

SEQUENCE LISTING

<110> MacroGenics, Inc.
 Liu, Ligin
 Kao, Chia-Ying
 Diedrich, Gundo
 Johnson, Leslie
 Moore, Paul
 Bonvini, Ezio

<120> Bispecific Binding Molecules That Are Capable of Binding CD137
 and Tumor Antigens, and Uses Thereof

<130> 1301.0149PCT

<150> US 62/597,594
 <151> 2017-12-12

<150> US 62/463,353
 <151> 2017-02-24

<160> 232

<170> PatentIn version 3.5

<210> 1
 <211> 107
 <212> PRT
 <213> Homo sapiens

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 <222> (1)..(107)
 <223> Human IgG CL Kappa Domain

<400> 1

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15

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

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

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

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

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

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

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<223> Human IgG CL Lambda Domain

<400> 2

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

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

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
35 40 45

Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
50 55 60

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
65 70 75 80

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

Thr Val Ala Pro Thr Glu Cys Ser
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<213> Homo sapiens

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<222> (1)..(98)
<223> Human IgG1 CH1 Domain

<400> 3

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

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

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

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

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

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

Arg Val

<210> 4
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<213> Homo sapiens

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<223> Human IgG2 CH1 Domain

<400> 4

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

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

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

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

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

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

Thr Val

<210> 5
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<213> Homo sapiens

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<223> Human IgG3 CH1 Domain

<400> 5

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

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

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

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

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

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

Arg Val

<210> 6
<211> 98
<212> PRT
<213> Homo sapiens

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<223> Human IgG4 CH1 Domain

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

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

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

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

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

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

Arg Val

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 <213> Homo sapiens

<220>
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 <223> Human IgG1 Hinge Region

<400> 7

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10 15

<210> 8
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 <212> PRT
 <213> Homo sapiens

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 <223> Human IgG2 Hinge Region

<400> 8

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
 1 5 10

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 <211> 62
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 <213> Homo sapiens

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 <222> (1)..(62)
 <223> Human IgG3 Hinge Region

<400> 9

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
 1 5 10 15

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 20 25 30

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
 35 40 45

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 50 55 60

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 <213> Homo sapiens

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 <222> (1)..(12)
 <223> Human IgG4 Hinge Region

 <400> 10
 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
 1 5 10

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 <400> 11
 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1 5 10

 <210> 12
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 <212> PRT
 <213> Homo sapiens

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 <223> Exemplary Human IgG1 CH2-CH3 Domain

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 <223> Xaa is Lysine (K) or Is Absent

 <400> 12
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1 5 10 15

 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 20 25 30

 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 35 40 45

 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60

 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80

 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 85 90 95

 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 Page 6

100 105 110
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 115 120 125
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 130 135 140
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 145 150 155 160
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 165 170 175
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 180 185 190
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 195 200 205
 Lys Ser Leu Ser Leu Ser Pro Gly Xaa
 210 215

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<220>
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 <222> (1)..(216)
 <223> Exemplary Human IgG2 CH2-CH3 Domain

<220>
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 <222> (216)..(216)
 <223> Xaa is Lysine (K) or Is Absent

<400> 13

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1 5 10 15
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 20 25 30
 Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
 35 40 45
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 50 55 60
 Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
 65 70 75 80

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
 85 90 95
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
 100 105 110
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 115 120 125
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 130 135 140
 Asp Ile Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 145 150 155 160
 Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 165 170 175
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 180 185 190
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 195 200 205
 Ser Leu Ser Leu Ser Pro Gly Xaa
 210 215

<210> 14
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 <213> Homo sapiens

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 <223> Exemplary Human IgG3 CH2-CH3 Domain

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 <222> (217)..(217)
 <223> Xaa is Lysine (K) or Is Absent

<400> 14

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

50

55

60

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

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<223> Exemplary Human IgG1 CH2-CH3 Domain

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<223> Xaa is Lysine (K) or Is Absent

<400> 15

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Xaa
210 215

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Intervening Spacer Peptide (Linker 1)

<400> 16

Gly Gly Gly ser Gly Gly Gly Gly
1 5

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Intervening Spacer Peptide (Linker 1) for scFv Molecules
<400> 17

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Intervening Spacer Peptide (Linker 2)
<400> 18

Gly Gly Cys Gly Gly Gly
1 5

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Alternative Intervening Spacer Peptide (Linker 2)
<400> 19

Ala Ser Thr Lys Gly
1 5

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Heterodimer-Promoting Domain (Linker 3)
<400> 20

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 21
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Alternative Heterodimer-Promoting Domain (Linker 3)
<400> 21

Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 22
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> Preferred Intervening Spacer Peptide (Linker 4)

<400> 22

Ala Pro Ser Ser Ser
1 5

<210> 23

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Alternative Preferred Intervening Spacer Peptide (Linker 4)

<400> 23

Ala Pro Ser Ser Ser Pro Met Glu
1 5

<210> 24

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Alternative Preferred Intervening Spacer Peptide (Linker 4)

<400> 24

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
1 5 10

<210> 25

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Alternative Linker

<400> 25

Leu Gly Gly Gly Ser Gly
1 5

<210> 26

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Alternative Linker

<400> 26

Gly Gly Gly Ser
1

<210> 27

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

<220>
<223> Alternative Linker

<400> 27

Leu Glu Pro Lys Ser Ser
1 5

<210> 28
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Alternative Linker

<400> 28

Val Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 29
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Alternative Linker

<400> 29

Leu Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 30
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Alternative Linker

<400> 30

Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 31
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Heterodimer-Promoting Domain

<400> 31

Gly Val Glu Pro Lys Ser Cys
1 5

<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Heterodimer-Promoting Domain

<400> 32

Val Glu Pro Lys Ser Cys
1 5

<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Heterodimer-Promoting Domain

<400> 33

Ala Glu Pro Lys Ser Cys
1 5

<210> 34
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<213> Artificial Sequence

<220>
<223> Preferred Heterodimer-Promoting Domain

<400> 34

Gly Phe Asn Arg Gly Glu Cys
1 5

<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Heterodimer-Promoting Domain

<400> 35

Phe Asn Arg Gly Glu Cys
1 5

<210> 36
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> E-Coil Heterodimer-Promoting Domain

<400> 36

Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
Page 14

1 5 10 15

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
20 25

<210> 37
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> K-Coil Heterodimer-Promoting Domain

<400> 37

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
1 5 10 15

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
20 25

<210> 38
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing E-Coil Heterodimer-Promoting Domain

<400> 38

Glu Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
1 5 10 15

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
20 25

<210> 39
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing K-Coil Heterodimer-Promoting Domain

<400> 39

Lys Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
1 5 10 15

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
20 25

<210> 40
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 CH2-CH3 Domain Variant Comprising Kabat L234A and
Page 15

L235A Substitutions

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<222> (217)..(217)

<223> Xaa is Lysine (K) or Is Absent

<400> 40

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

<210> 41

<211> 217

<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 CH2-CH3 Domain Variant Comprising Kabat M252Y, S254T and T256E Substitutions

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa is Lysine (K) or Is Absent

<400> 41

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa

210

215

<210> 42
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IgG1 CH2-CH3 Domain Variant Comprising Kabat L234A, L235A, M252Y, S254T and T256E Substitutions

<220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa is Lysine (K) or Is Absent

<400> 42

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
 20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

<210> 43
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG4 CH2-CH3 Domain Variant Comprising Kabat M252Y, S254T and T256E Substitutions

<220>
<221> misc_feature
<222> (217)..(217)
<223> Xaa can be any naturally occurring amino acid

<400> 43

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Xaa
210 215

<210> 44
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary "Knob-Bearing" IgG1 CH2-CH3 Domain

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa is Lysine (K) or Is Absent

<400> 44

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

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

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

<210> 45
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary "Knob-Bearing" IgG1 CH2-CH3 Domain

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa is Lysine (K) or Is Absent

<400> 45

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

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

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

Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Xaa
210 215

<210> 46
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary "Knob-Bearing" IgG1 CH2-CH3 Domain

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa is Lysine (K) or Is Absent

<400> 46

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

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

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

<210> 47
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary "Hole-Bearing" IgG1 CH2-CH3 Domain

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa is Lysine (K) or Is Absent

<400> 47

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

<210> 48
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary "Hole-Bearing" IgG1 CH2-CH3 Domain

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa is Lysine (K) or Is Absent

<400> 48

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Val Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Xaa
210 215

<210> 49
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary "Hole-Bearing" IgG1 CH2-CH3 Domain

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa is Lysine (K) or Is Absent

<400> 49

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
115 120 125

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
130 135 140

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

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

<210> 50
<211> 46
<212> PRT
<213> Streptococcus dysgalactiae

<220>
<221> MISC_FEATURE
<222> (1)..(46)
<223> Albumin-Binding Domain 3 (ABD3) of Protein G of Streptococcus
Strain G148

<400> 50

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asp Asn Ala Lys Ser Ala Glu
20 25 30

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

<210> 51
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Deimmunized Albumin-Binding Domain 3 (ABD3) of Protein G of Streptococcus Strain G148

<400> 51

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asp Asn Ala Lys Ser Ala Glu
20 25 30

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

<210> 52
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Deimmunized Albumin-Binding Domain 3 (ABD3) of Protein G of Streptococcus Strain G148

<400> 52

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

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

Gly Val Lys Ala Leu Ile Ala Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 53
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Deimmunized Albumin-Binding Domain 3 (ABD3) of Protein G of Streptococcus Strain G148

<400> 53

Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
1 5 10 15

Val Ser Asp Tyr Tyr Lys Asn Leu Ile Ser Asn Ala Lys Ser Val Glu
20 25 30

Gly Val Lys Ala Leu Ile Ala Glu Ile Leu Ala Ala Leu Pro
35 40 45

<210> 54
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> VH Domain of Margetuximab

<400> 54

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

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

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

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

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

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

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

Gly Ala Ser Val Thr Val Ser Ser
115 120

<210> 55

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of Margetuximab

<400> 55

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

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

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

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

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

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

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

<210> 56
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Trastuzumab
<400> 56

Glu Val Gln Leu Val 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 Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 57
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of Trastuzumab
<400> 57

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

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

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

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

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

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

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

<210> 58

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> VH Domain of Pertuzumab

<400> 58

Glu Val Gln Leu Val 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 Thr Asp Tyr
20 25 30

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 59

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of Pertuzumab

<400> 59

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

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

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

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

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

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

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

<210> 60

<211> 119

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(119)

<223> Murine Anti-HER2/neu Monoclonal Antibody HER2-MAB-1 VH Domain

<400> 60

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

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

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

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

Lys Gly Arg Phe Ala Phe Ser Leu Gly Thr Ser Ala Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

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

Thr Leu Val Thr Val Ser Ala
115

<210> 61
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(107)
<223> Murine Anti-HER2/neu Monoclonal Antibody HER2-MAB-1 VL Domain
<400> 61

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

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

Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45

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

Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln His Asp Glu Phe Pro Trp
85 90 95

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

<210> 62
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VH Domain

<220>
<221> MISC_FEATURE
<222> (100)..(100)
<223> Xaa is Asparatate (D) or Glutamate (E)

<220>
<221> MISC_FEATURE
<222> (101)..(101)
<223> Xaa is Glycine (G) or Isoleucine (I)

<400> 62

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

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

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

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

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

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

Ala Arg Asp Xaa Xaa Tyr Gly Asn Arg Val Ser Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 63

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VL Domain

<220>

<221> MISC_FEATURE

<222> (30)..(30)

<223> Xaa is Asparagine (N) or Serine (S)

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa is Serine (S), Threonine (T) or Asparagine (N)

<220>

<221> MISC_FEATURE

<222> (55)..(55)

<223> Xaa is Valine (V) or Glutamine (Q)

<220>

<221> MISC_FEATURE

<222> (56)..(56)

<223> Xaa is Aspartate (D), Glutamate (E) or Serine (S)

<400> 63

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

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

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

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

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

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

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

<210> 64

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VH1
Domain

<400> 64

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 65
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VH2 Domain

<400> 65

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

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

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

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

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

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

Ala Arg Asp Glu Gly Tyr Gly Asn Arg Val Ser Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 66
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VH3 Domain

<400> 66

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

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

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

Gly Trp Ile Asn Thr Asn Ile Gly Glu Pro Thr Tyr Thr Glu Glu Phe
Page 35

50

55

60

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

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

Ala Arg Asp Asp Ile Tyr Gly Asn Arg Val Ser Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 67

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VL1
Domain

<400> 67

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

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

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

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

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

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

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

<210> 68

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VL2
Domain

<400> 68

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

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

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

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

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

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

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

<210> 69

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized Anti-HER2/neu Monoclonal Antibody hHER2-MAB-1 VL3
Domain

<400> 69

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

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

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

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

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

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

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

<210> 70
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of CD137 MAB-1 (CD137 MAB-1 VH)

<400> 70

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

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

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Tyr Gly Pro Gly Asn Tyr Asp Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 71
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of CD137 MAB-1 (CD137 MAB-1 VL)

<400> 71

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

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

<210> 72
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of CD137 MAB-2 (CD137 MAB-2 VH)

<400> 72

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

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Ser Thr Tyr
20 25 30

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

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

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

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

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

Thr Val Ser Ser
115

<210> 73
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of CD137 MAB-2 (CD137 MAB-2 VL)

<400> 73

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

Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Ile Gly Asp Gln Tyr Ala
20 25 30

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

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

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

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

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

<210> 74
<211> 119
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(119)
<223> VH Domain of CD137 MAB-3 (CD137 MAB-3 VH)

<400> 74

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

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

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

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

Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 75
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> VL Domain of CD137 MAB-3 (CD137 MAB-3 VL)

<400> 75

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

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

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

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

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

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

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

<210> 76
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH Domain of Humanized CD137 MAB-3 (hCD137 MAB-3 VH1)

<400> 76

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

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

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

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

Lys Asp Lys Ala 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

Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 77
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Optimized Humanized CD137 MAB-3 (hCD137 MAB-3 VH1)

<220>
<221> MISC_FEATURE
<222> (103)..(103)
<223> Xaa is Alanine (A) or Serine (S)

<220>
<221> MISC_FEATURE
<222> (104)..(104)
<223> Xaa is Tyrosine (Y)

<220>
<221> MISC_FEATURE
<222> (105)..(105)
<223> Xaa is Serine (S)

<220>
<221> MISC_FEATURE
<222> (106)..(106)
<223> Xaa is Phenylalanine (F), Methionine (M) or Tyrosine (Y)

<220>
<221> MISC_FEATURE
<222> (107)..(107)
<223> Xaa is Histidine (H), Serine (S) or Asparagine (N)

<220>
<221> MISC_FEATURE
<222> (108)..(108)
<223> Xaa is Proline (P), Threonine (T), Leucine or Valine (V)

<400> 77

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

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

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

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

Lys Asp Lys Ala 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

Thr Arg Asp Tyr Gly Ser Xaa Xaa Xaa Xaa Xaa Xaa Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 78
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Residues 103-108 of SEQ ID NO:77 Variant 1A

<400> 78

Ala Tyr Ser Phe His Pro
1 5

<210> 79
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Residues 103-108 of SEQ ID NO:77 Variant 1B

<400> 79

Ala Tyr Ser Met Ser Thr
1 5

<210> 80
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Residues 103-108 of SEQ ID NO:77 Variant 1C

<400> 80

Ala Tyr Ser Tyr Ser Leu
1 5

<210> 81
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
 <223> Preferred Residues 103-108 of SEQ ID NO:77 Variant 1D
 <400> 81
 Ser Tyr Ser Tyr Asn Val
 1 5
 <210> 82
 <211> 107
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> VL Domain of Optimized Humanized Antibody hCD137 MAB-3 (hCD137 MAB-3 VL)

<220>
 <221> MISC_FEATURE
 <222> (41)..(41)
 <223> Xaa is Asparatate (D) or Glycine (G)

<220>
 <221> MISC_FEATURE
 <222> (42)..(42)
 <223> Xaa is Glycine (G) or Lysine (K)

<400> 82
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Asn Trp Tyr Gln Gln Lys Pro Xaa Xaa Thr Val Lys Leu Leu Ile
 35 40 45

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

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

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

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

<210> 83
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD137 MAB-3 VH1A

<400> 83

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Ala 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
 Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Phe His Pro Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

<210> 84
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD137 MAB-3 VH1B

<400> 84

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

100

105

110

Thr Thr Val Thr Val Ser Ser
115

<210> 85
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD137 MAB-3 VH1C

<400> 85

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

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

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

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

Lys Asp Lys Ala 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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 86
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> hCD137 MAB-3 VH1D

<400> 86

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

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

Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
Page 46

35

40

45

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

Lys Asp Lys Ala 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

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

Thr Thr Val Thr Val Ser Ser
 115

<210> 87
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD137 MAB-3 VL1

<400> 87

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

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

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

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

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

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

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

<210> 88
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD137 MAB-3 VL2

<400> 88

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

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

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

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

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

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

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

<210> 89

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> hCD137 MAB-3 VL3

<400> 89

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 90
 <211> 123
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(123)
 <223> VH Domain of CD137 MAB-4 (CD137 MAB-4 VH)

<400> 90

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala
 1 5 10 15

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

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

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

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

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

Thr Lys Ser Gly Glu Tyr Gly Lys Ile Gly Tyr Tyr Ala Met Asp Tyr
 100 105 110

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

<210> 91
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> VL Domain of CD137 MAB-4 (CD137 MAB-4 VL)

<400> 91

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 Page 49

35

40

45

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

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

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

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

<210> 92

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> VH Domain of Humanized CD137 MAB-4 (hCD137 MAB-4 VH1)

<400> 92

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

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

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

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

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

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

Thr Lys Ser Gly Glu Tyr Gly Lys Ile Gly Tyr Tyr Ala Met Asp Tyr
100 105 110

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

<210> 93

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of Humanized CD137 MAB-4 (hCD137 MAB-4 VL)

<220>
 <221> MISC_FEATURE
 <222> (87)..(87)
 <223> Xaa is Phenylalanine (F) or Tyrosine (Y)

<400> 93

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45

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

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

Glu Asp Ile Ala Thr Tyr Xaa Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

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

<210> 94
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL Domain of Humanized CD137 MAB-4 (hCD137 MAB-4 VL1)

<400> 94

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45

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

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

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr

85

90

95

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

<210> 95
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of Humanized CD137 MAB-4 (hCD137 MAB-4 VL2)
<400> 95

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

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

<210> 96
<211> 111
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> VH Domain of CD137 MAB-5 (CD137 MAB-5 VH)
<400> 96

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Asp Ile Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Val Trp Thr Gly Gly Gly Thr Asn Tyr Asn Ser Ala Phe Met
50 55 60

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

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

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

<210> 97
<211> 112
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(112)
<223> VL Domain of CD137 MAB-5 (CD137 MAB-5 VL)

<400> 97

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

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

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

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

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

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

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

<210> 98
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> First and Third Polypeptide Chains of DART-A

<400> 98

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Thr Tyr
 20 25 30
 Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Thr Leu Ile
 35 40 45
 Tyr Arg Ala Asn Arg Leu Val Glu Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asp Glu Phe Pro Trp
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110
 Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140
 Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160
 Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
 165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
 225 230 235 240
 Glu Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
 245 250 255
 Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Leu Glu Pro Lys
 260 265 270

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

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
290 295 300

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305 310 315 320

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
325 330 335

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
340 345 350

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
355 360 365

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
370 375 380

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385 390 395 400

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
405 410 415

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
420 425 430

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
435 440 445

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
450 455 460

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465 470 475 480

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
485 490 495

Leu Ser Pro Gly
500

<210> 99
<211> 268
<212> PRT
<213> Artificial sequence

<220>
<223> Second and Fourth Polypeptide Chains of DART-A
Page 55

<400> 99

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Glu Glu Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Ala Arg Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp
210 215 220

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
225 230 235 240

Lys Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
245 250 255

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
Page 56

260

265

<210> 100
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> First and Third Polypeptide Chain of DART-B

<400> 100

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp
 210 215 220

Gly 225 Gln Gly Thr Thr Val 230 Thr Val Ser Ser Gly 235 Gly Cys Gly Gly Gly 240
 Glu Val Ala Ala Cys 245 Glu Lys Glu Val Ala 250 Ala Leu Glu Lys Glu Val 255
 Ala Ala Leu Glu 260 Lys Glu Val Ala 265 Leu Glu Lys Leu Glu 270 Pro Lys
 Ser Ala Asp 275 Lys Thr His Thr Cys 280 Pro Pro Cys Pro Ala 285 Pro Glu Ala
 Ala Gly 290 Gly Pro Ser Val Phe 295 Leu Phe Pro Pro Lys 300 Pro Lys Asp Thr
 Leu 305 Met Ile Ser Arg Thr 310 Pro Glu Val Thr Cys 315 Val Val Val Asp Val 320
 Ser His Glu Asp Pro 325 Glu Val Lys Phe Asn 330 Trp Tyr Val Asp Gly 335 Val
 Glu Val His Asn 340 Ala Lys Thr Lys Pro 345 Arg Glu Glu Gln Tyr Asn Ser 350
 Thr Tyr Arg 355 Val Val Ser Val Leu 360 Thr Val Leu His Gln Asp Trp Leu 365
 Asn Gly 370 Lys Glu Tyr Lys Cys 375 Lys Val Ser Asn Lys 380 Ala Leu Pro Ala
 Pro 385 Ile Glu Lys Thr Ile 390 Ser Lys Ala Lys Gly 395 Gln Pro Arg Glu Pro 400
 Gln Val Tyr Thr Leu 405 Pro Pro Ser Arg Glu 410 Glu Met Thr Lys Asn Gln 415
 Val Ser Leu Thr 420 Cys Leu Val Lys Gly 425 Phe Tyr Pro Ser Asp Ile Ala 430
 Val Glu Trp 435 Glu Ser Asn Gly Gln 440 Pro Glu Asn Asn Tyr 445 Lys Thr Thr
 Pro Pro 450 Val Leu Asp Ser Asp 455 Gly Ser Phe Phe Leu 460 Tyr Ser Lys Leu
 Thr 465 Val Asp Lys Ser Arg 470 Trp Gln Gln Gly Asn 475 Val Phe Ser Cys Ser 480
 Val Met His Glu 485 Ala Leu His Asn His Tyr 490 Thr Gln Lys Ser Leu Ser 495

Leu Ser Pro Gly
500

<210> 101
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fourth Polypeptide Chain of DART-B

<400> 101

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Glu Glu Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Ala Arg Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp
Page 59

210

215

220

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
 225 230 235 240

Lys Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
 245 250 255

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
 260 265

<210> 102

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> First and Third Polypeptide Chains of DART-C

<400> 102

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140

Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160

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

Glu Glu Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Ala Arg Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp
 210 215 220
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
 225 230 235 240
 Glu Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
 245 250 255
 Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Leu Glu Pro Lys
 260 265 270
 Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 275 280 285
 Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 290 295 300
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 305 310 315 320
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 325 330 335
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 340 345 350
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 355 360 365
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 370 375 380
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 385 390 395 400
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 405 410 415
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 420 425 430
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 435 440 445

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
450 455 460

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
465 470 475 480

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
485 490 495

Leu Ser Pro Gly
500

<210> 103
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fourth Polypeptide Chains of DART-C

<400> 103

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
Page 62

165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
 225 230 235 240
 Lys Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
 245 250 255
 Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
 260 265
 <210> 104
 <211> 449
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> First Polypeptide Chain of DART-D
 <400> 104
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Asn Ile Gly Glu Pro Thr Tyr Thr Glu Glu Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu 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 Arg 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 Pro 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 Glu Glu Met 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 Arg Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 105
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fifth Polypeptide Chains of DART-D

<400> 105

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu 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
Page 65

165 170 175

Ser Thr Leu Thr 180 Leu Ser Lys Ala Asp 185 Tyr Glu Lys His Lys 190 Val Tyr

Ala Cys Glu 195 Val Thr His Gln Gly 200 Leu Ser Ser Pro Val 205 Thr Lys Ser

Phe Asn 210 Arg Gly Glu Cys

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 Arg 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 Pro 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 Glu Glu Met 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 Ser Gly Gly Gly Ser Gly Gly Gly Asp Ile Gln Met Thr
 450 455 460
 Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
 465 470 475 480
 Ser Cys Arg Pro Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
 485 490 495
 Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
 500 505 510
 Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 515 520 525
 Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr
 530 535 540
 Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr Thr Phe Gly Gly Gly
 545 550 555 560
 Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Gln Val
 565 570 575
 Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val
 580 585 590
 Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Ile
 595 600 605
 Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asn
 610 615 620
 Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
 625 630 635 640
 Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr Met Gln
 645 650 655
 Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Arg
 660 665 670
 Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Thr
 675 680 685
 Leu Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu Val Ala Ala Leu
 690 695 700
 Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
 705 710 715 720

Glu Val Ala Ala Leu Glu Lys
725

<210> 107
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Fourth Polypeptide Chain of DART-D

<400> 107

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg
115 120 125

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
180 185 190

Thr Ala Tyr Met Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp
Page 69

210

215

220

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
 225 230 235 240

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
 245 250 255

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
 260 265

<210> 108

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> First Polypeptide Chain of DART-E

<400> 108

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala
 1 5 10 15

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

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

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

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

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

Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu 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 Arg 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 Pro 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 Glu Glu Met 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 Arg Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 109
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fifth Polypeptide Chain of DART-E

<400> 109

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu 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> 110
<211> 727
<212> PRT
<213> Artificial Sequence

<220>
<223> Third Polypeptide Chain of DART-E

<400> 110

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

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

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

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

Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu 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 Arg 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
 290 300
 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 Pro 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 Glu Glu Met 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 Ser Gly Gly Gly Ser Gly Gly Gly Asp Ile Gln Met Thr
 450 455 460
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 465 470 475 480
 Thr Cys Lys Ala Ser Gln Asp Ile Ser Asn Tyr Leu Ser Trp Phe Gln
 485 490 495

Gln Lys Pro Gly Lys Ala Pro Lys Thr Leu Ile Tyr Arg Ala Asn Arg
500 505 510

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
515 520 525

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
530 535 540

Tyr Tyr Cys Leu Gln His Asp Glu Phe Pro Trp Thr Phe Gly Gln Gly
545 550 555 560

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

Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val
580 585 590

Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met
595 600 605

Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp
610 615 620

Ile Asn Thr Asn Ile Gly Glu Pro Thr Tyr Thr Glu Glu Phe Lys Gly
625 630 635 640

Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu
645 650 655

Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
660 665 670

Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp Gly Gln Gly Thr Leu
675 680 685

Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu Val Ala Ala Leu
690 695 700

Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
705 710 715 720

Glu Val Ala Ala Leu Glu Lys
725

<210> 111
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Fourth Polypeptide Chain of DART-E

<400> 111

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Glu Glu Phe Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Ala Arg Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp
210 215 220

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
225 230 235 240

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
245 250 255

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu

260

265

<210> 112
 <211> 731
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Third Polypeptide Chain of DART-F

<400> 112

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

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

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

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

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

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

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

Thr Leu 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 Arg 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 Pro 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 Glu Glu Met 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 Ser Gly Gly Gly Ser Gly Gly Gly Asp Ile Gln Met Thr
 450 455 460
 Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
 465 470 475 480
 Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
 485 490 495

Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
500 505 510

Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
515 520 525

Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr
530 535 540

Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly
545 550 555 560

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

Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val
580 585 590

Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Ile
595 600 605

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asn
610 615 620

Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asp Gln Lys Phe Lys Asp
625 630 635 640

Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr Met Gln
645 650 655

Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Lys
660 665 670

Ser Gly Glu Tyr Gly Lys Ile Gly Tyr Tyr Ala Met Asp Tyr Trp Gly
675 680 685

Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu
690 695 700

Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala
705 710 715 720

Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
725 730

<210> 113
<211> 272
<212> PRT
<213> Artificial sequence

<220>
<223> Fourth Polypeptide Chain of DART-F

<400> 113

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg
115 120 125

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
180 185 190

Thr Ala Tyr Met Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val
195 200 205

Tyr Tyr Cys Thr Lys Ser Gly Glu Tyr Gly Lys Ile Gly Tyr Tyr Ala
210 215 220

Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly
225 230 235 240

Cys Gly Gly Gly Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu
245 250 255

Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
Page 80

260

265

270

<210> 114
 <211> 727
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Third Polypeptide Chain of DART-G

<400> 114

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

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

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

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

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

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

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

Thr Leu 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 Arg 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
 290 300
 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 Pro 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 Glu Glu Met 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 Ser Gly Gly Gly Ser Gly Gly Gly Asp Ile Gln Met Thr
 450 455 460
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 465 470 475 480
 Thr Cys Arg Pro Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
 485 490 495

Gln Lys Pro Asp₅₀₀ Lys Thr Val Lys Leu₅₀₅ Leu Ile Tyr Tyr Thr₅₁₀ Ser Arg

Leu Arg Ser₅₁₅ Gly Val Pro Ser Arg₅₂₀ Phe Ser Gly Ser Gly₅₂₅ Ser Gly Thr

Asp Phe₅₃₀ Thr Phe Thr Ile Ser₅₃₅ Ser Leu Gln Pro Glu₅₄₀ Asp Ile Ala Thr

Tyr₅₄₅ Phe Cys Gln Gln Gly₅₅₀ Asp Thr Leu Pro Tyr₅₅₅ Thr Phe Gly Gln Gly₅₆₀

Thr Lys Leu Glu Ile₅₆₅ Lys Gly Gly Gly Ser₅₇₀ Gly Gly Gly Gly Gln₅₇₅ Val

Gln Leu Val Gln₅₈₀ Ser Gly Ala Glu Val₅₈₅ Lys Lys Pro Gly Ala₅₉₀ Ser Val

Lys Val Ser₅₉₅ Cys Lys Ala Ser Gly₆₀₀ Tyr Thr Phe Thr Ser₆₀₅ Tyr Trp Ile

Asn Trp₆₁₀ Val Lys Gln Ala Pro₆₁₅ Gly Gln Gly Leu Glu₆₂₀ Trp Ile Gly Asn

Ile₆₂₅ Tyr Pro Ser Asp Ser₆₃₀ Tyr Thr Asn Tyr Asn₆₃₅ Gln Lys Phe Lys Asp₆₄₀

Lys Ala Thr Ile Thr₆₄₅ Ala Asp Lys Ser Thr₆₅₀ Ser Thr Ala Tyr Met₆₅₅ Glu

Leu Ser Ser₆₆₀ Leu Arg Ser Glu Asp Thr₆₆₅ Ala Val Tyr Tyr Cys₆₇₀ Thr Arg

Asp Tyr Gly₆₇₅ Ser Ser Tyr Ser Phe₆₈₀ Asp Tyr Trp Gly Gln₆₈₅ Gly Thr Thr

Val Thr₆₉₀ Val Ser Ser Gly Gly₆₉₅ Cys Gly Gly Gly Glu₇₀₀ Val Ala Ala Leu

Glu₇₀₅ Lys Glu Val Ala Ala₇₁₀ Leu Glu Lys Glu Val₇₁₅ Ala Ala Leu Glu Lys₇₂₀

Glu Val Ala Ala Leu₇₂₅ Glu Lys

<210> 115

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Third Polypeptide Chain of Optimized DART-G1

<400> 115

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

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

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

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

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

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

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

Thr Leu 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 Arg 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
Page 84

	260							265					270				
Pro	Glu	Val 275	Lys	Phe	Asn	Trp	Tyr 280	Val	Asp	Gly	Val	Glu 285	Val	His	Asn		
Ala	Lys 290	Thr	Lys	Pro	Arg	Glu 295	Glu	Gln	Tyr	Asn	Ser 300	Thr	Tyr	Arg	Val		
Val 305	Ser	Val	Leu	Thr	Val 310	Leu	His	Gln	Asp	Trp 315	Leu	Asn	Gly	Lys	Glu 320		
Tyr	Lys	Cys	Lys	Val 325	Ser	Asn	Lys	Ala	Leu 330	Pro	Ala	Pro	Ile	Glu 335	Lys		
Thr	Ile	Ser	Lys 340	Ala	Lys	Gly	Gln	Pro 345	Arg	Glu	Pro	Gln	Val 350	Tyr	Thr		
Leu	Pro	Pro 355	Ser	Arg	Glu	Glu	Met 360	Thr	Lys	Asn	Gln	Val 365	Ser	Leu	Trp		
Cys	Leu 370	Val	Lys	Gly	Phe	Tyr 375	Pro	Ser	Asp	Ile	Ala 380	Val	Glu	Trp	Glu		
Ser 385	Asn	Gly	Gln	Pro	Glu 390	Asn	Asn	Tyr	Lys	Thr 395	Thr	Pro	Pro	Val	Leu 400		
Asp	Ser	Asp	Gly	Ser 405	Phe	Phe	Leu	Tyr	Ser 410	Lys	Leu	Thr	Val	Asp 415	Lys		
Ser	Arg	Trp	Gln 420	Gln	Gly	Asn	Val	Phe 425	Ser	Cys	Ser	Val	Met 430	His	Glu		
Ala	Leu	His 435	Asn	His	Tyr	Thr	Gln 440	Lys	Ser	Leu	Ser	Leu 445	Ser	Pro	Gly		
Gly	Gly 450	Gly	Ser	Gly	Gly	Gly 455	Ser	Gly	Gly	Gly	Asp 460	Ile	Gln	Met	Thr		
Gln 465	Ser	Pro	Ser	Ser	Leu 470	Ser	Ala	Ser	Val	Gly 475	Asp	Arg	Val	Thr	Ile 480		
Thr	Cys	Arg	Pro	Ser 485	Gln	Asp	Ile	Ser	Asn 490	Tyr	Leu	Asn	Trp	Tyr 495	Gln		
Gln	Lys	Pro	Asp 500	Lys	Thr	Val	Lys	Leu 505	Leu	Ile	Tyr	Tyr	Thr 510	Ser	Arg		
Leu	Arg	Ser 515	Gly	Val	Pro	Ser	Arg 520	Phe	Ser	Gly	Ser	Gly 525	Ser	Gly	Thr		
Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr		

530

535

540

Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr Thr Phe Gly Gln Gly
545 550 555 560

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

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
580 585 590

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
595 600 605

Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
610 615 620

Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
625 630 635 640

Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
645 650 655

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
660 665 670

Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Phe His Pro Trp Gly Gln Gly
675 680 685

Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu Val Ala
690 695 700

Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu
705 710 715 720

Glu Lys Glu Val Ala Ala Leu Glu Lys
725

<210> 116

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Third Polypeptide Chain of Optimized DART-G2

<400> 116

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

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

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Asn Ile Gly Glu Pro Thr Tyr Thr Glu Glu Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu 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 Arg 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 Pro 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 Glu Glu Met 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 Ser Gly Gly Gly Ser Gly Gly Gly Asp Ile Gln Met Thr
 450 455 460
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 465 470 475 480
 Thr Cys Arg Pro Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
 485 490 495
 Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
 500 505 510
 Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 515 520 525
 Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
 530 535 540
 Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr Thr Phe Gly Gln Gly
 545 550 555 560
 Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Gln Val
 565 570 575

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 580 585 590
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 595 600 605
 Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 610 615 620
 Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
 625 630 635 640
 Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 645 650 655
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 660 665 670
 Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Met Ser Thr Trp Gly Gln Gly
 675 680 685
 Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu Val Ala
 690 695 700
 Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu
 705 710 715 720
 Glu Lys Glu Val Ala Ala Leu Glu Lys
 725

<210> 117
 <211> 729
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Third Polypeptide Chain of Optimized DART-G3
 <400> 117

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Asn Ile Gly Glu Pro Thr Tyr Thr Glu Glu Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 Page 89

65		70		75		80									
Met	Glu	Leu	Ser	Arg ₈₅	Leu	Arg	Ser	Asp	Asp ₉₀	Thr	Ala	Val	Tyr	Tyr ₉₅	Cys
Ala	Arg	Asp	Asp ₁₀₀	Gly	Tyr	Gly	Asn	Arg ₁₀₅	Val	Ser	Tyr	Trp	Gly ₁₁₀	Gln	Gly
Thr	Leu	Val ₁₁₅	Thr	Val	Ser	Ser	Ala ₁₂₀	Ser	Thr	Lys	Gly	Pro ₁₂₅	Ser	Val	Phe
Pro	Leu ₁₃₀	Ala	Pro	Ser	Ser	Lys ₁₃₅	Ser	Thr	Ser	Gly	Gly ₁₄₀	Thr	Ala	Ala	Leu
Gly ₁₄₅	Cys	Leu	Val	Lys	Asp ₁₅₀	Tyr	Phe	Pro	Glu	Pro ₁₅₅	Val	Thr	Val	Ser	Trp ₁₆₀
Asn	Ser	Gly	Ala	Leu ₁₆₅	Thr	Ser	Gly	Val	His ₁₇₀	Thr	Phe	Pro	Ala	Val ₁₇₅	Leu
Gln	Ser	Ser	Gly ₁₈₀	Leu	Tyr	Ser	Leu	Ser ₁₈₅	Ser	Val	Val	Thr	Val ₁₉₀	Pro	Ser
Ser	Ser	Leu ₁₉₅	Gly	Thr	Gln	Thr	Tyr ₂₀₀	Ile	Cys	Asn	Val	Asn ₂₀₅	His	Lys	Pro
Ser	Asn ₂₁₀	Thr	Lys	Val	Asp	Lys ₂₁₅	Arg	Val	Glu	Pro	Lys ₂₂₀	Ser	Cys	Asp	Lys
Thr ₂₂₅	His	Thr	Cys	Pro	Pro ₂₃₀	Cys	Pro	Ala	Pro	Glu ₂₃₅	Ala	Ala	Gly	Gly	Pro ₂₄₀
Ser	Val	Phe	Leu	Phe ₂₄₅	Pro	Pro	Lys	Pro	Lys ₂₅₀	Asp	Thr	Leu	Met	Ile ₂₅₅	Ser
Arg	Thr	Pro	Glu ₂₆₀	Val	Thr	Cys	Val	Val ₂₆₅	Val	Asp	Val	Ser	His ₂₇₀	Glu	Asp
Pro	Glu	Val ₂₇₅	Lys	Phe	Asn	Trp	Tyr ₂₈₀	Val	Asp	Gly	Val	Glu ₂₈₅	Val	His	Asn
Ala	Lys ₂₉₀	Thr	Lys	Pro	Arg	Glu ₂₉₅	Glu	Gln	Tyr	Asn	Ser ₃₀₀	Thr	Tyr	Arg	Val
Val ₃₀₅	Ser	Val	Leu	Thr	Val ₃₁₀	Leu	His	Gln	Asp	Trp ₃₁₅	Leu	Asn	Gly	Lys	Glu ₃₂₀
Tyr	Lys	Cys	Lys	Val ₃₂₅	Ser	Asn	Lys	Ala	Leu ₃₃₀	Pro	Ala	Pro	Ile	Glu ₃₃₅	Lys
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr

340	345	350
Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp	355	360
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu	370	375
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu	385	390
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys	405	410
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu	420	425
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly	435	440
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Asp Ile Gln Met Thr	450	455
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile	465	470
Thr Cys Arg Pro Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln	485	490
Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg	500	505
Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr	515	520
Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr	530	535
Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr Thr Phe Gly Gln Gly	545	550
Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Gln Val	565	570
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	580	585
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr	595	600
Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile		

610 615 620
 Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
 625 630 635 640
 Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 645 650 655
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 660 665 670
 Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Tyr Ser Leu Trp Gly Gln Gly
 675 680 685
 Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu Val Ala
 690 695 700
 Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu
 705 710 715 720
 Glu Lys Glu Val Ala Ala Leu Glu Lys
 725

<210> 118
 <211> 729
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Third Polypeptide Chain of Optimized DART-G4

<400> 118

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Asn Ile Gly Glu Pro Thr Tyr Thr Glu Glu Phe
 50 55 60
 Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu 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 Arg 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 Pro 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 Glu Glu Met 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 Ser Gly Gly Gly Ser Gly Gly Gly Asp Ile Gln Met Thr
 450 455 460
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 465 470 475 480
 Thr Cys Arg Pro Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
 485 490 495
 Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
 500 505 510
 Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 515 520 525
 Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
 530 535 540
 Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr Thr Phe Gly Gln Gly
 545 550 555 560
 Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Gln Val
 565 570 575
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 580 585 590
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 595 600 605
 Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 610 615 620
 Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
 625 630 635 640
 Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 645 650 655

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
660 665 670

Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Tyr Asn Val Trp Gly Gln Gly
675 680 685

Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu Val Ala
690 695 700

Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu
705 710 715 720

Glu Lys Glu Val Ala Ala Leu Glu Lys
725

<210> 119
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Fourth Polypeptide Chain of DART-G

<400> 119

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
Page 95

145 150 155 160
 Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
 165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
 225 230 235 240
 Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
 245 250 255
 Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
 260 265

<210> 120
 <211> 268
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fourth Polypeptide Chain of Optimized DART-G1

<400> 120

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Pro Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Arg Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Phe His Pro Trp
210 215 220

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
225 230 235 240

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
245 250 255

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
260 265

<210> 121
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Fourth Polypeptide Chain of Optimized DART-G2

<400> 121

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
Page 97

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Arg Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110
 Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140
 Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160
 Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
 165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Tyr Ser Leu Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
 225 230 235 240
 Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
 245 250 255
 Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
 260 265

<210> 123
 <211> 268
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fourth Polypeptide Chain of Optimized DART-G4
 Page 99

<400> 123

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Tyr Asn Val Trp
210 215 220

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
225 230 235 240

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
245 250 255

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
Page 100

260

265

<210> 124
 <211> 118
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(118)
 <223> VH Domain of Anti-Fluorescein Antibody 4-4-20

<400> 124

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

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

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

Ala Gln Ile Arg Asn Lys Pro Tyr Asn Tyr Glu Thr Tyr Tyr Ser Asp
 50 55 60

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

Val Tyr Leu Gln Met Asn Asn Leu Arg Val Glu Asp Met Gly Ile Tyr
 85 90 95

Tyr Cys Thr Gly Ser Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Ser Val Thr Val Ser Ser
 115

<210> 125
 <211> 112
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(112)
 <223> VL Domain of Anti-Fluorescein Antibody 4-4-20

<400> 125

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

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

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

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

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

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

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

<210> 126
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Palivizumab

<400> 126

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60

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

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 127
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of Palivizumab

<400> 127

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 Val Gly Tyr Met
20 25 30

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

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

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

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

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

<210> 128
<211> 118
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(118)
<223> VH Domain of EphA2 MAB-1

<400> 128

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Tyr
20 25 30

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

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

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

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

Arg Lys His Gly Asn Tyr Tyr Thr Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Ser Val Thr Val Ser Ser
 115

<210> 129
 <211> 106
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(106)
 <223> VL Domain of EphA2 MAB-1

<400> 129

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

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

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

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

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

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

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

<210> 130
 <211> 118
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(118)
 <223> VH Domain of EphA2 MAB-2

<400> 130

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

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

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

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

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

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

Thr Leu Thr Val Ser Ser
115

<210> 131
<211> 111
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> VL Domain of EphA2 MAB-2

<400> 131

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

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

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

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

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

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

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

<210> 132
 <211> 118
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(118)
 <223> VH Domain of EphA2 MAB-3

<400> 132

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

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

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

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

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

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

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

Leu Val Thr Val Ser Ser
 115

<210> 133
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> VL Domain of EphA2 MAB-3

<400> 133

Asp Ile Val Leu Thr Gln Ser His Arg Ser Met Ser Thr Ser Val Gly
 1 5 10 15

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 Page 106

35

40

45

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

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

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

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

<210> 134
 <211> 118
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(118)
 <223> VH Domain of 5T4 MAB-1

<400> 134

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

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

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

Gly Arg Ile Asp Pro Asn Arg Gly Gly Thr Glu Tyr Asn Glu Lys Ala
 50 55 60

Lys Ser Arg Val Thr Met 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 Gly Gly Asn Pro Tyr Tyr Pro Met Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser
 115

<210> 135
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> VL Domain of 5T4 MAB-1

<400> 135

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

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

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

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

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

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

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

<210> 136
 <211> 127
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(127)
 <223> VH Domain of 5T4 MAB-2

<400> 136

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

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

Trp Ile Thr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

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

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

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

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

Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120 125

<210> 137
<211> 112
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(112)
<223> VL Domain of 5T4 MAB-2

<400> 137

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

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

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

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

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

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

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

<210> 138
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Fc-Optimized Anti-Human B7-H3 Antibody Enoblituzumab

<400> 138

Glu Val Gln Leu Val 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 Phe
20 25 30

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

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

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

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

Gly Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp
100 105 110

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

<210> 139

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of Fc-Optimized Anti-Human B7-H3 Antibody Enoblituzumab

<400> 139

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

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

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

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

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

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

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

<210> 140

<211> 120
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(120)
<223> VH Domain of Anti-Human B7-H3 Antibody BRCA69D

<400> 140

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

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

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

Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr Gln Lys Phe
50 55 60

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

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

Ala Arg Arg Gly Ile Pro Arg Leu Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 141
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(107)
<223> VL Domain of Anti-Human B7-H3 Antibody BRCA69D

<400> 141

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

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

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

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

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

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

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

<210> 142
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Humanized Anti-Human B7-H3 Antibody BRCA69D
(hBRCA69D VH1)

<400> 142

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

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

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

Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr Gln Lys Phe
50 55 60

Lys 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 Arg Gly Ile Pro Arg Leu Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 143
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Humanized Anti-Human B7-H3 Antibody BRCA69D
(hBRCA69D VH2)

<400> 143

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 144

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of Humanized Anti-Human B7-H3 Antibody BRCA69D
(hBRCA69D VL1)

<400> 144

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

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Pro
85 90 95

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

<210> 145
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of Humanized Anti-Human B7-H3 Antibody BRCA69D
(hBRCA69D VL2)

<400> 145

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

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Pro
85 90 95

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

<210> 146
<211> 117
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(117)
<223> VH Domain of Anti-Human B7-H3 Antibody PRCA157

<400> 146

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

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

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

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

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

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

Ala Arg His Asp Gly Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 147
<211> 108
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(108)
<223> VL Domain of Anti-Human B7-H3 Antibody PRCA157

<400> 147

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

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

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

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

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

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

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

<210> 148
<211> 119
<212> PRT
<213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(119)
 <223> VH Domain of Anti-gpA33 Antibody gpA33 MAB-1

<400> 148

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Ser
 20 25 30
 Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Tyr Pro Gly Asp Gly Glu Thr Asn Tyr Asn Gly Lys Phe
 50 55 60
 Lys Asp 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 Ile Tyr Gly Asn Asn Val Tyr Phe Asp Val Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

<210> 149
 <211> 106
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(106)
 <223> VL Domain of Anti-gpA33 Antibody gpA33 MAB-1

<400> 149

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

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65 70 75 80

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

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

<210> 150
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Humanized Anti-CEACAM5/CEACAM6 Antibody 16C3
<400> 150

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

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

Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
35 40 45

Gly Leu Ile Ser Thr Tyr Ser Gly Asp Thr Lys Tyr Asn Gln Asn Phe
50 55 60

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 151
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of Humanized Anti-CEACAM5/CEACAM6 Antibody 16C3
<400> 151

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

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

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

Trp Gly Ala Ser Asn Leu Ala Asp Gly Met Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Gln Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

<210> 152
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of Humanized Anti-CEACAM5/CEACAM6 Antibody hMN15
<400> 152

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

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

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

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

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

Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr
85 90 95

Phe Cys Ala Arg Asp Met Gly Ile Arg Trp Asn Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Pro Val Thr Val Ser Ser
115 120

<210> 153

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

<220>
<223> VL Domain of Humanized Anti-CEACAM5/CEACAM6 Antibody hMN15

<400> 153

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

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

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

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

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

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

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

<210> 154
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of Murine Anti-CD137 Monoclonal Antibody (CD137 MAB-3 VH)

<400> 154

Ser Tyr Trp Ile Asn
1 5

<210> 155
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of Murine Anti-CD137 Monoclonal Antibody (CD137 MAB-3 VH)

<400> 155

Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
Page 119

1 5 10 15

Asp

<210> 156
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> CDRH3 of Murine Anti-CD137 Monoclonal Antibody (CD137 MAB-3 VH)
<400> 156

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

<210> 157
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRL1 of Murine Anti-CD137 Monoclonal Antibody (CD137 MAB-3 VL)
<400> 157

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

<210> 158
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of Murine Anti-CD137 Monoclonal Antibody (CD137 MAB-3 VL)
<400> 158

Tyr Thr Ser Arg Leu Arg Ser
1 5

<210> 159
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDRL3 of Murine Anti-CD137 Monoclonal Antibody (CD137 MAB-3 VL)
Page 120

<400> 159

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 160

<211> 6

<212> PRT

<213> Mus musculus

<220>

<221> 1MISC_FEATURE

<222> (1)..(6)

<223> Residues 103-108 of SEQ ID NO:74

<400> 160

Ser Tyr Ser Phe Asp Tyr
1 5

<210> 161

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 of hCD137 MAB-3 VH1A

<400> 161

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

<210> 162

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 of hCD137 MAB-3 VH1B

<400> 162

Asp Tyr Gly Ser Ala Tyr Ser Met Ser Thr
1 5 10

<210> 163

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 of hCD137 MAB-3 VH1C

<400> 163

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

<210> 164

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 of hCD137 MAB-3 VH1D

<400> 164

Asp Tyr Gly Ser Ser Tyr Ser Tyr Asn Val
1 5 10

<210> 165
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of CD137 MAB-4 VH

<400> 165

Ser Tyr Trp Ile Asn
1 5

<210> 166
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of CD137 MAB-4 VH

<400> 166

Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asp Gln Lys Phe Lys
1 5 10 15

Asp

<210> 167
<211> 14
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> CDRH3 of CD137 MAB-4 VH

<400> 167

Ser Gly Glu Tyr Gly Lys Ile Gly Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 168

<211> 11
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(11)
<223> CDRL1 of CD137 MAB-4 VL

<400> 168

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

<210> 169
<211> 7
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(7)
<223> CDRL2 of CD137 MAB-4 VL

<400> 169

Tyr Thr Ser Arg Leu His Ser
1 5

<210> 170
<211> 9
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(9)
<223> CDRL3 of CD137 MAB-4 VL

<400> 170

Gln Gln Gly Asn Thr Leu Pro Tyr Thr
1 5

<210> 171
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of CD137 MAB-5 VH

<400> 171

Ser Tyr Asp Ile Ser
1 5

<210> 172

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

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> CDRH2 of CD137 MAB-5 VH

<400> 172

Val Val Trp Thr Gly Gly Gly Thr Asn Tyr Asn Ser Ala Phe Met Ser
1 5 10 15

<210> 173

<400> 173
000

<210> 174
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> CDRL1 of CD137 MAB-5 VL

<400> 174

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 175
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of CD137 MAB-5 VL

<400> 175

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 176
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDRL3 of CD137 MAB-5 VL

<400> 176

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 177
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of Murine Anti-HER2/neu Monoclonal Antibody HER2 MAB-1 VH
<400> 177

Asn Tyr Gly Met Asn
1 5

<210> 178
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of Murine Anti-HER2/neu Monoclonal Antibody HER2 MAB-1 VH
<400> 178

Trp Ile Asn Thr Asn Ile Gly Glu Pro Thr Tyr Thr Glu Glu Phe Lys
1 5 10 15

Gly

<210> 179
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> CDRH3 of Murine Anti-HER2/neu Monoclonal Antibody HER2 MAB-1 VH
<400> 179

Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr
1 5 10

<210> 180
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)

<223> CDR1 of Murine Anti-HER2/neu Monoclonal Antibody HER2 MAB-1 VL

<400> 180

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

<210> 181

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> CDR2 of Murine Anti-HER2/neu Monoclonal Antibody HER2 MAB-1 VL

<400> 181

Arg Ala Asn Arg Leu Val Asp
1 5

<210> 182

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDR3 of Murine Anti-HER2/neu Monoclonal Antibody HER2 MAB-1 VL

<400> 182

Leu Gln His Asp Glu Phe Pro Trp Thr
1 5

<210> 183

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 of VH Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VH1)

<400> 183

Asp Asp Gly Tyr Gly Asn Arg Val Ser Tyr
1 5 10

<210> 184

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3 of VH Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VH2)

<400> 184

Asp Glu Gly Tyr Gly Asn Arg Val Ser Tyr
1 5 10

<210> 185
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 of VH Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VH3)

<400> 185

Asp Asp Ile Tyr Gly Asn Arg Val Ser Tyr
1 5 10

<210> 186
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1 of VL Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VL1)

<400> 186

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

<210> 187
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1 of VL Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VL2)

<400> 187

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

<210> 188
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1 of VL Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VL3)

<400> 188

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

<210> 189
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of VL Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VL1)

<400> 189

Arg Ala Asn Arg Leu Val Asp
1 5

<210> 190
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of VL Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VL2)

<400> 190

Arg Ala Asn Arg Leu Val Glu
1 5

<210> 191
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of VL Domain of Humanized Anti-Human HER2/neu Antibody
(hHER2 MAB-1 VL3)

<400> 191

Arg Ala Asn Arg Leu Gln Ser
1 5

<210> 192
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of TRIDENT-A

<400> 192

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
Page 128

65					70					75				80
Glu	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asp	Thr	Leu	Pro
				85					90				95	Tyr
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Ser
			100					105					110	Gly
Gly	Gly	Gly	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys
			115				120					125		Lys
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr
	130					135					140			Phe
Thr	Ser	Tyr	Trp	Ile	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly
145					150					155				Leu
Glu	Trp	Ile	Gly	Asn	Ile	Tyr	Pro	Ser	Asp	Ser	Tyr	Thr	Asn	Tyr
				165					170					175
Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr
			180					185					190	Ser
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala
		195					200					205		Val
Tyr	Tyr	Cys	Thr	Arg	Asp	Tyr	Gly	Ser	Ser	Tyr	Ser	Phe	Asp	Tyr
	210					215					220			Trp
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
225					230					235				Glu
Val	Ala	Ala	Cys	Glu	Lys	Glu	Val	Ala	Ala	Leu	Glu	Lys	Glu	Val
				245					250					255
Ala	Leu	Glu	Lys	Glu	Val	Ala	Ala	Leu	Glu	Lys	Gly	Gly	Gly	Asp
			260					265					270	Lys
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly
		275					280					285		Pro
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
	290					295					300			Ser
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
305					310					315				320
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
				325					330					335
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
														Val

340 345 350
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp
 405 410 415
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 435 440 445
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495

Lys

<210> 193
 <211> 497
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> First Polypeptide Chain of TRIDENT-A1

<400> 193

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110
 Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140
 Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160
 Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
 165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Phe His Pro Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Glu
 225 230 235 240
 Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala
 245 250 255
 Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asp Lys
 260 265 270
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 275 280 285
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385 390 395 400

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp
405 410 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
420 425 430

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495

Lys

<210> 194
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of TRIDENT-A2
<400> 194

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
Page 132

50

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Met Ser Thr Trp
210 215 220

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Glu
225 230 235 240

Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala
245 250 255

Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asp Lys
260 265 270

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
290 295 300

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
Page 133

Tyr Tyr Thr Ser Arg Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110
 Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140
 Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160
 Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
 165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Tyr Ser Leu Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Glu
 225 230 235 240
 Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala
 245 250 255
 Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asp Lys
 260 265 270
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 275 280 285
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
325 330 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385 390 395 400

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp
405 410 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
420 425 430

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495

Lys

<210> 196
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of TRIDENT-A4

<400> 196

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
Page 136

35

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45

Tyr Tyr Thr Ser Arg Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110
 Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140
 Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160
 Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
 165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Tyr Asn Val Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Glu
 225 230 235 240
 Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala
 245 250 255
 Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Gly Gly Gly Asp Lys
 260 265 270
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 275 280 285
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 Page 137

305 310 315 320
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp
 405 410 415
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 420 425 430
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 435 440 445
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495
 Lys

<210> 197
 <211> 267
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Second Polypeptide Chain of TRIDENT-A

<400> 197

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Pro Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Arg Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110
 Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140
 Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160
 Glu Trp Ile Gly Asn Ile Tyr Pro Ser Asp Ser Tyr Thr Asn Tyr Asn
 165 170 175
 Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Phe Asp Tyr Trp
 210 215 220
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Lys
 225 230 235 240
 Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala
 245 250 255
 Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
 260 265

<210> 198
 <211> 267
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Second Polypeptide Chain of TRIDENT-A1
 Page 139

<400> 198

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Phe His Pro Trp
210 215 220

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Lys
225 230 235 240

Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala
245 250 255

Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
Page 140

260

265

<210> 199
 <211> 267
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Second Polypeptide Chain of TRIDENT-A2

<400> 199

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
 100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
 180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Met Ser Thr Trp
 210 215 220

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Lys
225 230 235 240

Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala
245 250 255

Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
260 265

<210> 200
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> Second Polypeptide Chain of TRIDENT-A3

<400> 200

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
Page 142

180							185						190					
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val			
		195					200					205						
Tyr	Tyr	Cys	Thr	Arg	Asp	Tyr	Gly	Ser	Ala	Tyr	Ser	Tyr	Ser	Leu	Trp			
	210					215						220						
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Lys			
225					230					235					240			
Val	Ala	Ala	Cys	Lys	Glu	Lys	Val	Ala	Ala	Leu	Lys	Glu	Lys	Val	Ala			
				245					250					255				
Ala	Leu	Lys	Glu	Lys	Val	Ala	Ala	Leu	Lys	Glu								
			260					265										

Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15	Gly
Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Pro 25	Ser	Gln	Asp	Ile	Ser 30	Asn	Tyr
Leu	Asn	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Asp	Lys	Thr	Val	Lys 45	Leu	Leu	Ile
Tyr	Tyr 50	Thr	Ser	Arg	Leu	Arg 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly
Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser	Leu	Gln	Pro 80
Glu	Asp	Ile	Ala	Thr 85	Tyr	Phe	Cys	Gln	Gln 90	Gly	Asp	Thr	Leu	Pro 95	Tyr
Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Leu	Glu 105	Ile	Lys	Gly	Gly	Gly 110	Ser	Gly
Gly	Gly	Gly 115	Gln	Val	Gln	Leu	Val 120	Gln	Ser	Gly	Ala	Glu 125	Val	Lys	Lys
Pro	Gly 130	Ala	Ser	Val	Lys	Val 135	Ser	Cys	Lys	Ala	Ser 140	Gly	Tyr	Thr	Phe

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ser Tyr Ser Tyr Asn Val Trp
210 215 220

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Lys
225 230 235 240

Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala
245 250 255

Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
260 265

<210> 202
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of hPRCA157 VH1

<400> 202

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys 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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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 His Asp Gly Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr
Page 144

100

105

110

Val Thr Val Ser Ser
115

<210> 203
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of hPRCA157 VL1
<400> 203

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

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

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

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

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

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

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

<210> 204
<211> 120
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(120)
<223> VH Domain of CD19 MAB-1

<400> 204

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ala
50 55 60

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

Phe Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Met Glu Leu Trp Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 205
<211> 106
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(106)
<223> VL Domain of CD19 MAB-1

<400> 205

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

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

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

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

Gly Ser Gly Thr Asp His Thr Leu Thr Ile Ser Ser Leu Glu Ala Glu
65 70 75 80

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

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

<210> 206
<211> 120
<212> PRT
<213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(120)
 <223> VH Domain of CD123 MAB-1

<400> 206

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 207
 <211> 113
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(113)
 <223> VL Domain of CD123 MAB-1

<400> 207

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

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

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

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

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

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

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

Lys

<210> 208
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain oif of hCD137 MAB-3 VH1E

<400> 208

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

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

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

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

Lys Asp Lys Ala 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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 209
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain oif of hCD137 MAB-3 VH1F

<400> 209

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

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

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

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

Lys Asp Lys Ala 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

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

Thr Thr Val Thr Val Ser Ser
115

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

<220>
<223> VH Domain oif of hCD137 MAB-3 VH1G

<400> 210

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

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

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

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

Lys Asp Lys Ala 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

Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Met Ser Thr Trp Gly Gln Gly
Page 149

100

105

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Thr Thr Val Thr Val Ser Ser
115

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

<220>
<223> VL Domain oif of hCD137 MAB-3 VL4
<400> 211

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

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

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

<220>
<223> VL Domain oif of hCD137 MAB-3 VL5
<400> 212

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

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

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

Tyr Tyr Thr Ser Arg Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
Page 150

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

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

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

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

<220>
 <223> VL Domain oif of hCD137 MAB-3 VL6

<400> 213

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45

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

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

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

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

<210> 214
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL Domain oif of hCD137 MAB-3 VL7

<400> 214

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

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
 Page 151

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

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

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

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

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

<210> 215

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain oif of hCD137 MAB-3 VL8

<400> 215

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

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

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

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

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

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

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

<210> 216

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain oif of hCD137 MAB-3 VL9

<400> 216

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 217

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain oif of hCD137 MAB-3 VL10

<400> 217

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 218
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL Domain oif of hCD137 MAB-3 VL11

<400> 218

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
 35 40 45

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

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

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

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

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

<220>
 <223> VL Domain oif of hCD137 MAB-3 VL12

<400> 219

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

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

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

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

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

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

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

<210> 220
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain oif of hCD137 MAB-3 VL13

<400> 220

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

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

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

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

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

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

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

<210> 221
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain oif of hCD137 MAB-3 VL14

<400> 221

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 222
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain oif of hCD137 MAB-3 VL15

<400> 222

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

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

<210> 223
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1 of hCD137 MAB-3 VL4, hCD137 MAB-3 VL7, hCD137 MAB-3 VL8,
hCD137 MAB-3 VL9, hCD137 MAB-3 VL14 and hCD137 MAB-3 VL15

<400> 223

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

<210> 224
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of hCD137 MAB-3 VL6, hCD137 MAB-3 VL8 and hCD137 MAB-3 VL9
<400> 224

Tyr Thr Ser Arg Ala Arg Ser
1 5

<210> 225
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of hCD137 MAB-3 VL10 and hCD137 MAB-3 VL12
<400> 225

Tyr Thr Thr Arg Leu Arg Ser
1 5

<210> 226
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of hCD137 MAB-3 VL11 and hCD137 MAB-3 VL13
<400> 226

Tyr Thr Gly Arg Leu Arg Ser
1 5

<210> 227
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of hCD137 MAB-3 VL14
<400> 227

Tyr Thr Thr Arg Ala Arg Ser
1 5

<210> 228
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of hCD137 MAB-3 VL15
<400> 228

Tyr Thr Gly Arg Ala Arg Ser
1 5

<210> 229
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of TRIDENT-A5

<400> 229

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Met Ser Thr Trp
210 215 220

Gly 225 Gln Gly Thr Thr Val 230 Thr Val Ser Ser Ala 235 Ser Thr Lys Gly Glu 240
 Val Ala Ala Cys Glu 245 Lys Glu Val Ala Ala 250 Leu Glu Lys Glu Val 255 Ala
 Ala Leu Glu Lys 260 Glu Val Ala Ala Leu 265 Glu Lys Gly Gly Gly 270 Asp Lys
 Thr His Thr 275 Cys Pro Pro Cys Pro 280 Ala Pro Glu Ala Ala 285 Gly Gly Pro
 Ser Val 290 Phe Leu Phe Pro Pro 295 Lys Pro Lys Asp Thr 300 Leu Met Ile Ser
 Arg Thr Pro Glu Val Thr 310 Cys Val Val Val Asp 315 Val Ser His Glu Asp 320
 Pro Glu Val Lys Phe 325 Asn Trp Tyr Val Asp 330 Gly Val Glu Val His 335 Asn
 Ala Lys Thr Lys 340 Pro Arg Glu Glu Gln 345 Tyr Asn Ser Thr Tyr 350 Arg Val
 Val Ser Val 355 Leu Thr Val Leu His 360 Gln Asp Trp Leu Asn 365 Gly Lys Glu
 Tyr Lys 370 Cys Lys Val Ser Asn 375 Lys Ala Leu Pro Ala 380 Pro Ile Glu Lys
 Thr 385 Ile Ser Lys Ala Lys 390 Gly Gln Pro Arg Glu 395 Pro Gln Val Tyr Thr 400
 Leu Pro Pro Ser Arg 405 Glu Glu Met Thr Lys 410 Asn Gln Val Ser Leu 415 Trp
 Cys Leu Val Lys 420 Gly Phe Tyr Pro Ser 425 Asp Ile Ala Val Glu 430 Trp Glu
 Ser Asn Gly 435 Gln Pro Glu Asn Asn 440 Tyr Lys Thr Thr Pro 445 Pro Val Leu
 Asp Ser 450 Asp Gly Ser Phe Phe 455 Leu Tyr Ser Lys Leu 460 Thr Val Asp Lys
 Ser Arg Trp Gln Gln Gly 470 Asn Val Phe Ser Cys 475 Ser Val Met His Glu 480
 Ala Leu His Asn His 485 Tyr Thr Gln Lys Ser 490 Leu Ser Leu Ser Pro 495 Gly

Lys

<210> 230
<211> 267
<212> PRT
<213> Artificial Sequence

<220>
<223> Second Polypeptide Chain of TRIDENT-A5
<400> 230

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Thr Val Lys Leu Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
115 120 125

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
130 135 140

Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
145 150 155 160

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

Gln Lys Phe Lys Asp Lys Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser
180 185 190

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Thr Arg Asp Tyr Gly Ser Ala Tyr Ser Met Ser Thr Trp
210 215 220

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Lys
225 230 235 240

Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala
245 250 255

Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
260 265

<210> 231
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Third Polypeptide Chain of TRIDENT-B

<400> 231

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

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

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

Gly Arg Ile Asp Pro Asn Arg Gly Gly Thr Glu Tyr Asn Glu Lys Ala
50 55 60

Lys Ser Arg Val Thr Met 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 Gly Gly Asn Pro Tyr Tyr Pro Met 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 Arg 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 Pro 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 Glu Glu Met 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 Arg Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 232
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fourth Polypeptide Chain of TRIDENT-B

<400> 232

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu 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