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac      1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac      1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc      1320
tccctgtctc cgggtaaa                                           1338

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<210> 190

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> 1G4 P329GLALA IgG1 light chain

<400> 190

```

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

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

```

```

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

```

```

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

```

```

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

```

```

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ile Ser Tyr Ser Met
85           90           95

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

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Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 191
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1G4 P329GLALA IgG1 heavy chain

<400> 191

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro

245

250

255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 192
 <211> 642
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DNA 20B7 P329GLALA IgG1 light chain

<400> 192
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctgggttg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag tatcaggctt ttctgcttac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 193
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 20B7 P329GLALA IgG1 heavy chain

<400> 193
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatggggagg atcatcccta tctttggtac agcaaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

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atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac      300
taccctgact cttactgggg tgacttcgac tactggggcc aaggggaccac cgtgaccgtc      360
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc      420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg      480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag      540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc      600
cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaagggtgga caagaaagtt      660
gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaagctgca      720
gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      780
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      960
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcg gcgcccccat cgagaaaacc     1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg     1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc     1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct     1200
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc     1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac     1320
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1356

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<210> 194
<211> 214
<212> PRT
<213> Artificial

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<220>
<223> 20B7 P329GLALA IgG1 Light chain

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```

<400> 194

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Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly

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

Phe Asn Arg Gly Glu Cys
210

<210> 195

<211> 452

<212> PRT

<213> Artificial

<220>

<223> 20B7 P329GLALA IgG1 heavy chain

<400> 195

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Val Asn Tyr Pro Tyr Ser Tyr Trp Gly Asp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

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

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

340

345

350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro Gly Lys
 450

<210> 196
 <211> 645
 <212> DNA
 <213> Artificial

<220>
 <223> DNA CLC-563 P329GLALA IgG1 light chain

<400> 196
 gagatcgtgc tgacccagag ccccggcaca ctctccctgt ctcctgggga aagggccacc 60
 ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag 120
 ccaggacaag cccccgcct cctgatttac ggcgcttcct ctcgggcaac tggtatccct 180
 gacaggttct caggggagcgg aagcggaaca gattttacct tgactatttc tagactggag 240
 ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagccccct cacctttggc 300

caggggacaa aagtcgaaat caagcgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatcccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
 ggcttgagct cgcccgctac aaagagcttc aacaggggag agtgt 645

<210> 197
 <211> 1338
 <212> DNA
 <213> Artificial

<220>
 <223> DNA CLC-563 P329GLALA IgG1 heavy chain

<400> 197
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcttgacgtt 300
 ggtgctttcg actactgggg ccaaggagcc ctggtcaccg tctcgagtgc tagcaccaag 360
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tggtaagga ctacttcccc gaaccgggtga cgggtgctgt gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtagc 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

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gtggagggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt      900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc      960
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg    1020
cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac    1080
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg    1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac    1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac    1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc    1320
tccctgtctc cgggtaaa                                     1338

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<210> 198
<211> 215
<212> PRT
<213> Artificial

```

```

<220>
<223> CLC-563 P329GLALA IgG1 light chain

```

```

<400> 198

```

```

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

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
          20           25           30

```

```

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

```

```

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

```

```

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

```

```

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

```

85

90

95

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

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 199

<211> 446

<212> PRT

<213> Artificial

<220>

<223> CLC-563 P329GLALA IgG1 heavy chain

<400> 199

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Leu Asp Val Gly Ala Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His

420

425

430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 200

<211> 645

<212> DNA

<213> Artificial

<220>

<223> DNA CLC-564 P329GLALA IgG1 light chain

<400> 200

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gagatcgtgc tgaccagag ccccggcaca ctctccctgt ctctgggga aaggccacc      60
ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag    120
ccaggacaag ccccccgcct cctgatttac ggcgcttcct ctcgggcaac tggatatcct    180
gacaggttct caggagcgg aagcggaca gattttacct tgactatttc tagactggag     240
ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagccccct cacctttggc    300
caggggacaa aagtcgaaat caagcgtacg gtggctgcac catctgtctt catcttcccg   360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc   420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtactcc     480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg    540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag    600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt                    645

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<210> 201

<211> 1338

<212> DNA

<213> Artificial

<220>

<223> DNA CLC-564 P329GLALA IgG1 heavy chain

<400> 201

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gagggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc    60

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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gttcgacgtt	300
gggccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgtcgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac	660
aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc	720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	780
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gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	960
aagggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg	1020
cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac	1080
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg	1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtaaa	1338

<210> 202
 <211> 215
 <212> PRT
 <213> Artificial

<220>

<223> CLC-564 P329GLALA IgG1 light chain

<400> 202

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

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

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

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

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

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

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val

180

185

190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 203
 <211> 446
 <212> PRT
 <213> Artificial

<220>
 <223> CLC-564 P329GLALA IgG1 heavy chain

<400> 203

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Phe Asp Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

115

120

125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 204

<211> 639

<212> DNA

<213> Artificial

<220>

<223> DNA 17A9 P329GLALA IgG1 light chain

<400> 204

tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactcccgt gttatgcctc ataatcgcgt attcggcgga 300
 gggaccaagc tgaccgtcct aggtcaaccc aaggctgccc ccagcgtgac cctgttcccc 360
 cccagcagcg aggaactgca ggccaacaag gccaccctgg tctgcctgat cagcgacttc 420
 taccagggcg ccgtgaccgt ggcctggaag gccgacagca gccccgtgaa ggccggcgtg 480
 gagaccacca cccccagcaa gcagagcaac aacaagtacg ccgccagcag ctacctgagc 540
 ctgacccccg agcagtggaa gagccacagg tcctacagct gccaggtgac ccacgagggc 600
 agcaccgtgg agaaaaccgt ggccccccacc gagtgcagc 639

<210> 205
 <211> 1350
 <212> DNA
 <213> Artificial

<220>
 <223> DNA 17A9 P329GLALA IgG1 heavy chain

<400> 205
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 tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttttc 300
 taccgtgggtg gtgttttctat ggactactgg ggccaaggaa ccctgggtcac cgtctcgagt 360
 gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
 ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga 720
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 780

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gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
tacgtggacg gcgtggagggt gcataatgcc aagacaaaagc cgcgaggagga gcagtacaac      900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc     1020
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag     1080
ctgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg     1260
cagcaggggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                     1350

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<210> 206
<211> 213
<212> PRT
<213> Artificial

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<220>
<223> 17A9 P329GLALA IgG1 light chain

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<400> 206

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

```

```

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

```

```

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

```

```

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

```

```

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65           70           75          80

```

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Val Met Pro His Asn Arg
 85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
 100 105 110

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
 115 120 125

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

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
 145 150 155 160

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
 165 170 175

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 180 185 190

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
 195 200 205

Pro Thr Glu Cys Ser
 210

<210> 207

<211> 450

<212> PRT

<213> Artificial

<220>

<223> 17A9 P329GLALA IgG1 heavy chain

<400> 207

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Val Phe Tyr Arg Gly Gly Val Ser Met Asp Tyr Trp Gly Gln
 100 105 110

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

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp

210

215

220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 208
 <211> 663
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> human OX40 His nucleotide sequence

<400> 208
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 ggcaacggca tgggtgtccc gtgcagccgg tcccagaaca ccgtgtgcag accttgcggc 120
 cctggcttct acaacgacgt ggtgtccagc aagccctgca agccttgtag ctggtgcaac 180
 ctgcggagcg gcagcgagcg gaagcagctg tgtaccgcca cccaggatac cgtgtgccgg 240
 tgtagagccg gcacccagcc cctggacagc tacaaccccg gcgtggactg cgccccttgc 300
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 ctggccggca agcacaccct gcagcccgcc agcaatagca gcgacgccat ctgcgaggac 420
 cgggatcctc ctgccacca gcctcaggaa acccagggcc ctcccgccag acccatcacc 480
 gtgcagccta cagaggcctg gcccagaacc agccaggggc ctagcaccag acccgtggaa 540
 gtgcctggcg gcagagccgt cgacgaacag ttatatatttc agggcgggctc aggcctgaac 600
 gacatcttcg agggccagaa gatcgagtgg cacgaggctc gagctcacca ccatcaccat 660
 cac 663

<210> 209
 <211> 221
 <212> PRT

<213> Artificial Sequence

<220>

<223> human OX40 His

<400> 209

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
1 5 10 15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
35 40 45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
50 55 60

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

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
100 105 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
130 135 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
165 170 175

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

Phe Gln Gly Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
 195 200 205

Glu Trp His Glu Ala Arg Ala His His His His His His
 210 215 220

<210> 210
 <211> 681
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA murine OX40 His

<400> 210
 gtgaccgcca gacggctgaa ctgctgaag cacacctacc ccagcggcca caagtgtctgc 60
 agagagtgcc agcccgcca cgcatggtg tccagatgcg accacacacg ggacaccctg 120
 tgccaccctt gcgagacagg cttctacaac gaggccgtga actacgatac ctgcaagcag 180
 tgcaccagt gcaaccacag aagcggcagc gagctgaagc agaactgcac cccacccag 240
 gataccgtgt gcagatgcag acccggcacc cagcccagac aggacagcgg ctacaagctg 300
 ggcgtggact gcgtgccctg ccctcctggc cacttcagcc ccggcaacaa ccaggcctgc 360
 aagccctgga ccaactgcac cctgagcggc aagcagacca gacacccgc cagcgacagc 420
 ctggatgccg tgtgcgagga cagaagcctg ctggccaccc tgctgtggga gacacagcgg 480
 cccaccttca gacccaccac cgtgcagagc accaccgtgt ggcccagaac cagcgagctg 540
 cccagtcctc ctaccctcgt gacacctgag ggccccgtcg acgaacagtt atattttcag 600
 ggcggctcag gcctgaacga catcttcgag gccagaaga tcgagtggca cgaggctcga 660
 gctcaccacc atcaccatca c 681

<210> 211
 <211> 226
 <212> PRT

<213> Artificial Sequence

<220>

<223> murine OX40 His

<400> 211

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

Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg Cys
20 25 30

Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu Thr Gly Phe Tyr
35 40 45

Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr Gln Cys Asn
50 55 60

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

Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg Gln Asp Ser Gly
85 90 95

Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly His Phe Ser
100 105 110

Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu Ser
115 120 125

Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu Asp Ala Val Cys
130 135 140

Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg Pro
145 150 155 160

Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val Trp Pro Arg Thr
165 170 175

Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro Glu Gly Pro Val
 180 185 190

Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Gly Leu Asn Asp Ile Phe
 195 200 205

Glu Ala Gln Lys Ile Glu Trp His Glu Ala Arg Ala His His His His
 210 215 220

His His
 225

<210> 212
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence dimeric human OX40 antigen Fc

<400> 212
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 cctggcttct acaacgacgt ggtgtccagc aagccctgca agccttgtag ctggtgcaac 180
 ctgctggagcgc gcagcgagcgc gaagcagctg tgtaccgcca cccaggatac cgtgtgccgg 240
 tgttagagccg gcacccagcc cctggacagc taaaaacccg gcgtggactg cggcccttgc 300
 cctcctggcc acttcagccc tggcgacaac caggcctgca agccttggac caactgcacc 360
 ctggccggca agcacaccct gcagcccgcc agcaatagca gcgacgccat ctgcgaggac 420
 cgggatcctc ctgccaccca gcctcaggaa acccagggcc ctcccgccag acccatcacc 480
 gtgcagccta cagaggcctg gccagaacc agccaggggc ctagcaccag acccgtggaa 540
 gtgcctggcg gcagagccgt cgacgaacag ttatatatttc agggcggctc acccaaattct 600
 gcagacaaaa ctacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 660
 gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc 720

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acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg      780
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg      840
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac      900
aagtgcaagg tctccaacaa agccctcggc gccccatcg agaaaacat ctccaaagcc      960
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc     1020
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg     1080
gagtgggaga gcaatgggca gccggagAAC aactacaaga ccacgcctcc cgtgctggac     1140
tccgacggct ctttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag     1200
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag     1260
agcctctccc tgtctccggg taaatccggc tacccatacg atgttccaga ttacgct      1317

```

```

<210> 213
<211> 439
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> dimeric human OX40 antigen Fc

```

```

<400> 213

```

```

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
1           5           10           15

```

```

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
          20           25           30

```

```

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
          35           40           45

```

```

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
          50           55           60

```

```

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

```

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
100 105 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
130 135 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
165 170 175

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

Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
195 200 205

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
210 215 220

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
225 230 235 240

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
245 250 255

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
260 265 270

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

275

280

285

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 290 295 300

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 305 310 315 320

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 325 330 335

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 340 345 350

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 355 360 365

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 370 375 380

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 385 390 395 400

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 405 410 415

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Tyr Pro
 420 425 430

Tyr Asp Val Pro Asp Tyr Ala
 435

<210> 214

<211> 2064

<212> DNA

<213> Artificial Sequence

<220>

<223> (8B9) VHCH1-Heavy chain-(28H1) VHCL

<400> 214
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagt gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300
ggttggtatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360
ggcccatccg tgttcctct ggccccttcc agcaagtcta cctctggcgg cacagccgct 420
ctgggctgcc tcgtgaagga ctacttcccc gagcctgtga cagtgtcctg gaactctggc 480
gccctgacat ccggcgtgca cacctttcca gctgtgctgc agtcctccgg cctgtactcc 540
ctgtcctccg tcgtgacagt gccctccagc tctctgggca cccagaccta catctgcaac 600
gtgaaccaca agccctccaa caccaagggt gacaagaagg tggaacccaa gtcctgcgac 660
aagaccacaca cctgtcccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc 720
ctgttcccc caaagcccaa ggacaccctg atgatctccc ggacccccga agtgacctgc 780
gtggtggtgg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840
gtggaagtgc acaatgccaa gaccaagcct agagaggaac agtacaactc cacctaccgg 900
gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaaaga gtacaagtgc 960
aaggtgtcca acaaggccct gggagcccc atcgaaaaga ccatctccaa ggccaagggc 1020
cagcctcgcg agcctcaggt gtacaccctg ccccttagca gagatgagct gaccaagaac 1080
caggtgtccc tgacctgtct cgtgaaaggc ttctaccct ccatatcgc cgtggaatgg 1140
gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgac 1200
ggctcattct tcctgtactc taagctgaca gtggacaagt cccggtggca gcagggaac 1260
gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacacca gaagtccctg 1320
tccctgtctc ccgggggagg cggaggatct ggcgaggcg gatccggtgg tggcggatct 1380
gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc 1440

ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt 1500
 tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggccctccggc 1560
 gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcggga taacagcaag 1620
 aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc 1680
 gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg 1740
 agcgcttctg tggccgctcc ctccgtgttc atcttccac cttccgacga gcagctgaag 1800
 tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcggga agccaagggtg 1860
 cagtggaaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag 1920
 gactccaagg acagcaccta ctccctgagc agcaccctga ccctgtccaa ggccgactac 1980
 gagaagcaca aggtgtacgc ctgtgaagtg acccaccagg gcctgtccag ccccgtagacc 2040
 aagtccttca accggggcga gtgc 2064

<210> 215

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA VLCH1-Light chain 2 (28H1)

<400> 215

gagatcgtgc tgacccagtc tcccggcacc ctgagcctga gccctggcga gagagccacc 60
 ctgagctgca gagccagcca gagcgtgagc cggagctacc tggcctggta tcagcagaag 120
 cccggccagg cccccagact gctgatcatc ggccgagca cccgggccac cggcatcccc 180
 gatagattca gcggcagcgg ctccggcacc gacttcaccc tgaccatcag ccggctggaa 240
 cccgaggact tcgccgtgta ctactgccag cagggccagg tgatcccccc caccttcggc 300
 cagggcacca aggtggaaat caagagctcc gctagcacca agggcccctc cgtgtttcct 360
 ctggcccccga gcagcaagag cacctctggc ggaacagccg ccctgggctg cctggtgaaa 420
 gactacttcc ccgagcccgt gaccgtgtcc tggaactctg gcgccctgac cagcggcgtg 480
 cacacctttc cagccgtgct gcagagcagc ggccgtgtact ccctgagcag cgtggtgaca 540

gtgccctcca gcagcctggg caccagacc tacatctgca acgtgaacca caagcccagc 600

aacaccaaag tggacaagaa ggtggaaccc aagagctgcg ac 642

<210> 216

<211> 688

<212> PRT

<213> Artificial Sequence

<220>

<223> (8B9) VHCH1-Heavy chain-(28H1) VHCL

<400> 216

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Trp Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

340

345

350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
 435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 465 470 475 480

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
 485 490 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 500 505 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
 515 520 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 530 535 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 545 550 555 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 565 570 575

Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
 580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 675 680 685

<210> 217

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> VLCH1-Light chain 2 (28H1)

<400> 217

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Ser
 20 25 30

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

Ile Ile Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

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

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ala Ser
 100 105 110

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

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 145 150 155 160

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

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
 180 185 190

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 195 200 205

Glu Pro Lys Ser Cys Asp

210

<210> 218
 <211> 2070
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (49B4) VHCH1-Heavy chain-(28H1) VHCL

<400> 218
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300
 taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360
 accaagggcc catccgtgtt cctcttgccc ccttccagca agtctacctc tggcggcaca 420
 gccgctcttg gctgcctcgt gaaggactac ttccccgagc ctgtgacagt gtcctggaac 480
 tctggcgccc tgacatccgg cgtgcacacc tttccagctg tgctgcagtc ctccggcctg 540
 tactccctgt cctccgtcgt gacagtgtccc tccagctctc tgggcaccca gacctacatc 600
 tgcaacgtga accacaagcc ctccaacacc aagggtggaca agaagggtgga acccaagtcc 660
 tgcgacaaga cccacacctg tcccccttgt cctgcccctg aagctgctgg cggccctagc 720
 gtgttcctgt tcccccaaaa gcccaaggac accctgatga tctcccggac ccccgaagtg 780
 acctgcgtgg tgggtgatgt gtcccacgag gaccctgaag tgaagttcaa ttggtacgtg 840
 gacggcgtgg aagtgcacaa tgccaagacc aagcctagag aggaacagta caactccacc 900
 taccgggtgg tgtccgtgct gaccgtgctg caccaggatt ggctgaacgg caaagagtac 960
 aagtgcagg tgccaacaa ggccctggga gccccatcg aaaagaccat ctccaaggcc 1020
 aagggccagc ctcgcgagcc tcaggtgtac accctgcccc ctagcagaga tgagctgacc 1080
 aagaaccagg tgtccctgac ctgtctcgtg aaaggcttct acccctccga tatcgccgtg 1140

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gaatgggaga gcaacggcca gcccgagaac aactacaaga ccaccccccc tgtgctggac      1200
tccgacggct cattcttcct gtactctaag ctgacagtgg acaagtcccc gtggcagcag      1260
ggcaacgtgt tctcctgctc cgtgatgcac gaggccctgc acaaccacta caccagaag      1320
tccctgtccc tgtctcccgg gggaggcgga ggatctggcg gaggcggatc cgggtggtggc      1380
ggatctgggg gcggtggatc tgaggtgcag ctgctggaat ctgggggagg actggtgcag      1440
ccaggcggat ctctgaggct gtcctgcgct gcttccggct ttaccttctc cagccacgcc      1500
atgagttggg tgcgccaggc acccggaaaa ggactggaat ggggtgtcagc catctgggcc      1560
tccggcgagc agtactacgc cgatagcgtg aagggccggt tcaccatctc tcgggataac      1620
agcaagaata ctctgtacct gcagatgaac tccctgcgcg ctgaagatac cgctgtgtat      1680
tactgcgcca agggctggct gggcaacttc gattactggg gccagggaac cctcgtgact      1740
gtctcgagcg cttctgtggc cgctccctcc gtgttcatct tcccaccttc cgacgagcag      1800
ctgaagtccg gcactgcctc tgctgtgtgc ctgctgaaca acttctaccc tcgggaagcc      1860
aaggtgcagt ggaaagtgga taacgccctg cagtccggca actcccagga atccgtgacc      1920
gagcaggact ccaaggacag cacctactcc ctgagcagca ccctgaccct gtccaaggcc      1980
gactacgaga agcacaaggt gtacgcctgt gaagtgaccc accagggcct gtccagcccc      2040
gtgaccaagt ccttcaaccg gggcgagtgc      2070

```

<210> 219

<211> 690

<212> PRT

<213> Artificial Sequence

<220>

<223> (49B4) VHCH1-Heavy chain-(28H1) VHCL

<400> 219

```

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

```

```

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

```

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 485 490 495

Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 500 505 510

Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp
 515 520 525

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 545 550 555 560

Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly
 565 570 575

Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe
 580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 610 615 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr

625	630	635	640
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr			
	645	650	655
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val			
	660	665	670
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly			
	675	680	685
Glu Cys			
690			

<210> 220
 <211> 2064
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (1G4) VHCH1-Heavy chain-(28H1) VHCL

<400> 220	
cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac	300
ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag	360
ggcccatccg tgttccctct ggccccttcc agcaagtcta cctctggcgg cacagccgct	420
ctgggctgcc tcgtgaagga ctacttcccc gagcctgtga cagtgtcctg gaactctggc	480
gccctgacat ccggcgtgca cacctttcca gctgtgctgc agtcctccgg cctgtactcc	540
ctgtcctccg tcgtgacagt gccctccagc tctctgggca cccagaccta catctgcaac	600
gtgaaccaca agccctccaa caccaagggtg gacaagaagg tggaacccaa gtcctgcgac	660

aagacccaca cctgtccccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc	720
ctgttccccc caaagcccaa ggacaccctg atgatctccc ggacccccga agtgacctgc	780
gtggtggtgg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc	840
gtggaagtgc acaatgccaa gaccaagcct agagaggaac agtacaactc cacctaccgg	900
gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaaaga gtacaagtgc	960
aaggtgtcca acaaggccct gggagccccc atcgaaaaga ccatctccaa ggccaagggc	1020
cagcctcgcg agcctcaggt gtacaccctg ccccttagca gagatgagct gaccaagaac	1080
caggtgtccc tgacctgtct cgtgaaaggc ttctaccctt ccgatatcgc cgtggaatgg	1140
gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgac	1200
ggctcattct tcctgtactc taagctgaca gtggacaagt cccgggtggca gcagggcaac	1260
gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacacca gaagtccttg	1320
tccctgtctc ccgggggagg cggaggatct ggcgaggcg gatccggtgg tggcggatct	1380
gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc	1440
ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt	1500
tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggctccggc	1560
gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcgga taacagcaag	1620
aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc	1680
gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg	1740
agcgcttctg tggccgctcc ctccgtgttc atcttccac cttccgacga gcagctgaag	1800
tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcggga agccaaggtg	1860
cagtggaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag	1920
gactccaagg acagcaccta ctccctgagc agcacctga ccctgtccaa ggccgactac	1980
gagaagcaca aggtgtacgc ctgtgaagtg acccaccagg gcctgtccag ccccgtagc	2040
aagtccttca accggggcga gtgc	2064

<211> 688
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (1G4) VHCH1-Heavy chain-(28H1) VHCL

<400> 221

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser

165

170

175

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
 435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 465 470 475 480

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
 485 490 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 500 505 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
 515 520 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 530 535 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 545 550 555 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu

565

570

575

Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
 580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 675 680 685

<210> 222

<211> 2082

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (20B7) VHCH1-Heavy chain-(28H1) VHCL

<400> 222

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac 300

tacccgtact cttactgggg tgacttcgac tactggggcc aaggggaccac cgtgaccgtc	360
tcctcagcta gcaccaaggg cccatccgtg ttccctctgg ccccttccag caagtctacc	420
tctggcggca cagccgctct gggctgcctc gtgaaggact acttccccga gcctgtgaca	480
gtgtcctgga actctggcgc cctgacatcc ggcgtgcaca cttttccagc tgtgctgcag	540
tcctccggcc tgtactccct gtcctccgtc gtgacagtgc cctccagctc tctgggcacc	600
cagacctaca tctgcaacgt gaaccacaag ccctccaaca ccaaggtgga caagaaggtg	660
gaacccaagt cctgcgacaa gaccacacc tgtccccctt gtcctgcccc tgaagctgct	720
ggcggcccta gcgtgttcct gttccccca aagccaagg acaccctgat gatctcccgg	780
acccccgaag tgacctgcgt ggtggtggat gtgtcccacg aggaccctga agtgaagttc	840
aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagcctag agaggaacag	900
tacaactcca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac	960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgg gagccccat cgaaaagacc	1020
atctccaagg ccaagggcca gcctcgcgag cctcaggtgt acaccctgcc ccctagcaga	1080
gatgagctga ccaagaacca ggtgtccctg acctgtctcg tgaaaggctt ctaccctcc	1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc	1200
cctgtgctgg actccgacgg ctcatcttct ctgtactcta agctgacagt ggacaagtcc	1260
cgggtggcagc agggcaacgt gttctcctgc tccgtgatgc acgaggccct gcacaaccac	1320
tacaccacga agtccctgtc cctgtctccc gggggaggcg gaggatctgg cggaggcgga	1380
tccggtggtg gcggatctgg gggcgggtgga tctgaggtgc agctgctgga atctggggga	1440
ggactggtgc agccaggcgg atctctgagg ctgtcctgcg ctgcttccgg ctttaccttc	1500
tccagccacg ccatgagttg ggtgcgccag gcacccggaa aaggactgga atgggtgtca	1560
gccatctggg cctccggcga gcagtactac gccgatagcg tgaagggccg gttcaccatc	1620
tctcgggata acagcaagaa tactctgtac ctgcagatga actccctgcg cgctgaagat	1680
accgctgtgt attactgcgc caagggtggt ctgggcaact tcgattactg gggccaggga	1740
accctcgtga ctgtctcgag cgcttctgtg gccgctccct ccgtgttcat cttccacct	1800

tccgacgagc agctgaagtc cggcactgcc tctgtcgtgt gcctgctgaa caacttctac 1860
 cctcgggaag ccaaggtgca gtggaaaagtg gataacgccc tgcagtccgg caactcccag 1920
 gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgagcag caccctgacc 1980
 ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gtgaagtgac ccaccagggc 2040
 ctgtccagcc ccgtgaccaa gtccttcaac cggggcgagt gc 2082

<210> 223
 <211> 694
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (20B7) VHCH1-Heavy chain-(28H1) VHCL

<400> 223

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Val Asn Tyr Pro Tyr Ser Tyr Trp Gly Asp Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro

115

120

125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

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

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 450 455 460

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
 465 470 475 480

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 485 490 495

Gly Phe Thr Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro
 500 505 510

Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln

515

520

525

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 530 535 540

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 545 550 555 560

Thr Ala Val Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr
 565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala
 580 585 590

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 595 600 605

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 610 615 620

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 625 630 635 640

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 645 650 655

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 660 665 670

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 675 680 685

Phe Asn Arg Gly Glu Cys
 690

<210> 224

<211> 2064

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (CLC-563) VHCH1-Heavy chain-(28H1) VHCL

<400> 224

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcttgacgtt	300
ggtgctttcg actactgggg ccaaggagcc ctggtcaccg tctcgagtgc tagcaccaag	360
ggcccatccg tgttccctct ggccccttcc agcaagtcta cctctggcgg cacagccgct	420
ctgggctgcc tcgtgaagga ctacttcccc gagcctgtga cagtgtcctg gaactctggc	480
gccctgacat ccggcgtgca cacctttcca gctgtgctgc agtcctccgg cctgtactcc	540
ctgtcctccg tcgtgacagt gccctccagc tctctgggca cccagaccta catctgcaac	600
gtgaaccaca agccctccaa caccaagggtg gacaagaagg tggaacccaa gtcctgcgac	660
aagaccaca cctgtcccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc	720
ctgttcccc caaagcccaa ggacaccctg atgatctccc ggacccccga agtgacctgc	780
gtggtgggtg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc	840
gtggaagtgc acaatgcaa gaccaagcct agagaggaac agtacaactc cacctaccgg	900
gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaaaga gtacaagtgc	960
aaggtgtcca acaaggccct gggagcccc atcgaaaaga ccatctccaa ggccaagggc	1020
cagcctcgcg agcctcaggt gtacaccctg ccccttagca gagatgagct gaccaagaac	1080
cagggtgtcc tgacctgtct cgtgaaaggc ttctaccct ccatatcgc cgtggaatgg	1140
gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgac	1200
ggctcattct tcctgtactc taagctgaca gtggacaagt cccggtggca gcagggaac	1260
gtgttctcct gtcctgtgat gcacgaggcc ctgcacaacc actacacca gaagtccttg	1320

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tccctgtctc ccgggggagg cggaggatct ggcggaggcg gatccggtgg tggcggatct      1380
gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc      1440
ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt      1500
tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggcctccggc      1560
gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcgga taacagcaag      1620
aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc      1680
gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg      1740
agcgcttctg tggccgctcc ctccgtgttc atcttccac cttccgacga gcagctgaag      1800
tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcgga agccaagggtg      1860
cagtggaaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag      1920
gactccaagg acagcaccta ctccctgagc agcaccctga ccctgtccaa ggccgactac      1980
gagaagcaca aggtgtacgc ctgtgaagtg acccaccagg gcctgtccag ccccgtagacc      2040
aagtccttca accggggcga gtgc                                             2064

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<210> 225

<211> 688

<212> PRT

<213> Artificial Sequence

<220>

<223> (CLC-563) VHCH1-Heavy chain-(28H1) VHCL

<400> 225

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

```

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20           25           30

```

```

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

```

```

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

```

50

55

60

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

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

Ala Leu Asp Val Gly Ala Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
 435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

450

455

460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 465 470 475 480

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
 485 490 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 500 505 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
 515 520 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 530 535 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 545 550 555 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 565 570 575

Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
 580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 675 680 685

<210> 226
 <211> 2064
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (CLC-564) VHCH1-Heavy chain-(28H1) VHCL

<400> 226
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 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gttcgacgtt 300
 ggtccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaag 360
 ggcccatccg tgttccctct ggccccttcc agcaagtcta cctctggcgg cacagccgct 420
 ctgggctgcc tcgtgaagga ctacttcccc gagcctgtga cagtgtcctg gaactctggc 480
 gccctgacat ccggcgtgca cacctttcca gctgtgctgc agtcctccgg cctgtactcc 540
 ctgtcctccg tcgtgacagt gccctccagc tctctgggca cccagaccta catctgcaac 600
 gtgaaccaca agccctccaa caccaagggtg gacaagaagg tggaacccaa gtcctgacgac 660
 aagaccaca cctgtcccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc 720
 ctgttcccc caaagccaa ggacaccctg atgatctccc ggacccccga agtgacctgc 780
 gtggtggtgg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840
 gtggaagtgc acaatgccaa gaccaagcct agagaggaac agtacaactc cacctaccgg 900
 gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaaaga gtacaagtgc 960

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aaggtgtcca acaaggccct gggagccccc atcgaaaaga ccatctccaa ggccaagggc 1020
cagcctcgcg agcctcaggt gtacaccctg ccccttagca gagatgagct gaccaagaac 1080
caggtgtccc tgacctgtct cgtgaaaggc ttctaccctt ccgatatcgc cgtggaatgg 1140
gagagcaacg gccagcccgga gaacaactac aagaccaccc cccctgtgct ggactccgac 1200
ggctcattct tcctgtactc taagctgaca gtggacaagt cccgggtggca gcagggaac 1260
gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacacca gaagtccctg 1320
tccctgtctc ccgggggagg cggaggatct ggcgaggcg gatccggtgg tggcggatct 1380
gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc 1440
ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt 1500
tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggccctcggc 1560
gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcggga taacagcaag 1620
aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc 1680
gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg 1740
agcgcttctg tggccgctcc ctccgtgttc atcttccac cttccgacga gcagctgaag 1800
tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcggga agccaagggtg 1860
cagtggaaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag 1920
gactccaagg acagcaccta ctccctgagc agcaccctga ccctgtccaa ggccgactac 1980
gagaagcaca aggtgtacgc ctgtgaagtg acccaccagg gcctgtccag ccccgtgacc 2040
aagtccttca accggggcga gtgc 2064

```

<210> 227

<211> 688

<212> PRT

<213> Artificial Sequence

<220>

<223> (CLC-564) VHCH1-Heavy chain-(28H1) VHCL

<400> 227

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp

405

410

415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
 435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 465 470 475 480

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
 485 490 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 500 505 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
 515 520 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 530 535 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 545 550 555 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 565 570 575

Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
 580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 675 680 685

<210> 228
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (28H1) VHCL-heavy chain hole

<400> 228
 gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
 tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt cgcacaggct 120
 cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180
 gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
 cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca gggctggctg 300
 ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcgtggcc 360
 gctcccagcg tgttcatctt cccaccagc gacgagcagc tgaagtccgg cacagccagc 420
 gtggtgtgcc tgctgaacaa cttctacccc cgcgaggcca aggtgcagtg gaaggtggac 480
 aacgccctgc agagcggcaa cagccaggaa tccgtgaccg agcaggacag caaggactcc 540
 acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaaggtg 600

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tacgcctgcg aagtgaccca ccagggcctg tccagccccg tgaccaagag cttcaaccgg      660
ggcgagtgcg acaagaccca cacctgtccc ccttgccctg cccctgaagc tgctgggtggc      720
ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc      780
gaagtgacct gcgtgggtggc cgatgtgtcc cacgaggacc ctgaagtga gttcaattgg      840
tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac      900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc     1020
aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag     1080
ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcagggtgg     1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                     1350

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<210> 229
<211> 450
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> (28H1) VHCL-heavy chain hole

```

```

<400> 229

```

```

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

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
20           25           30

```

```

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

```

```

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys

```

50

55

60

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

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

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro
115 120 125

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155 160

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
165 170 175

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
180 185 190

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
195 200 205

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys

450

<210> 230
 <211> 1343
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (49B4) VHCH1-heavy chain knob

<400> 230
 aggtgcaatt ggtgcagtct ggggctgagg tgaagaagcc tgggtcctcg gtgaaggtct 60
 cctgcaaggc ctccggaggc acattcagca gctacgctat aagctgggtg cgacaggccc 120
 ctggacaagg gctcgagtgg atgggaggga tcatccctat ctttgggtaca gcaaactacg 180
 cacagaagtt ccagggcagg gtcaccatta ctgcagacaa atccacgagc acagcctaca 240
 tggagctgag cagcctgaga tctgaggaca ccgccgtgta ttactgtgcg agagaatact 300
 accgtggtcc gtacgactac tggggccaag ggaccaccgt gaccgtctcc tcagctagca 360
 ccaagggccc tagcgtgttc cctctggccc ctagcagcaa gagcacaagt ggaggaacag 420
 ccgccctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg tcctggaatt 480
 ctggcgccct gacaagcggc gtgcacacat ttccagccgt gctgcagagc agcggcctgt 540
 actctctgag cagcgtcgtg accgtgccct ctagctctct gggcaccag acctacatct 600
 gcaacgtgaa ccacaagccc agcaacacca aagtggacaa gaaggtggaa cccaagagct 660
 gcgacaagac ccacacctgt ccccttgcc ctgcccctga agctgctggt ggcccttccg 720
 tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc cccgaagtga 780
 cctgcgtggt ggtcgatgtg tcccacgagg accctgaagt gaagttcaat tggtagctgg 840
 acggcgtgga agtgcacaat gccaagacca agccgcggga ggagcagtac aacagcacgt 900
 accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc aaggagtaca 960
 agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc tccaaagcca 1020
 aagggcagcc ccgagaacca caggtgtaca ccctgcccc atgccgggat gagctgacca 1080
 agaaccaggt cagcctgtgg tgcctgggtca aaggcttcta tcccagcgac atcgccgtgg 1140

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agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact      1200
ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg tggcagcagg      1260
ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac acgcagaaga      1320
gcctctccct gtctccgggt aaa                                             1343

```

```

<210> 231
<211> 448
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> (49B4) VHCH1-heavy chain knob

```

```

<400> 231

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60

```

```

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
          100          105          110

```

```

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
          115          120          125

```


Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr

325

330

335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 232

<211> 1338

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (1G4) VHCH1-heavy chain knob

<400> 232

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagt gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

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ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag      360
ggcccctagcg tgttccctct ggcccctagc agcaagagca caagtggagg aacagccgcc      420
ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccggtgcctg gaattctggc      480
gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct      540
ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac      600
gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac      660
aagaccacaca cctgtcccc ttgccctgcc cctgaagctg ctggtggccc ttccgtgttc      720
ctgttcccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc      780
gtggtggtcg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc      840
gtggaagtgc acaatgccaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt      900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc      960
aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg     1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac     1080
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg     1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac     1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac     1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc     1320
tcctgtctc cggtgtaa                                1338

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<210> 233

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> (1G4) VHCH1-heavy chain knob

<400> 233

```

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

```

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr

210

215

220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 234
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (20B7) VHCH1-heavy chain knob

<400> 234
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggctc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttgttac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac 300
 taccgtact cttactgggg tgacttcgac tactggggcc aagggaccac cgtgaccgtc 360
 tcctcagcta gcaccaaggg ccctagcgtg ttccctctgg cccctagcag caagagcaca 420
 agtggaggaa cagccgccct gggctgcctg gtcaaggact acttccccga gcccgtgacc 480
 gtgtcctgga attctggcgc cctgacaagc ggcgtgcaca catttccagc cgtgctgcag 540
 agcagcggcc tgtactctct gagcagcgtc gtgaccgtgc cctctagctc tctgggcacc 600
 cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaagtgga caagaagggtg 660
 gaaccaaga gctgcgacaa gaccacacc tgtccccctt gccctgcccc tgaagctgct 720
 ggtggccctt ccgtgttcct gttccccca aagccaagg acaccctgat gatcagccgg 780
 accccgaag tgacctgcgt ggtggtcgat gtgtcccacg aggacctga agtgaagttc 840
 aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagccgcg ggaggagcag 900
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

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ggcaaggagt acaagtgcaa ggtctccaac aaagccctcg gcgcccccat cgagaaaacc      1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg      1080
gatgagctga ccaagaacca ggtcagcctg tggcgcctgg tcaaaggctt ctatcccagc      1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1200
cccggtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc      1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1320
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1356

```

```

<210> 235
<211> 452
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> (20B7) VHCH1-heavy chain knob

```

```

<400> 235

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50              55              60

```

```

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Val Asn Tyr Pro Tyr Ser Tyr Trp Gly Asp Phe Asp Tyr Trp

```

100					105					110					
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
		115					120					125			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	130					135					140				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145					150					155					160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			165						170					175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
		180						185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
	195						200					205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			245						250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
		260						265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
	275						280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	290					295					300				

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro Gly Lys
 450

<210> 236

<211> 1338

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (CLC-563) VHCH1-heavy chain knob

<400> 236

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcttgacgtt 300
 ggtgctttcg actactgggg ccaaggagcc ctggtcaccg tctcgagtgc tagcaccaag 360
 ggcccctagcg tgttccctct ggcccctagc agcaagagca caagtggagg aacagccgcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaattctggc 480
 gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct 540
 ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac 600
 gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac 660
 aagaccaca cctgtcccc ttgccctgcc cctgaagctg ctgggtggccc ttccgtgttc 720
 ctgttcccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc 780
 gtgggtggtcg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840
 gtggaagtgc acaatgcaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
 caggtcagcc tgtgggtgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg 1140
 gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
 gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
 tccctgtctc cgggtaaa 1338

<210> 237

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> (CLC-563) VHCH1-heavy chain knob

<400> 237

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Leu Asp Val Gly Ala Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

370

375

380

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 238
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (CLC-564) VHCH1-heavy chain knob

<400> 238
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gttcgacgtt 300
 ggtccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaag 360
 ggccctagcg tgttccctct ggcccctagc agcaagagca caagtggagg aacagccgcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaattctggc 480
 gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct 540
 ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac 600
 gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac 660

```

aagacccaca cctgtccccc ttgccctgcc cctgaagctg ctggtggccc ttccgtgttc      720
ctgttccccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc      780
gtggtggctcg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc      840
gtggaagtgc acaatgccaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt      900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc      960
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg    1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac    1080
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg    1140
gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac    1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac    1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc    1320
tccctgtctc cgggtaaa                                1338

```

<210> 239

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> (CLC-564) VHCH1-heavy chain knob

<400> 239

```

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

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20          25          30

```

```

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

```

```

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50          55          60

```

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

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

Ala Phe Asp Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val

260

265

270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 240

<211> 163

<212> PRT

<213> cynomolgus

<400> 240

Leu Gln Asp Leu Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
 1 5 10 15

Asn Arg Ser Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
 20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
 35 40 45

Phe Lys Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
 50 55 60

Cys Ile Ser Gly Tyr His Cys Leu Gly Ala Glu Cys Ser Met Cys Glu
 65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
 85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
 100 105 110

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

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
 130 135 140

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

Ser Pro Gln

<210> 241

<211> 164

<212> PRT

<213> Mus musculus

<400> 241

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
 1 5 10 15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
 20 25 30

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
 35 40 45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
 50 55 60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
 65 70 75 80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys
 85 90 95

Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro
 100 105 110

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

Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe Ser Pro
 130 135 140

Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly His Ser
 145 150 155 160

Leu Gln Val Leu

<210> 242

<211> 1266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA human 4-1BB antigen Fc knob chain

<400> 242
 ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag 60
 atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac 120
 atctgcagac agtgcaaggg cgtgttcaga acccggaag agtgcagcag caccagcaac 180
 gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag 240
 caggactgca agcagggcca ggaactgacc aagaagggt gcaaggactg ctgcttcggc 300
 accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc 360
 aagagcgtgc tgggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct 420
 gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac 480
 tctcctcagg tcgacgaaca gttatatattt cagggcggct caccctaatc tgcagacaaa 540
 actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 600
 ttcccccaa aaccaagga caccctcatg atctccgga cccctgaggt cacatgcgtg 660
 gtgggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 720
 gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 780
 gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag 840
 gtctccaaca aagccctccc agccccatc gagaaaacca tctccaaagc caaagggcag 900
 ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 960
 gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1020
 agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1080
 tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1140
 ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1200
 ctgtctccgg gtaaattccg aggcctgaac gacatcttcg aggccagaa gattgaatgg 1260

cacgag

1266

<210> 243

<211> 1266

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA cynomolgus 4-1BB antigen Fc knob chain

<400> 243

ttgcaggatc tgtgtagtaa ctgcccagct ggtacattct gtgataataa caggagtcag	60
atttgcagtc cctgtcctcc aaatagtttc tccagcgcag gtggacaaag gacctgtgac	120
atatgcaggc agtgtaaagg tgttttcaag accaggaagg agtgttcctc caccagcaat	180
gcagagtgtg actgcatttc agggatatcac tgcctggggg cagagtgcag catgtgtgaa	240
caggattgta aacaagggtca agaattgaca aaaaaagggt gttaaagactg ttgctttggg	300
acatttaatg accagaaaacg tggcatctgt cgcccctgga caaactgttc tttggatgga	360
aagtctgtgc ttgtgaatgg gacgaaggag agggacgtgg tctgcggacc atctccagcc	420
gacctctctc caggagcatc ctctgcgacc ccgcctgccc ctgcgagaga gccaggacac	480
tctccgcagg tcgacgaaca gttatatattt cagggcggct cacccaaadc tgcagacaaa	540
actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc	600
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	660
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	720
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	780
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag	840
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag	900
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag	960
gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1020
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1080
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc	1140

ttctcatgct ccgatgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc	1200
ctgtctccgg gtaaatccgg aggctgaac gacatcttcg aggcccagaa gattgaatgg	1260
cacgag	1266

<210> 244
 <211> 1269
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA murine 4-1BB antigen Fc knob chain

<400> 244	
gtgcagaaca gctgcgacaa ctgccagccc ggcaccttct gccggaagta caaccccggtg	60
tgcaagagct gcccccccag caccttcagc agcatcggcg gccagcccaa ctgcaacatc	120
tgcaagagct gcgccggcta cttccggttc aagaagttct gcagcagcac ccacaacgcc	180
gagtgcgagt gcatcgaggg cttccactgc ctgggcccc agtgcaccag atgcgagaag	240
gactgcagac ccggccagga actgaccaag cagggtgtga agacctgcag cctgggcacc	300
ttcaacgacc agaacgggac cggcgtgtgc cggccttgga ccaattgcag cctggacggg	360
agaagcgtgc tgaaaaccgg caccaccgag aaggacgtcg tgtgcggccc tcccgtggtg	420
tccttcagcc ctagcaccac catcagcgtg acccctgaag gcggccctgg cggacactct	480
ctgcaggtcc tggctgacga acagttatat tttcagggcg gctcacccaa atctgcagac	540
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc	600
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	660
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	720
gtggaggtgc ataatgcca gacaaagccg cgggaggagc agtacaacag cacgtaccgt	780
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	840
aaggctctcca acaaagccct ccagcccc atcgagaaaa ccatctccaa agccaaaggg	900
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac	960
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg	1020

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1080
 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1140
 gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1200
 tccctgtctc cgggtaaatac cggaggcctg aacgacatct tcgaggccca gaagattgaa 1260
 tggcacgag 1269

<210> 245
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human 4-1BB antigen Fc knob chain

<400> 245

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
 1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
 20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
 35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
 50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
 65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
 85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
 100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr

115

120

125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
 130 135 140

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
 145 150 155 160

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
 165 170 175

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 180 185 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 195 200 205

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 210 215 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 225 230 235 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 245 250 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 260 265 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 275 280 285

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 290 295 300

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
 305 310 315 320

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

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 340 345 350

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 355 360 365

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 370 375 380

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 385 390 395 400

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
 405 410 415

Lys Ile Glu Trp His Glu
 420

<210> 246

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> cynomolgus 4-1BB antigen

Fc knob chain

<400> 246

Leu Gln Asp Leu Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
 1 5 10 15

Asn Arg Ser Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
 20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val

35

40

45

Phe Lys Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
 50 55 60

Cys Ile Ser Gly Tyr His Cys Leu Gly Ala Glu Cys Ser Met Cys Glu
 65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
 85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
 100 105 110

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

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
 130 135 140

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

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
 165 170 175

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 180 185 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 195 200 205

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 210 215 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 225 230 235 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
245 250 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
260 265 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
275 280 285

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
290 295 300

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
305 310 315 320

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

Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
			340					345					350		

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
355 360 365

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
370 375 380

Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
385					390					395					400

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
405 410 415

Lys Ile Glu Trp His Glu
420

<211> 423
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> murine 4-1BB antigen Fc knob chain

<400> 247

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
 1 5 10 15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
 20 25 30

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
 35 40 45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
 50 55 60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
 65 70 75 80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys
 85 90 95

Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro
 100 105 110

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

Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe Ser Pro
 130 135 140

Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly His Ser
 145 150 155 160

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

165

170

175

Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 180 185 190

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 195 200 205

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 210 215 220

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 225 230 235 240

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 245 250 255

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 260 265 270

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 275 280 285

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 290 295 300

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
 305 310 315 320

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 325 330 335

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 340 345 350

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 355 360 365

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 370 375 380

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 385 390 395 400

Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala
 405 410 415

Gln Lys Ile Glu Trp His Glu
 420

<210> 248
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer MS63

<400> 248
 tttcgcacag taatatacgg ccgtgtcc 28

<210> 249
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 4-1BB(12B3) VL

<400> 249
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag tatcattcgt atccgcagac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 250
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 4-1BB(12B3) VH

<400> 250
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagt gatgggaggg atcatcccta tctttgttac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300
 ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

<210> 251
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 4-1BB(25G7) VL

<400> 251
 tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60
 acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120
 caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180
 ttctctggct ccagctcagg aaacacagct tccttgacca tcaactggggc tcaggcggaa 240
 gatgaggctg actattactg taactccctt gataggcgcg gtatgtgggt attcggcgga 300
 gggaccaagc tgaccgtc 318

<210> 252
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>

<223> DNA 4-1BB(25G7) VH

<400> 252

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300
 ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagt 354

<210> 253

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA 4-1BB(11D5) VL

<400> 253

gacatccaga tgaccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag ctttaattcgt atcctcagac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 254

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA 4-1BB(11D5) VH

<400> 254

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggctc 60

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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact      300
ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctca        357

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<210> 255
<211> 321
<212> DNA
<213> Artificial Sequence

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<220>
<223> DNA 4-1BB(9B11) VL

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<400> 255
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gtgccagtca gagtattagt agctgggttg cctggatatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca      180
cgtttcagcg gcagtggatc cgggacagaa ttcaacttca ccatcagcag cttgcagcct      240
gatgattttg caacttatta ctgccaacag gttaattctt atccgcagac gtttggccag      300
ggcaccaaag tcgagatcaa g                                              321

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<210> 256
<211> 360
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> DNA 4-1BB(9B11) VH

```

```

<400> 256
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240

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atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300
 ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

<210> 257
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 4-1BB(20G2) VL

<400> 257
 gacatccaga tgaccagtc tccatccacc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctggatatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag cagcactcgt attatacgtt tggccagggc 300
 accaaagtcg agatcaag 318

<210> 258
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 4-1BB(20G2) VH

<400> 258
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttac 300
 tactgggaat cttacccgtt cgactactgg ggccaaggga ccaccgtgac cgtctccagc 360

<210> 259

<211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 12B3 P329GLALA IgG1 light chain

<400> 259
 gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag tatcattcgt atccgcagac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 260
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 12B3 P329GLALA IgG1 heavy chain

<400> 260
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggctc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttgttac agcaaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

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ttccgtttct acgtgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca      360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg      480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc      600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660
aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga      720
ccgtcagtct tcctcttccc ccaaaaaccc aaggacaccc tcatgatctc ccggaccct      780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgaggagga gcagtacaac      900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaagggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc     1020
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag     1080
ctgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg     1260
cagcaggggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                     1350

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<210> 261

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 12B3 P329GLALA IgG1 light chain

<400> 261

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys

210

<210> 262
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 12B3 P329GLALA IgG1 heavy chain

<400> 262

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser

145		150		155		160									
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165					170						175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
		180						185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
	210					215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly
225					230					235					240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
			245						250					255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
		260						265					270		
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
	275						280					285			
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	290					295					300				
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
305					310					315					320
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro	Ile	Glu
				325					330					335	
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
			340					345					350		

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 263
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 25G7 P329GLALA IgG1 light chain

<400> 263
 tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60
 acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120
 caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180
 ttctctggct ccagctcagg aaacacagct tccttgacca tcaactggggc tcaggcggaa 240
 gatgaggctg actattactg taactccctt gataggcgcg gtatgtgggt attcggcgga 300
 gggaccaagc tgaccgtcct aggtcaaccc aaggctgccc ccagcgtgac cctgttcccc 360

cccagcagcg aggaactgca ggccaacaag gccaccctgg tctgcctgat cagcgacttc 420
 taccagggcg ccgtgaccgt ggccctggaag gccgacagca gccccgtgaa ggccggcgtg 480
 gagaccacca ccccccagcaa gcagagcaac aacaagtacg ccgccagcag ctacctgagc 540
 ctgacccccg agcagtggaa gagccacagg tcctacagct gccagggtgac ccacgagggc 600
 agcaccgtgg agaaaaccgt ggccccacc gagtgcagc 639

<210> 264
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 25G7 P329GLALA IgG1 heavy chain

<400> 264
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300
 ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgtagc 360
 accaagggcc catcggctct ccccttgga ccctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggg gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct 660
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720
 gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ctttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320
agcctctccc tgtctccggg taaa 1344

<210> 265

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 25G7 P329GLALA IgG1 light chain

<400> 265

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

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

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

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

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Asp Arg Arg Gly Met Trp
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
 100 105 110

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
 115 120 125

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

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
 145 150 155 160

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
 165 170 175

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 180 185 190

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
 195 200 205

Pro Thr Glu Cys Ser
 210

<210> 266

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> 25G7 P329GLALA IgG1 heavy chain

<400> 266

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser

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

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 267
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 11D5 P329GLALA IgG1 light chain

<400> 267
 gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag cttaattcgt atcctcagac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 268
 <211> 1347
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 11D5 P329GLALA IgG1 heavy chain

<400> 268
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

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cctggacaag ggctcgagt gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact      300
ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctctcagct      360
agcaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc      420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      480
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga      540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac      600
atctgcaacg tgaatcaca gcccagcaac accaagggtg acaagaaagt tgagcccaaa      660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg      720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag      780
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac      840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc      900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag      960
tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa     1020
gccaaagggc agccccgaga accacagggtg tacaccctgc ccccatcccg ggatgagctg     1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc     1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg     1200
gactccgacg gtccttctt cctctacagc aagctcaccg tggacaagag caggtggcag     1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag     1320
aagagcctct ccctgtctcc gggtaaa                                           1347

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<210> 269

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> 11D5 P329GLALA IgG1 light chain

<400> 269

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 270

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> 11D5 P329GLALA IgG1 heavy chain

<400> 270

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys

325

330

335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 271

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA 9B11 P329GLALA IgG1 light chain

<400> 271

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctgggttg cctgggtatca gcagaaacca 120

gggaaagccc ctaagtcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240
 gatgatTTTT caacttatta ctgccaacag gtttaattctt atccgcagac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacgggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 272

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA 9B11 P329GLALA IgG1 heavy chain

<400> 272

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggctc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagt gatgggaggg atcatcccta tctttgttac agcaaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300
 ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360
 gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
 ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga 720

```

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt      780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgcggggagga gcagtacaac      900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc     1020
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag     1080
ctgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg     1260
cagcaggggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                     1350

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<210> 273
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 9B11 P329GLALA IgG1 light chain

<400> 273

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

```

```

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

```

```

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

```

```

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

```

```

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

```

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

<210> 274

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> 9B11 P329GLALA IgG1 heavy chain

<400> 274

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

405

410

415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 275
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA 20G2 P329GLALA IgG1 light chain

<400> 275
 gacatccaga tgacccagtc tccatccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
 cgtttcagcg gcagtggatc cgggacagaa ttactctca ccatcagcag cttgcagcct 240
 gatgattttg caacttatta ctgccaacag cagcactcgt attatacggtt tggccagggc 300
 accaaagtcg agatcaagcg tacggtggct gcaccatctg tcttcatctt cccgccatct 360
 gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420
 agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480
 agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540
 agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg 600
 agctcgccccg tcacaaagag cttcaacagg ggagagtgt 639

<210> 276
 <211> 1350
 <212> DNA

<213> Artificial Sequence

<220>

<223> DNA 20G2 P329GLALA IgG1 heavy chain

<400> 276

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttac	300
tactgggaat cttacccgtt cgactactgg ggccaaggga ccaccgtgac cgtctccagc	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttggtg acaaaaactca cacatgcca cctgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggctct caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accaggctcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320

cagaagagcc tctccctgtc tccgggtaaa

1350

<210> 277

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 20G2 P329GLALA IgG1 light chain

<400> 277

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

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

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

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

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

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

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys
 210

<210> 278
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> 20G2 P329GLALA IgG1 heavy chain

<400> 278

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Tyr Tyr Trp Glu Ser Tyr Pro Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 279
 <211> 421
 <212> PRT
 <213> Artificial Sequence

<220>

<223> mu4-1BB D1 / hu4-1BB D2 Fc knob

<400> 279

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
 1 5 10 15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
 20 25 30

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
 35 40 45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
 50 55 60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
 65 70 75 80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Asp Cys
 85 90 95

Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro Trp
 100 105 110

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

Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro Gly
 130 135 140

Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His Ser
 145 150 155 160

Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys Ser
 165 170 175

Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

180

185

190

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 195 200 205

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 210 215 220

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 225 230 235 240

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 245 250 255

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 260 265 270

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 275 280 285

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 290 295 300

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
 305 310 315 320

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 340 345 350

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 355 360 365

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 370 375 380

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 385 390 395 400

Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys
 405 410 415

Ile Glu Trp His Glu
 420

<210> 280
 <211> 424
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu4-1BB D1 / mu4-1BB D2 Fc knob

<400> 280

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
 1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
 20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
 35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
 50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
 65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Thr
 85 90 95

Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg
 100 105 110

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

Thr Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe Ser
 130 135 140

Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly His
 145 150 155 160

Ser Leu Gln Val Leu Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser
 165 170 175

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 180 185 190

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 195 200 205

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 210 215 220

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 225 230 235 240

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 245 250 255

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 260 265 270

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 275 280 285

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 290 295 300

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys

305 310 315 320

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 325 330 335

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 340 345 350

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 355 360 365

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 370 375 380

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 385 390 395 400

Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu
 405 410 415

Ala Gln Lys Ile Glu Trp His Glu
 420

<210> 281
 <211> 354
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu 4-1BB D1 Fc knob

<400> 281

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
 1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
 20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val

35

40

45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
 50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
 65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Val
 85 90 95

Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys
 100 105 110

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 115 120 125

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 145 150 155 160

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 165 170 175

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 180 185 190

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

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 210 215 220

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

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 260 265 270

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 290 295 300

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 305 310 315 320

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 325 330 335

Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
 340 345 350

His Glu

<210> 282

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine 4-1BB domain D1 (N-terminus)

<400> 282

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
 1 5 10 15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
 20 25 30

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
 35 40 45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
 50 55 60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
 65 70 75 80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys
 85 90

<210> 283

<211> 68

<212> PRT

<213> Artificial Sequence

<220>

<223> Human 4-1BB domain D2 (C-terminus)

<400> 283

Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg
 1 5 10 15

Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly
 20 25 30

Thr Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser
 35 40 45

Pro Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly
 50 55 60

His Ser Pro Gln
 65

<210> 284

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> Human 4-1BB domain D1 (N-terminus)

<400> 284

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys
85 90 95

<210> 285

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine 4-1BB domain D2 (C-terminus)

<400> 285

Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys
1 5 10 15

Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr
20 25 30

Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe

35

40

45

Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly
 50 55 60

His Ser Leu Gln Val Leu
 65 70

<210> 286
 <211> 2076
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (12B3) VHCH1-Heavy chain-(28H1) VHCL

<400> 286
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tcttttgttac agcaaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300
 ttccgtttct acgtgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360
 gctagcacca agggcccatc cgtgttccct ctggcccctt ccagcaagtc tacctctggc 420
 ggacagccg ctctgggctg cctcgtgaag gactacttcc ccgagcctgt gacagtgtcc 480
 tggaactctg gcgccctgac atccggcgtg cacacctttc cagctgtgct gcagtcctcc 540
 ggctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg caccagacc 600
 tacatctgca acgtgaacca caagccctcc aacaccaagg tggacaagaa ggtggaaccc 660
 aagtcctgcg acaagacca cacctgtccc cttgtcctg cccctgaagc tgctggcggc 720
 cctagcgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccgaccccc 780
 gaagtgacct gcgtgggtgt ggatgtgtcc cacgaggacc ctgaagtga gttcaattgg 840
 tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ctagagagga acagtacaac 900

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tccacctacc ggggtggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaaa      960
gagtacaagt gcaagggtgtc caacaaggcc ctgggagccc ccatcgaaaa gaccatctcc      1020
aaggccaagg gccagcctcg cgagcctcag gtgtacaccc tgccccctag cagagatgag      1080
ctgaccaaga accagggtgtc cctgacctgt ctctgtgaaag gcttctaccc ctccgatatc      1140
gccgtggaat gggagagcaa cggccagccc gagaacaact acaagaccac cccccctgtg      1200
ctggactccg acggctcatt cttcctgtac tctaagctga cagtggacaa gtccccggtg      1260
cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc      1320
cagaagtccc tgtccctgtc tcccggggga ggcggaggat ctggcggagg cggatccggt      1380
ggtggcggat ctgggggcgg tggatctgag gtgcagctgc tggaatctgg gggaggactg      1440
gtgcagccag gcggatctct gaggctgtcc tgcgctgctt ccggctttac cttctccagc      1500
cacgccatga gttgggtgcg ccaggcaccc ggaaaaggac tggaatgggt gtcagccatc      1560
tgggcctccg gcgagcagta ctacgccgat agcgtgaagg gccggttcac catctctcgg      1620
gataacagca agaatactct gtacctgcag atgaactccc tgcgcgctga agataccgct      1680
gtgtattact gcgccaaggg ctggctgggc aacttcgatt actggggcca gggaaacctc      1740
gtgactgtct cgagcgcttc tgtggccgct ccctccgtgt tcatcttccc accttccgac      1800
gagcagctga agtccggcac tgcctctgtc gtgtgcctgc tgaacaactt ctaccctcgg      1860
gaagccaagg tgcagtggaa agtggataac gccctgcagt ccggcaactc ccaggaatcc      1920
gtgaccgagc aggactccaa ggacagcacc tactccctga gcagcaccct gaccctgtcc      1980
aaggccgact acgagaagca caaggtgtac gcctgtgaag tgaccaccca gggcctgtcc      2040
agccccgtga ccaagtcctt caaccggggc gagtgc                                2076

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<210> 287

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> (12B3) VHCH1-Heavy chain-(28H1) VHCL

<400> 287

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys

195

200

205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 485 490 495

Thr Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510

Gly Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr
 515 520 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 530 535 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 545 550 555 560

Val Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly
 565 570 575

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser
 580 585 590

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala

595

600

605

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
 610 615 620

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
 625 630 635 640

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
 645 650 655

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
 660 665 670

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 675 680 685

Arg Gly Glu Cys
 690

<210> 288
 <211> 2070
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (25G7) VHCH1-Heavy chain-(28H1) VHCL

<400> 288
 gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggttag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300
 ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgctagc 360
 accaagggcc catccgtgtt ccctctggcc ccttccagca agtctacctc tggcggcaca 420

gccgctctgg gctgcctcgt gaaggactac ttccccgagc ctgtgacagt gtcctggaac	480
tctggcgccc tgacatccgg cgtgcacacc tttccagctg tgctgcagtc ctccggcctg	540
tactccctgt cctccgtcgt gacagtgtccc tccagctctc tgggcaccca gacctacatc	600
tgcaacgtga accacaagcc ctccaacacc aagggtggaca agaaggtgga acccaagtcc	660
tgcgacaaga cccacacctg tcccccttgt cctgccccctg aagctgctgg cggccctagc	720
gtgttcctgt tcccccaaaa gcccgaaggac accctgatga tctcccggac ccccgaagtg	780
acctgcgtgg tgggtggatgt gtcccacgag gaccctgaag tgaagttcaa ttggtacgtg	840
gacggcgtgg aagtgcacaa tgccaagacc aagcctagag aggaacagta caactccacc	900
taccgggtgg tgtccgtgct gaccgtgctg caccaggatt ggctgaacgg caaagagtac	960
aagtgcgaagg tgtccaacaa ggccctggga gccccatcg aaaagaccat ctccaaggcc	1020
aagggccagc ctgcgagcc tcaggtgtac accctgcccc ctagcagaga tgagctgacc	1080
aagaaccagg tgtccctgac ctgtctcgtg aaaggcttct acccctccga tatcgccgtg	1140
gaatgggaga gcaacggcca gcccgagaac aactacaaga ccaccccccc tgtgctggac	1200
tccgacggct cattcttcct gtactctaag ctgacagtgg acaagtcccc gtggcagcag	1260
ggcaacgtgt tctcctgctc cgtgatgcac gaggccctgc acaaccacta caccagaag	1320
tccctgtccc tgtctcccgg gggaggcgga ggatctggcg gaggcggatc cgggtggtggc	1380
ggatctgggg gcggtggatc tgaggtgcag ctgctggaat ctgggggagg actggtgcag	1440
ccaggcggat ctctgaggct gtcctgcgct gcttccggct ttaccttctc cagccacgcc	1500
atgagttggg tgcgccaggc acccggaata ggactggaat ggggtgtcagc catctgggcc	1560
tccggcgagc agtactacgc cgatagcgtg aagggccggt tcaccatctc tcgggataac	1620
agcaagaata ctctgtacct gcagatgaac tccctgcgcg ctgaagatac cgctgtgtat	1680
tactgcgcca agggctggct gggcaacttc gattactggg gccagggaac cctcgtgact	1740
gtctcgagcg cttctgtggc cgctccctcc gtgttcatct tcccaccttc cgacgagcag	1800
ctgaagtccg gcaactgcctc tgtcgtgtgc ctgctgaaca acttctaccc tcgggaagcc	1860
aagggtgcagt ggaaagtgga taacgccctg cagtccggca actcccagga atccgtgacc	1920

gagcaggact ccaaggacag cacctactcc ctgagcagca ccctgaccct gtccaaggcc 1980
gactacgaga agcacaaggt gtacgcctgt gaagtgaccc accagggcct gtccagcccc 2040
gtgaccaagt ccttcaaccg gggcgagtgc 2070

<210> 289
<211> 690
<212> PRT
<213> Artificial Sequence

<220>
<223> (25G7) VHCH1-Heavy chain-(28H1) VHCL

<400> 289

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130

135

140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 485 490 495

Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 500 505 510

Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp
 515 520 525

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

530

535

540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 545 550 555 560

Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly
 565 570 575

Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe
 580 585 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 595 600 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 610 615 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 645 650 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 660 665 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 675 680 685

Glu Cys
 690

<210> 290

<211> 2073

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (11D5) VHCH1-Heavy chain-(28H1) VHCL

<400> 290

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact	300
ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctctcagct	360
agcaccaagg gcccatccgt gttccctctg gcccttcca gcaagtctac ctctggcggc	420
acagccgctc tgggctgcct cgtgaaggac tacttccccg agcctgtgac agtgcctgg	480
aactctggcg ccctgacatc cggcgtgcac acctttccag ctgtgctgca gtcctccggc	540
ctgtactccc tgtcctccgt cgtgacagtg ccctccagct ctctgggcac ccagacctac	600
atctgcaacg tgaaccacaa gccctccaac accaagggtg acaagaagg ggaaccaag	660
tcctgcgaca agaccacac ctgtccccct tgtcctgccc ctgaagctgc tggcggccct	720
agcgtgttcc tgttcccccc aaagcccaag gacaccctga tgatctcccc gacccccgaa	780
gtgacctgcg tgggtggtgga tgtgtccac gaggacctg aagtgaagtt caattggtac	840
gtggacggcg tggaaagtga caatgccaa accaagccta gagaggaaca gtacaactcc	900
acctaccggg tgggtgtccgt gctgaccgtg ctgcaccagg attggctgaa cggcaaagag	960
tacaagtga aggtgtccaa caaggccctg ggagcccca tcgaaaagac catctccaag	1020
gccaagggcc agcctcgcga gcctcagggtg tacaccctgc cccctagcag agatgagctg	1080
accaagaacc aggtgtccct gacctgtctc gtgaaaggct tctaccctc cgatatcgcc	1140
gtggaatggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg	1200
gactccgacg gctcattctt cctgtactct aagctgacag tggacaagtc ccggtggcag	1260
cagggaacg tgttctcctg ctccgtgatg cacgaggccc tgcacaacca ctacaccag	1320
aagtcctgt ccctgtctcc cgggggaggc ggaggatctg gcggaggcgg atccggtggt	1380
ggcggatctg ggggcgggtg atctgagggtg cagctgctgg aatctggggg aggactggtg	1440

cagccaggcg gatctctgag gctgtcctgc gctgcttccg gctttacctt ctccagccac 1500
 gccatgagtt ggggtgcgcca ggcacccgga aaaggactgg aatgggtgtc agccatctgg 1560
 gcctccggcg agcagtacta cgccgatagc gtgaagggcc gggttcacat ctctcgggat 1620
 aacagcaaga atactctgta cctgcagatg aactccctgc gcgctgaaga taccgctgtg 1680
 tattactgcg ccaagggtg gctgggcaac ttcgattact ggggccaggg aaccctcgtg 1740
 actgtctcga gcgcttctgt ggccgctccc tccgtgttca tcttcccacc ttccgacgag 1800
 cagctgaagt ccggcactgc ctctgtcgtg tgcctgctga acaacttcta ccctcgggaa 1860
 gccaagggtgc agtggaaagt ggataacgcc ctgcagtccg gcaactcca ggaatccgtg 1920
 accgagcagg actccaagga cagcacctac tccctgagca gcaccctgac cctgtccaag 1980
 gccgactacg agaagcaciaa ggtgtacgcc tgtgaagtga cccaccaggg cctgtccagc 2040
 cccgtgacca agtccttcaa ccggggcgag tgc 2073

<210> 291
 <211> 691
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (11D5) VHCH1-Heavy chain-(28H1) VHCL

<400> 291

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 450 455 460

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val

465		470		475		480									
Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr
				485					490					495	
Phe	Ser	Ser	His	Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly
			500					505					510		
Leu	Glu	Trp	Val	Ser	Ala	Ile	Trp	Ala	Ser	Gly	Glu	Gln	Tyr	Tyr	Ala
		515					520					525			
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn
	530					535					540				
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val
545					550					555					560
Tyr	Tyr	Cys	Ala	Lys	Gly	Trp	Leu	Gly	Asn	Phe	Asp	Tyr	Trp	Gly	Gln
				565					570					575	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Val	Ala	Ala	Pro	Ser	Val
			580					585					590		
Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser
		595					600					605			
Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln
	610					615					620				
Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val
625					630					635					640
Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu
				645					650					655	
Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu
			660					665					670		

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
 675 680 685

Gly Glu Cys
 690

<210> 292
 <211> 2076
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (9B11) VHCH1-Heavy chain-(28H1) VHCL

<400> 292
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300
 ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360
 gctagcacca agggcccatc cgtgttccct ctggcccctt ccagcaagtc tacctctggc 420
 ggacagccg ctctgggctg cctcgtgaag gactacttcc ccgagcctgt gacagtgtcc 480
 tggaactctg gcgccctgac atccggcgtg cacacctttc cagctgtgct gcagtcctcc 540
 ggctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg caccagacc 600
 tacatctgca acgtgaacca caagccctcc aacaccaagg tggacaagaa ggtggaaccc 660
 aagtcctgcg acaagaccca cacctgtccc cttgtcctg cccctgaagc tgctggcggc 720
 cctagcgtgt tcctgttccc ccaaagccc aaggacaccc tgatgatctc ccggaccccc 780
 gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtga gttcaattgg 840
 tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ctagagagga acagtacaac 900
 tccacctacc ggggtggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaaa 960

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gagtacaagt gcaagggtgtc caacaaggcc ctgggagccc ccatcgaaaa gaccatctcc 1020
aaggccaagg gccagcctcg cgagcctcag gtgtacaccc tgccccctag cagagatgag 1080
ctgaccaaga accagggtgtc cctgacctgt ctcgtgaaag gcttctaccc ctccgatatc 1140
gccgtggaat gggagagcaa cggccagccc gagaacaact acaagaccac cccccctgtg 1200
ctggactccg acggctcatt cttcctgtac tctaagctga cagtggacaa gtccccggtg 1260
cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320
cagaagtccc tgtccctgtc tcccggggga ggcgaggagg ctggcgagg cggatccggt 1380
ggtggcggtat ctggggggcg tggatctgag gtgcagctgc tggaatctgg gggaggactg 1440
gtgcagccag gcggatctct gaggctgtcc tgcgctgctt ccggctttac cttctccagc 1500
cacgccatga gttgggtgcg ccaggcaccc ggaaaaggac tggaatgggt gtcagccatc 1560
tgggcctccg gcgagcagta ctacccgat agcgtgaagg gccggttcac catctctcgg 1620
gataacagca agaatactct gtacctgcag atgaactccc tgcgcgctga agataccgct 1680
gtgtattact gcgccaaggg ctggctgggc aacttcgatt actggggcca gggaaacctc 1740
gtgactgtct cgagcgcttc tgtggccgct ccctccgtgt tcatcttccc accttccgac 1800
gagcagctga agtccggcac tgcctctgtc gtgtgcctgc tgaacaactt ctaccctcgg 1860
gaagccaagg tgcaaggtaa agtggataac gccctgcagt ccggcaactc ccaggaatcc 1920
gtgaccgagc aggactccaa ggacagcacc tactccctga gcagcaccct gaccctgtcc 1980
aaggccgact acgagaagca caaggtgtac gcctgtgaag tgaccaccca gggcctgtcc 2040
agccccgtga ccaagtcctt caaccggggc gagtgc 2076

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<210> 293

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> (9B11) VHCH1-Heavy chain-(28H1) VHCL

<400> 293

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

405

410

415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 485 490 495

Thr Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510

Gly Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr
 515 520 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 530 535 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 545 550 555 560

Val Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly
 565 570 575

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser
 580 585 590

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
 595 600 605

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
 610 615 620

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
 625 630 635 640

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
 645 650 655

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
 660 665 670

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 675 680 685

Arg Gly Glu Cys
 690

<210> 294

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (12B3) VHCH1-heavy chain knob

<400> 294

cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggccctag cgtgttcctt ctggccccta gcagcaagag cacaagtgga 420

ggaacagccg ccctgggctg cctggtcaag gactacttcc ccgagcccgt gaccgtgtcc 480

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tggaattctg gcgccctgac aagcggcgtg cacacatttc cagccgtgct gcagagcagc      540
ggcctgtact ctctgagcag cgtcgtgacc gtgccctcta gctctctggg caccagacc      600
tacatctgca acgtgaacca caagcccagc aacaccaaag tggacaagaa ggtggaaccc      660
aagagctgcg acaagacca cacctgtccc ccttgccctg cccctgaagc tgctggtggc      720
ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc      780
gaagtgacct gcgtggtggt cgatgtgtcc cacgaggacc ctgaagtga gttcaattgg      840
tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac      900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggcttc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc     1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatg ccgggatgag     1080
ctgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg     1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                     1350

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<210> 295

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> (12B3) VHCH1-heavy chain knob

<400> 295

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

```

```

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

```

```

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

```

35

40

45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

435

440

445

Gly Lys
450

<210> 296
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA (25G7) VHCH1-heavy chain knob

<400> 296
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300
ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgcctagc 360
accaagggcc ctagcgtgtt ccctctggcc cctagcagca agagcacaag tggaggaaca 420
gccgccctgg gctgcctggg caaggactac ttccccgagc ccgtgaccgt gtcctggaat 480
tctggcgccc tgacaagcgg cgtgcacaca tttccagccg tgctgcagag cagcggcctg 540
tactctctga gcagcgtcgt gaccgtgccc tctagctctc tgggcaccca gacctacatc 600
tgcaacgtga accacaagcc cagcaacacc aaagtggaca agaagggtgga acccaagagc 660
tgcgacaaga cccacacctg tcccccttgc cctgcccctg aagctgctgg tggcccttcc 720
gtgttcctgt tcccccaaaa gccaaggac accctgatga tcagccggac ccccgaaagt 780
acctgcgtgg tggctgatgt gtccacgag gaccctgaag tgaagttcaa ttggtacgtg 840
gacggcgtgg aagtgcacaa tgccaagacc aagccgcggg aggagcagta caacagcacg 900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
aagtgcagg tctccaacaa agccctcggc gccccatcg agaaaacat ctccaaagcc 1020


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aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc      1080
aagaaccagg tcagcctgtg gtgcctgggtc aaaggcttct atcccagcga catcgccgtg      1140
gagtggggaga gcaatgggca gccgggagaac aactacaaga ccacgcctcc cgtgctggac      1200
tccgacggct ctttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag      1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag      1320
agcctctccc tgtctccggg taaa                                             1344

```

```

<210> 297
<211> 448
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> (25G7) VHCH1-heavy chain knob
<400> 297

```

```

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

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20              25              30

```

```

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

```

```

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50              55              60

```

```

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

```

```

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

```

```

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100              105              110

```

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys
		355					360					365			

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210>	298
<211>	1347
<212>	DNA
<213>	Artificial Sequence

<220>
<223> DNA (11D5) VHCH1-heavy chain knob

```
<400> 298
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggct      60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
```

```

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact      300
ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctcagct      360
agcaccaagg gccctagcgt gttccctctg gcccttagca gcaagagcac aagtggagga      420
acagccgccc tgggctgcct ggtcaaggac tacttccccg agcccgtgac cgtgtcctgg      480
aattctggcg ccctgacaag cggcgtgcac acatttccag ccgtgctgca gagcagcggc      540
ctgtactctc tgagcagcgt cgtgaccgtg ccctctagct ctctggggcac ccagacctac      600
atctgcaacg tgaaccacaa gccagcaac accaaagtgg acaagaaggt ggaaccaag      660
agctgcgaca agaccacac ctgtccccct tgccctgccc ctgaagctgc tgggtggcct      720
tccgtgttcc tgttcccccc aaagcccaag gacaccctga tgatcagccg gacccccgaa      780
gtgacctgcg tgggtggcga tgtgtccac gaggaccctg aagtgaagtt caattggtac      840
gtggacggcg tggaagtgca caatgccaag accaagccgc gggaggagca gtacaacagc      900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag      960
tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa     1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatgccg ggatgagctg     1080
accaagaacc aggtcagcct gtggtgcctg gtcaaaggct tctatcccag cgacatcgcc     1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg     1200
gactccgacg gtccttctt cctctacagc aagctcaccg tggacaagag caggtggcag     1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag     1320
aagagcctct ccctgtctcc gggtaaaa                                     1347

```

<210> 299

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> (11D5) VHCH1-heavy chain knob

<400> 299

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

195

200

205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 300
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (9B11) VHCH1-heavy chain knob

<400> 300
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagt gatgggaggg atcatcccta tctttgttac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300
 ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360
 gctagcacca agggccctag cgtgttccct ctggccccta gcagcaagag cacaagtgga 420
 ggaacagccg ccctgggctg cctgggtcaag gactacttcc ccgagcccgt gaccgtgtcc 480
 tggaattctg gcgccctgac aagcggcgtg cacacatttc cagccgtgct gcagagcagc 540
 ggcctgtact ctctgagcag cgtcgtgacc gtgccctcta gctctctggg caccagacc 600
 tacatctgca acgtgaacca caagcccagc aacaccaaag tggacaagaa ggtggaaccc 660
 aagagctgcg acaagacca cacctgtccc ccttgccctg cccctgaagc tgctggtggc 720

```

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc      780
gaagtgacct gcgtgggtgt cgatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg      840
tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcggggagga gcagtacaac      900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc     1020
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatg ccgggatgag     1080
ctgaccaaga accagggtcag cctgtgggtgc ctggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcagggtg     1260
cagcaggggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa                                     1350

```

<210> 301

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> (9B11) VHCH1-heavy chain knob

<400> 301

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50          55          60

```

```

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

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 302

<211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (8H9) VHCH1-heavy chain knob

<400> 302
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300
 ggttggatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360
 ggccctagcg tgttccctct ggccctagc agcaagagca caagtggagg aacagccgcc 420
 ctgggctgcc tggtaagga ctacttcccc gagcccgtga ccgtgtcctg gaattctggc 480
 gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct 540
 ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac 600
 gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac 660
 aagaccacaca cctgtcccc ttgccctgcc cctgaagctg ctggtggccc ttccgtgttc 720
 ctgttcccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc 780
 gtggtggctc atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840
 gtggaagtgc acaatgcaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
 caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg 1140
 gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
 ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 303

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> (8H9) VHCH1-heavy chain knob

<400> 303

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Gly Trp Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

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

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

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

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

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

340

345

350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 304

<211> 1752

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of (49B4) VHCH1 Fc knob VH (4B9)

<400> 304

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac	300
taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc	360
accaagggcc catcggctctt ccccttgcca cctcctcca agagcacctc tgggggcaca	420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttccccggtg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gcccaaattct 660
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720
 gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga cctgagggtc 780
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900
 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgcgaagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctccaaagcc 1020
 aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080
 aagaaccagg tgtccctgtg gtgtctggtc aagggttctt accccagcga tatcgccgtg 1140
 gagtgggaga gcaacggcca gcctgagaac aactacaaga ccaccccccc tgtgctggac 1200
 agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260
 ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta caccagaag 1320
 tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc tgggggcgga 1380
 ggttccggag gcggaggatc cgaggtgcag ctgctcgaaa gcggcggagg actggtgcag 1440
 cctggcggca gcctgagact gtcttgccg gccagcggct tcaccttcag cagctacgcc 1500
 atgagctggg tccgccaggc ccctggcaag ggactggaat ggggtgtccg catcatcggc 1560
 tctggcgcca gcacctacta cgccgacagc gtgaagggcc ggttcacat cagccgggac 1620
 aacagcaaga acaccctgta cctgcagatg aacagcctgc gggccgagga caccgccgtg 1680
 tactactgcg ccaagggatg gttcggcggc ttcaactact ggggacaggg caccctggtc 1740
 accgtgtcca gc 1752

<210> 305
 <211> 1725
 <212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of (49B4) VHCH1 Fc hole VL (4B9)

<400> 305

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac	300
taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc	360
accaagggcc catcggctctt ccccttgga ccctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggc caaggactac ttccccgaac cggtgacggc gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttccccggctg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggc gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca	720
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcaagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc	1080
aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ccttcttctt cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320


```

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggcggcgga      1380
ggttccggag gcggtggatc tgagatcgtg ctgaccaggt ctcccggcac cctgtctctg      1440
agccctggcg agagagccac cctgtcctgc agagcctccc agtccgtgac ctcctcctac      1500
ctcgcttggg atcagcagaa gcccggccag gccctctggc tgctgatcaa cgtgggcagt      1560
cggagagcca ccggcatccc tgaccggttc tccggctctg gctccggcac cgacttcacc      1620
ctgaccatct cccggctgga acccgaggac ttcgccgtgt actactgcca gcagggcatc      1680
atgctgcccc ccacctttgg ccagggcacc aaggtggaaa tcaag                        1725

```

```

<210> 306
<211> 584
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> (49B4) VHCH1 Fc knob VH (4B9)

```

```

<400> 306

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50           55           60

```

```

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr

```

100	105	110
Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
115	120	125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
130	135	140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
145	150	155
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
165	170	175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
180	185	190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser		
195	200	205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
210	215	220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser		
225	230	235
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
245	250	255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
260	265	270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
275	280	285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		
290	295	300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 485 490 495

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

500

505

510

Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala
 515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 545 550 555 560

Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln
 565 570 575

Gly Thr Leu Val Thr Val Ser Ser
 580

<210> 307

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> (49B4) VHCH1 Fc hole VL (4B9)

<400> 307

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu

465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile
545 550 555 560

Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210>	308
<211>	1749
<212>	DNA
<213>	Artificial Sequence

<220>
<223> nucleotide sequence of (49B4) VHCH1 Fc knob VH (28H1)

[illegible]

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttccccggtg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc 660
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720
 gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900
 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgcagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctccaaagcc 1020
 aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080
 aagaaccagg tgtccctgtg gtgtctggtc aagggttct accccagcga tatcgccgtg 1140
 gagtgggaga gcaacggcca gcctgagaac aactacaaga ccaccccccc tgtgctggac 1200
 agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260
 ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta caccagaag 1320
 tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc cggaggaggg 1380
 ggaagtggcg gcggaggatc tgaggtgcag ctgctggaat ccggcggagg cctggtgcag 1440
 cctggcggat ctctgagact gtcctgcgcc gcctccggct tcaccttctc ctcccacgcc 1500
 atgtcctggg tccgacaggc tcctggcaaa ggcctggaat ggggtgtccg catctgggcc 1560
 tccggcgagc agtactacgc cgactctgtg aagggccggt tcaccatctc ccgggacaac 1620
 tccaagaaca ccctgtacct gcagatgaac tccctgcggg ccgaggacac cgccgtgtac 1680
 tactgtgcca agggctggct gggcaacttc gactactggg gccagggcac cctggtcacc 1740
 gtgtccagc 1749

<210> 309
 <211> 1725
 <212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of (49B4) VHCH1 Fc hole VL (28H1)

<400> 309

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac	300
taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc	360
accaagggcc catcggctctt ccccttgga ccctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca	720
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgga ccctgaggtc	780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcaagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc	1080
aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttctt cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320

```

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggtggtggc      1380
ggatctgggg gcggtggatc tgagatcgtg ctgaccagct ctcccggcac cctgagcctg      1440
agccctggcg agagagccac cctgagctgc agagccagcc agagcgtgag ccggagctac      1500
ctggcctggt atcagcagaa gcccggccag gccccagac tgctgatcat cggcgccagc      1560
acccggggcca ccggcatccc cgatagattc agcggcagcg gctccggcac cgacttcacc      1620
ctgaccatca gccggctgga acccgaggac ttcgccgtgt actactgcca gcagggccag      1680
gtgatcccc ccaccttcgg ccagggcacc aaggtggaaa tcaag                        1725

```

```

<210> 310
<211> 583
<212> PRT
<213> Artificial Sequence

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<220>
<223> (49B4) VHCH1 Fc knob VH (28H1)

```

```

<400> 310

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50           55           60

```

```

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr

```

100	105	110
Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
115	120	125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
130	135	140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
145	150	155
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
165	170	175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
180	185	190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser		
195	200	205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
210	215	220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser		
225	230	235
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
245	250	255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
260	265	270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
275	280	285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		
290	295	300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 485 490 495

Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

500

505

510

Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp
 515 520 525

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 545 550 555 560

Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly
 565 570 575

Thr Leu Val Thr Val Ser Ser
 580

<210> 311

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> (49B4) VHCH1 Fc hole VL (28H1)

<400> 311

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu

465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Ser Arg Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Ile Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Gln
545 550 555 560

Val Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

$\langle 210 \rangle$	312
$\langle 211 \rangle$	1746
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial Sequence

```
<220>
<223> nucleotide sequence of (49B4) VHCH1 Fc knob VH (DP47)
```

<400>	312
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tcttttgtac agcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac	300
taccgtggtc cgtagcacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc	360
accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca	420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttccccggtg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gccc aaatct 660
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720
 gtcttcctct tcccccaaaa acccaaggac accctcatga tctcccgga cctgagggtc 780
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900
 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgc aagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctccaaagcc 1020
 aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080
 aagaaccagg tgtccctgtg gtgtctggtc aagggttctt accccagcga tatcgccgtg 1140
 gagtggggaga gcaacggcca gcctgagaac aactacaaga ccaccccccc tgtgctggac 1200
 agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260
 ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta caccagaag 1320
 tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc cggaggaggg 1380
 ggaagtggcg gcggaggatc tgagggtgcaa ttgttggagt ctgggggagg cttggtacag 1440
 cctgggggggt ccctgagact ctctgtgca gccagcggat tcacctttag cagttagtacc 1500
 atgagctggg tccgccaggc tccagggaag gggctggagt gggctctcagc tattagtgg 1560
 agtgggtgta gcacatacta cgcagactcc gtgaagggcc ggttcacat ctccagagac 1620
 aattccaaga acacgctgta tctgcagatg aacagcctga gagccgagga cacggccgta 1680
 tattactgtg cgaaaggcag cggatttgac tactggggcc aaggaaccct ggtcaccgtc 1740
 tcgagc 1746

<210> 313
 <211> 1725
 <212> DNA

<213> Artificial Sequence

<220>

<223> nucelotide sequence of (49B4) VHCH1 Fc hole VL (DP47)

<400> 313

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac	300
taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc	360
accaagggcc catcggctctt ccccttgga ccctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttccccggtg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gccc aaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca	720
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc	780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcaagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc	1080
aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttctt cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag	1320

```

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggaggcggc      1380
ggaagcggag ggggaggctc tgaaattgtg ctgaccacaga gccccggcac cctgtcactg      1440
tctccaggcg aaagagccac cctgagctgc agagccagcc agagcgtgtc cagctcttac      1500
ctggcctggt atcagcagaa gcccggacag gccccagac tgctgatcta cggcgcctct      1560
tctagagcca ccggcatccc cgatagattc agcggcagcg gctccggcac cgacttcacc      1620
ctgacaatca gcagactgga acccgaggac tttgccgtgt attactgcca gcagtacggc      1680
agcagcccc  tgacctttgg ccagggcacc aaggtggaaa tcaaa                        1725

```

```

<210> 314
<211> 582
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> (49B4) VHCH1 Fc knob VH (DP47)

```

```

<400> 314

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50              55              60

```

```

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr

```

100	105	110
Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
115	120	125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
130	135	140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
145	150	155
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
165	170	175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser		
180	185	190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser		
195	200	205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr		
210	215	220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser		
225	230	235
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
245	250	255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
260	265	270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
275	280	285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		
290	295	300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 485 490 495

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

500

505

510

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
 515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 545 550 555 560

Tyr Tyr Cys Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 565 570 575

Leu Val Thr Val Ser Ser
 580

<210> 315

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> (49B4) VHCH1 Fc hole VL (DP47)

<400> 315

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu

465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
545 550 555 560

Ser Ser Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

$\langle 210 \rangle$	316
$\langle 211 \rangle$	1758
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> DNA (12B3) VHCH1 Fc knob VH (4B9) (HC1)

[illegible]

ggacacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480
 tggaactcag gcgcccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcagcag cgtgggtgacc gtgcccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga 720
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900
 agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
 gagtacaagt gcaaggctct caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccctg cagagatgag 1080
 ctgaccaaga accaggtgtc cctgtgggtgt ctgggtcaagg gcttctaccc cagcgatatc 1140
 gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac cccccctgtg 1200
 ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccgggtgg 1260
 cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc 1320
 cagaagtccc tgagcctgag ccccggcgga ggcggcgga ggcggaggagg aggatctggg 1380
 ggcggagggtt ccggaggcgg tggatctgag gtgcagctgc tcgaaagcgg cggaggactg 1440
 gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc 1500
 tacgccatga gctgggtccg ccaggccccct ggcaaggac tggaatgggt gtccgccatc 1560
 atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccggtt caccatcagc 1620
 cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc 1680
 gccgtgtact actgcgcaa gggatgggtt ggcggcttca actactgggg acagggcacc 1740
 ctggtcaccg tgtccagc 1758

<210> 317
 <211> 1731
 <212> DNA

<213> Artificial Sequence

<220>

<223> DNA (12B3) VHCH1 Fc hole VL (4B9)

<400> 317

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctggagtg gatgggaggg atcatcccta tctttggtac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa	300
ttccgtttct acgtgactt cgactactgg ggccaaggga ccaccgtgac cgtctcgagt	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttggtg acaaaaactca cacatgcca cctgccccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaagggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accagggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320

```

cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccggc      1380
ggcggagggtt ccggaggcgg aggatccgag atcgtgctga cccagtctcc cggcaccctg      1440
tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc      1500
tcctacctcg cctggtatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg      1560
ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcaccgac      1620
ttcaccctga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag      1680
ggcatcatgc tgccccccac ctttggccag ggcaccaagg tggaaatcaa g                1731

```

```

<210> 318
<211> 586
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> (12B3) VHCH1 Fc knob VH (4B9)

```

```

<400> 318

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50           55           60

```

```

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln

```

100					105					110					
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
	210					215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly
225					230					235					240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
				245					250					255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
			260					265					270		
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
	275						280					285			
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	290					295					300				

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
485 490 495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys

500

505

510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
 515 520 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 530 535 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 545 550 555 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
 565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 580 585

<210> 319

<211> 577

<212> PRT

<213> Artificial Sequence

<220>

<223> (12B3) VHCH1 Fc hole VL (4B9)

<400> 319

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu

465 470 475 480

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
485 490 495

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
500 505 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
515 520 525

Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
	530					535					540				

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
545 550 555 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
565 570 575

Lys

$\langle 210 \rangle$	320
$\langle 211 \rangle$	1752
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> DNA (25G7) VHCH1 Fc knob VH (4B9)

[illegible]

ccctggcccc cctttgatta ttggggacag ggcaccctcg tgaccgtgtc cagcgctagc	360
accaagggcc catcggcttt cccctggca ccctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggg caaggactac ttccccgaac cggtgacggg gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggg gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaaagttga gccc aaatct	660
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca	720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc	780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgaagg tctccaacaa agccctcggc gccccatcg agaaaacat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc	1080
aagaaccagg tgtccctgtg gtgtctgggtc aagggttctt accccagcga tatcgccgtg	1140
gagtgggaga gcaacggcca gcctgagaac aactacaaga ccaccccccc tgtgctggac	1200
agcgacggca gcttcttct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag	1260
ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta caccagaag	1320
tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc tgggggcgga	1380
ggttccggag gcggtggatc tgagggtgcag ctgctcga aa gcggcggagg actggtgcag	1440
cctggcggca gcctgagact gtcttgccgc gccagcggct tcaccttcag cagctacgcc	1500
atgagctggg tccgccaggc ccctggcaag ggactggaat ggggtgtccgc catcatcggc	1560
tctggcgcca gcacctacta cgccgacagc gtgaagggcc gggttaccat cagccgggac	1620
aacagcaaga acacctgta cctgcagatg aacagcctgc gggccgagga caccgccgtg	1680
tactactgcg ccaagggatg gttcggcggc ttcaactact ggggacaggg caccctggtc	1740
accgtgtcca gc	1752

<210> 321
 <211> 1725
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (25G7) VHCH1 Fc hole VL (4B9)

<400> 321
 gaggtgcagc tgctggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60
 agctgtgccg ccagcggctt caccttcagc agctacgcca tgagctgggt gcgccaggcc 120
 cctggaaaag gcctggaatg ggtgtccgcc atctctggca gcggcggcag cacctactac 180
 gccgattctg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
 ctgcagatga acagcctgcg ggccgaggac accgccgtgt actattgcgc cagggacgac 300
 ccctggcccc cctttgatta ttggggacag ggcaccctcg tgaccgtgtc cagcgctagc 360
 accaagggcc catcggctct ccccttgga cctcctcca agagcacctc tgggggcaca 420
 gcggcccttg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaaagtga gccc aaatct 660
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720
 gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900
 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgcagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctcaaagcc 1020
 aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc 1080
 aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg 1140
 gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

```

tccgacggct ccttcttcct cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag      1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag      1320
agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggcggcggg      1380
ggttccggag gcggaggatc cgagatcgtg ctgaccaggt ctcccggcac cctgtctctg      1440
agccctggcg agagagccac cctgtcctgc agagcctccc agtccgtgac ctcttcctac      1500
ctcgcctggg atcagcagaa gcccggccag gcccctcggc tgctgatcaa cgtgggcagt      1560
cggagagcca ccggcatccc tgaccgggtt tccggctctg gctccggcac cgacttcacc      1620
ctgaccatct cccggctgga acccgaggac ttcgccgtgt actactgcca gcagggcatc      1680
atgctgcccc ccacctttgg ccagggcacc aaggtggaaa tcaag                        1725

```

```

<210> 322
<211> 584
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> (25G7) VHCH1 Fc knob VH

```

```

<400> 322

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

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20           25           30

```

```

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

```

```

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50           55           60

```

```

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

```

```

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

```

85

90

95

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

485

490

495

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 500 505 510

Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala
 515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 545 550 555 560

Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln
 565 570 575

Gly Thr Leu Val Thr Val Ser Ser
 580

<210> 323

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> (25G7) VHCH1 Fc hole VL (4B9)

<400> 323

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

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

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

450

455

460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
 465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
 485 490 495

Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 500 505 510

Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp
 515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile
 545 550 555 560

Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 565 570 575

<210> 324

<211> 1755

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (11D5) VHCH1 Fc knob VH (4B9)

<400> 324

caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg cttccggcgg caccttcagc agctacgcca tttcttgggt gcgccaggcc 120

cctggacagg gcctggaatg gatgggcggc atcatcccca tcttcggcac cgccaactac 180

gcccagaaat tccagggcag agtgaccatc accgccgaca agagcaccag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc cagaagcacc 300

ctgatctacg gctacttcga ctactggggc cagggcacca ccgtgaccgt gtctagcgct	360
agcaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc	420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	480
aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga	540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac	600
atctgcaacg tgaatcaciaa gcccagcaac accaaggtgg acaagaaaagt tgagcccaaa	660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg	720
tcagtcttcc tcttcccccc aaaaccaag gacaccctca tgatctcccg gaccctgag	780
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac	840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc	900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	960
tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa	1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccctgcag agatgagctg	1080
accaagaacc aggtgtccct gtggtgtctg gtcaagggtc tctaccccag cgatatcgcc	1140
gtggagtggg agagcaacgg ccagcctgag aacaactaca agaccacccc ccctgtgctg	1200
gacagcgacg gcagcttctt cctgtactcc aaactgaccg tggacaagag ccggtggcag	1260
cagggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacaccag	1320
aagtcctga gcctgagccc cggcggaggc ggcggaagcg gaggaggagg atctgggggc	1380
ggaggttccg gaggcgggtg atctgaggtg cagctgctcg aaagcggcgg aggactggtg	1440
cagcctggcg gcagcctgag actgtcttgc gccgccagcg gcttcacctt cagcagctac	1500
gccatgagct ggggtccgcca ggcccctggc aagggactgg aatgggtgtc cgccatcatc	1560
ggctctggcg ccagcaccta ctacccgac agcgtgaagg gccggttcac catcagccgg	1620
gacaacagca agaacaccct gtacctgcag atgaacagcc tgcgggccga ggacaccgcc	1680
gtgtactact gcgccaaggg atgggtcggc ggcttcaact actggggaca gggcacctg	1740
gtcaccgtgt ccagc	1755

<210> 325
 <211> 1728
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (11D5) VHCH1 Fc hole VL (4B9)

<400> 325
 caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60
 tcctgcaagg cttccggcgg caccttcagc agctacgcca tttcttgggt gcgccaggcc 120
 cctggacagg gcctggaatg gatgggcggc atcatcccca tcttcggcac cgccaactac 180
 gcccagaaaat tccagggcag agtgaccatc accgccgaca agagcaccag caccgcctac 240
 atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc cagaagcacc 300
 ctgatctacg gctacttcga ctactggggc cagggcacca ccgtgaccgt gtctagcgct 360
 agcaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
 acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
 aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 540
 ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
 atctgcaacg tgaatcaca gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
 tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc aggggggaccg 720
 tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag 780
 gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
 gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
 acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
 tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020
 gccaaagggc agccccgaga accacagggtg tgcaccctgc ccccatcccg ggatgagctg 1080
 accaagaacc aggtcagcct ctctgtgcga gtcaaaggct tctatcccag cgacatcgcc 1140
 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag 1260
 caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
 aagagcctct ccctgtctcc ggggtggaggc ggcggaagcg gaggaggagg atccggcggc 1380
 ggaggttccg gaggcggagg atccgagatc gtgctgaccc agtctcccgg caccctgtct 1440
 ctgagccctg gcgagagagc caccctgtcc tgcagagcct ccagtcctgt gacctcctcc 1500
 tacctcgcct ggtatcagca gaagcccggc caggcccctc ggctgctgat caacgtgggc 1560
 agtcggagag ccaccggcat ccctgaccgg ttctccggct ctggctccgg caccgacttc 1620
 accctgacca tctcccggct ggaacccgag gacttcgccg tgtactactg ccagcagggc 1680
 atcatgctgc ccccccacctt tggccagggc accaaggtgg aaatcaag 1728

<210> 326
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (11D5) VHCH1 Fc knob VH (4B9)

<400> 326

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 450 455 460

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
 465 470 475 480

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr

485

490

495

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
 500 505 510

Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr
 515 520 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 530 535 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 545 550 555 560

Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly
 565 570 575

Gln Gly Thr Leu Val Thr Val Ser Ser
 580 585

<210> 327

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> (11D5) VHCH1 Fc hole VL (4B9)

<400> 327

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

50

55

60

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
 340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser
 355 360 365

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

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

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

450

455

460

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
 465 470 475 480

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 485 490 495

Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 500 505 510

Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro
 515 520 525

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 530 535 540

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly
 545 550 555 560

Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 565 570 575

<210> 328

<211> 1758

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (9B11) VHCH1 Fc knob VH (4B9)

<400> 328

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tcttttgttac agcaaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc gcggggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgccccctg cagagatgag	1080
ctgaccaaga accaggtgtc cctgtgggtgt ctgggtcaagg gcttctaccc cagcgatatc	1140
gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac cccccctgtg	1200
ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccgggtg	1260
cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc	1320
cagaagtccc tgagcctgag ccccggcgga ggcggcgga ggcggaggagg aggatctggg	1380
ggcggagggt ccggaggcgg tggatctgag gtgcagctgc tcgaaagcgg cggaggactg	1440
gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc	1500
tacgccatga gctgggtccg ccaggcccct ggcaagggaac tggaatgggt gtccgccatc	1560
atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccggtt caccatcagc	1620
cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc	1680
gccgtgtact actgcgcaa gggatgggtt ggcggcttca actactgggg acagggcacc	1740
ctggtcaccg tgtccagc	1758

<210> 329
 <211> 1731
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (9B11) VHCH1 Fc hole VL (4B9)

<400> 329
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagt gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300
 ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360
 gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
 ggacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga 720
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 780
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
 tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgcgggagga gcagtacaac 900
 agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
 gagtacaagt gcaaggctct caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020
 aaagccaaaag ggagccccg agaaccacag gtgtgcaccc tgcccccac cgggatgag 1080
 ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

```

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcagggtgg      1260
cagcaggggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg      1320
cagaagagcc tctccctgtc tccgggtgga ggccggcggaa gcggaggagg aggatccggc      1380
ggcggagggtt ccggaggcgg aggatccgag atcgtgctga cccagtctcc cggcaccttg      1440
tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc      1500
tcctacctcg cctggtatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg      1560
ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcacccgac      1620
ttcacctga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag      1680
ggcatcatgc tgccccccac ctttggccag ggcaccaagg tggaaatcaa g              1731

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<210> 330
<211> 586
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> (9B11) VHCH1 Fc knob VH (4B9)

```

```

<400> 330

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50              55              60

```

```

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe

485

490

495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
 515 520 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 530 535 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 545 550 555 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
 565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 580 585

<210> 331

<211> 577

<212> PRT

<213> Artificial Sequence

<220>

<223> (9B11) VHCH1 Fc hole VL (4B9)

<400> 331

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

50

55

60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

450

455

460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
 465 470 475 480

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 485 490 495

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 500 505 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
 515 520 525

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 530 535 540

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 545 550 555 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 565 570 575

Lys

<210> 332
 <211> 1731
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (12B3) VHCH1 Fc knob VL (4B9)

<400> 332
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctggagtg gatgggaggg atcatcccta tcttttgttac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa	300
ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcgagt	360
gctagcacca agggcccatc ggtcttcccc ctggcacctt cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggctct caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggagccccg agaaccacag gtgtacaccc tgccccctg cagagatgag	1080
ctgaccaaga accagggtgc cctgtgggtgt ctgggtcaagg gcttctaccc cagcgatatc	1140
gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac cccccctgtg	1200
ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccgggtg	1260
cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc	1320
cagaagtccc tgagcctgag ccccggcgga ggccggcgga gcggaggagg aggatctggg	1380
ggcggagggtt ccggaggcgg tggatctgag atcgtgctga cccagtctcc cggcaccctg	1440
tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc	1500
tcctacctcg cctggatatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg	1560
ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcaccgac	1620
ttcaccttga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag	1680

ggcatcatgc tgccccccac ctttggccag ggcaccaagg tggaaatcaa g 1731

<210> 333

<211> 1758

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (12B3) VHCH1 Fc hole VH (4B9)

<400> 333

cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctggagtg gatgggaggg atcatcccta tctttgttac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa	300
ttccgtttct acgtgactt cgactactgg ggccaaggga ccaccgtgac cgtctcgagt	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg	480
tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt	780
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgagggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc	1140

```

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg      1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg      1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg      1320
cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccggc      1380
ggcggagggtt ccggaggcgg aggatccgag gtgcagctgc tcgaaagcgg cggaggactg      1440
gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc      1500
tacgcatga gctgggtccg ccaggcccct ggcaagggac tggaatgggt gtccgccatc      1560
atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccgggt caccatcagc      1620
cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc      1680
gccgtgtact actgcgcaa gggatgggtt ggcggttca actactgggg acagggcacc      1740
ctggtcaccg tgtccagc                                     1758

```

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<210> 334
<211> 577
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> (12B3) VHCH1 Fc knob VL (4B9)

```

```

<400> 334

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```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60

```

```

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

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
500 505 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
515 520 525

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
530 535 540

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
545 550 555 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
565 570 575

Lys

$\langle 210 \rangle$	335
$\langle 211 \rangle$	586
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> (12B3) VHCH1 Fc hole VH (4B9)

<400> 335

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

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

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

35

40

45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

435

440

445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 485 490 495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
 515 520 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 530 535 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 545 550 555 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
 565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 580 585

<210> 336

<211> 1725

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (25G7) VHCH1 Fc knob VL (4B9)

<400> 336

gagggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc

60

tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac	300
ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgctagc	360
accaagggcc catcggctctt ccccctggca ccctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctgggt caaggactac ttccccgaac cggtgacgggt gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	540
tactccctca gcagcgtgggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aagggtggaca agaaagttga gcccaaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca	720
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc	780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcagg tctccaacaa agccctcggc gccccatcg agaaaaccat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc	1080
aagaaccagg tgtccctgtg gtgtctggtc aagggttctt accccagcga tatcgccgtg	1140
gagtgggaga gcaacggcca gcctgagaac aactacaaga ccaccccccc tgtgctggac	1200
agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag	1260
ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta caccagaag	1320
tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc tgggggcgga	1380
ggttccggag gcggtggatc tgagatcgtg ctgaccagct ctcccggcac cctgtctctg	1440
agccctggcg agagagccac cctgtcctgc agagcctccc agtccgtgac ctctcctac	1500
ctgcctgggt atcagcagaa gcccggccag gcccctcggc tgctgatcaa cgtgggcagt	1560

cggagagcca ccggcatccc tgaccggttc tccggctctg gctccggcac cgacttcacc 1620
 ctgaccatct cccggctgga acccgaggac ttcgccgtgt actactgcca gcagggcatc 1680
 atgctgcccc ccacctttgg ccagggcacc aaggtggaaa tcaag 1725

<210> 337

<211> 1752

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (25G7) VHCH1 Fc hole VH (4B9)

<400> 337

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300
 ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgcctagc 360
 accaagggcc catcggctctt cccctggca cctcctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
 tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gccc aaatct 660
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720
 gtcttcctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780
 acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840
 gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900
 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgaagg tctccaacaa agccctcggc gccccatcg agaaaacat ctccaaagcc 1020


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aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc      1080
aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg      1140
gagtggggaga gcaatgggca gccgggagaac aactacaaga ccacgcctcc cgtgctggac      1200
tccgacggct ccttcttcct cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag      1260
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag      1320
agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggcggcgga      1380
ggttccggag gcggaggatc cgaggtgcag ctgctcgaaa gcggcggagg actggtgcag      1440
cctggcggca gcctgagact gtcttgcgcc gccagcggct tcaccttcag cagctacgcc      1500
atgagctggg tccgccaggc ccctggcaag ggactggaat ggggtgtccgc catcatcggc      1560
tctggcgcca gcacctacta cgccgacagc gtgaagggcc ggttcaccat cagccgggac      1620
aacagcaaga acacctgtga cctgcagatg aacagcctgc gggccgagga caccgccgtg      1680
tactactgcg ccaagggatg gttcggcggc ttcaactact ggggacaggg caccctggtc      1740
accgtgtcca gc                                              1752

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<210> 338
<211> 575
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> (25G7) VHCH1 Fc knob VL (4B9)

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```

<400> 338

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```

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

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```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20           25           30

```

```

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

```

```

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

```

50

55

60

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

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

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

450

455

460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
 465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
 485 490 495

Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 500 505 510

Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp
 515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile
 545 550 555 560

Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 565 570 575

<210> 339

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> (25G7) VHCH1 Fc hole VH (4B9)

<400> 339

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

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

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
 355 360 365

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

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

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly

435

440

445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 485 490 495

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 500 505 510

Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala
 515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 545 550 555 560

Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln
 565 570 575

Gly Thr Leu Val Thr Val Ser Ser
 580

<210> 340

<211> 1728

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (11D5) VHCH1 Fc knob VL (4B9)

<400> 340

cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc

60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagt gatgggaggg atcatcccta tctttggtac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact	300
ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctctcagct	360
agcaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc	420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	480
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga	540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac	600
atctgcaacg tgaatcaca gcccagcaac accaagggtg acaagaaagt tgagcccaaa	660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg	720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag	780
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac	840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc	900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	960
tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa	1020
gccaaagggc agccccgaga accacagggtg tacaccctgc cccctgcag agatgagctg	1080
accaagaacc aggtgtccct gtggtgtctg gtcaagggtc tctaccccag cgatatcgcc	1140
gtggagtggg agagcaacgg ccagcctgag aacaactaca agaccacccc ccctgtgctg	1200
gacagcgacg gcagcttctt cctgtactcc aaactgaccg tggacaagag ccggtggcag	1260
cagggaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacaccag	1320
aagtcctga gcctgagccc cggcggaggc ggcggaagcg gaggaggagg atctgggggc	1380
ggaggttccg gaggcgggtg atctgagatc gtgctgaccc agtctcccgg caccctgtct	1440
ctgagccctg gcgagagagc caccctgtcc tgcagagcct ccagtcctg gacctcctcc	1500
tacctcgctt ggtatcagca gaagcccggc caggcccctc ggctgctgat caacgtgggc	1560

agtcggagag ccaccggcat ccctgaccgg ttctccggct ctggctccgg caccgacttc 1620
 accctgacca tctcccggct ggaacccgag gacttcgccg tgtactactg ccagcagggc 1680
 atcatgctgc cccccacctt tggccagggc accaaggtgg aaatcaag 1728

<210> 341
 <211> 1755
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA (11D5) VHCH1 Fc hole VH (4B9)

<400> 341
 cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagt gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact 300
 ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctctcagct 360
 agcaccaagg gcccatcggc cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
 acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
 aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540
 ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600
 atctgcaacg tgaatcaciaa gccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
 tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg 720
 tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780
 gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840
 gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
 acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
 tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

```

gccaaagggc agccccgaga accacaggtg tgcaccctgc ccccatcccc ggatgagctg      1080
accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc      1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg      1200
gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag      1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag      1320
aagagcctct ccctgtctcc ggggtggaggc ggcggaagcg gaggaggagg atccggcggc      1380
ggaggttccg gaggcggagg atccgaggtg cagctgctcg aaagcggcgg aggactgggtg      1440
cagcctggcg gcagcctgag actgtcttgc gccgccagcg gcttcacctt cagcagctac      1500
gccatgagct ggggtccgcca ggcccctggc aagggaactgg aatgggtgtc cgccatcatc      1560
ggctctggcg ccagcaccta ctacgccgac agcgtgaagg gccgggttcac catcagccgg      1620
gacaacagca agaacaccct gtacctgcag atgaacagcc tgcggggccga ggacaccgcc      1680
gtgtactact gcgccaaggg atggttcggc ggcttcaact actggggaca gggcaccctg      1740
gtcaccgtgt ccagc                                          1755

```

<210> 342

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> (11D5) VHCH1 Fc knob VL (4B9)

<400> 342

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

```

50

55

60

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

450

455

460

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
 465 470 475 480

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 485 490 495

Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 500 505 510

Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro
 515 520 525

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 530 535 540

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly
 545 550 555 560

Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 565 570 575

<210> 343

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> (11D5) VHCH1 Fc hole VH (4B9)

<400> 343

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

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

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

35

40

45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
305					310					315					320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser
355 360 365

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

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

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

435

440

445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 450 455 460

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
 465 470 475 480

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 485 490 495

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
 500 505 510

Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr
 515 520 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 530 535 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 545 550 555 560

Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly
 565 570 575

Gln Gly Thr Leu Val Thr Val Ser Ser
 580 585

<210> 344

<211> 1731

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (9B11) VHCH1 Fc knob VL (4B9)

<400> 344

cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagt gatgggaggg atcatcccta tctttggtac agcaaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct	300
ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca	360
gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg	480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	780
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccctg cagagatgag	1080
ctgaccaaga accaggtgtc cctgtggtgt ctggtcaagg gcttctaccc cagcgatatc	1140
gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac cccccctgtg	1200
ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccggtgg	1260
cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc	1320
cagaagtccc tgagcctgag ccccggcgga ggccggcgga gcggaggagg aggatctggg	1380
ggcggagggt ccggaggcgg tggatctgag atcgtgctga ccagtcctcc cggcacctg	1440
tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc	1500
tcctacctcg cctggtatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg	1560

ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcaccgac 1620
 ttcaccctga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag 1680
 ggcatcatgc tgccccccac ctttggccag ggcaccaagg tggaaatcaa g 1731

<210> 345

<211> 1758

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA (9B11) VHCH1 Fc hole VH (4B9)

<400> 345

cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300
 ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360
 gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
 ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
 tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 600
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660
 aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaagc tgcaggggga 720
 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 780
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840
 tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgcgggagga gcagtacaac 900
 agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960
 gagtacaagt gcaaggctct caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

```

aaagccaaag ggcagccccc agaaccacag gtgtgcaccc tgcccccatc ccgggatgag      1080
ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc      1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg      1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg      1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg      1320
cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccggc      1380
ggcggagggtt ccggaggcgg aggatccgag gtgcagctgc tcgaaagcgg cggaggactg      1440
gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc      1500
tacgccatga gctgggtccg ccaggcccct ggcaagggaac tggaatgggt gtccgccatc      1560
atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccgggt caccatcagc      1620
cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc      1680
gccgtgtact actgcgcaa gggatggttc ggcggcttca actactgggg acagggcacc      1740
ctggtcaccg tgtccagc                                     1758

```

<210> 346
 <211> 577
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> (9B11) VHCH1 Fc knob VL (4B9)

<400> 346

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

```

50

55

60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

450

455

460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
 465 470 475 480

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 485 490 495

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 500 505 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
 515 520 525

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 530 535 540

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
 545 550 555 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 565 570 575

Lys

<210> 347

<211> 586

<212> PRT

<213> Artificial Sequence

<220>

<223> (9B11) VHCH1 Fc hole VH (4B9)

<400> 347

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

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

20

25

30

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

420

425

430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 485 490 495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
 515 520 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 530 535 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 545 550 555 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
 565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 580 585