

SEQUENCE LISTING

<110> MacroGenic, Inc.
 Shah, Kalpana
 Smith, Douglas
 La Motte-Mohs, Ross
 Johnson, Leslie
 Moore, Paul
 Bonvini, Ezio
 Koenig, Scott

<120> PD-1-Binding Molecules and Methods of Use Thereof

<130> 1301.0122PCT

<150> US 62/198,867
 <151> 2015-07-30

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<150> US 62/255,140
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 <151> 2016-04-15

<160> 298

<170> PatentIn version 3.5

<210> 1
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 <213> Homo sapiens

<220>
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 <222> (1)..(217)
 <223> Human IgG1 CH2-CH3 Domain

<220>
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 <222> (217)..(217)
 <223> Xaa is a lysine (K) or is absent

<400> 1

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
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> 2
 <211> 216
 <212> PRT
 <213> Homo sapiens

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

<220>
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 <222> (216)..(216)
 <223> Xaa is a lysine (K) or is absent

<400> 2

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> 3
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(217)
 <223> Human IgG3 CH2-CH3 Domain

<220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa is a lysine (K) or is absent

<400> 3

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

<210> 4
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<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
 <222> (1)..(217)
 <223> Human IgG4 CH2-CH3 Domain

 <220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa is a lysine (K) or is absent

<400> 4

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> 5

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IgG1 CH2-CH3 Domain Having L234A/L235A Substitutions

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> Xaa is a lysine (K) or is absent

<400> 5

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> 6

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> "Knob-Bearing" Human IgG1 CH2-CH3 Domain

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> Xaa is a lysine (K) or is absent

<400> 6

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

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

210

215

<210> 7

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> "Hole-Bearing" Human IgG1 CH2-CH3 Domain

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> Xaa is a lysine (K) or is absent

<400> 7

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> 8
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(107)
 <223> Human IgG CL Kappa Domain

<400> 8

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

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

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

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

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

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

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

<210> 9
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(104)
<223> Human IgG CL Lambda Domain

<400> 9

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
100

<210> 10
 <211> 98
 <212> PRT
 <213> Homo sapiens

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

<400> 10

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> 11
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(12)
 <223> Human IgG2 Hinge Region

<400> 11

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

<210> 12

<211> 12

<212> PRT

<213> Homo sapiens

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<221> MISC_FEATURE

<222> (1)..(12)

<223> Human IgG4 Hinge Region

<400> 12

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
1 5 10

<210> 13

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Stabilized IgG4 Hinge Region

<400> 13

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 14

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker 1

<400> 14

Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-containing Linker 2

<400> 15

Gly Gly Cys Gly Gly Gly
1 5

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

<220>
<223> Heterodimer-Promoting Domain

<400> 16

Gly Val Glu Pro Lys Ser Cys
1 5

<210> 17
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting Domain

<400> 17

Val Glu Pro Lys Ser Cys
1 5

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

<220>
<223> Heterodimer-Promoting Domain

<400> 18

Ala Glu Pro Lys Ser Cys
1 5

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting Domain

<400> 19

Gly Phe Asn Arg Gly Glu Cys
1 5

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting Domain

<400> 20

Phe Asn Arg Gly Glu Cys
1 5

<210> 21
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting (E-coil) Domain

<400> 21

Glu Val Ala Ala Leu 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> 22
<211> 28

<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting "K-coil" Domain

<400> 22

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> 23
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing Heterodimer-Promoting "E-coil" Domain

<400> 23

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> 24
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing Heterodimer-Promoting "K-coil" Domain

<400> 24

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> 25
 <211> 46
 <212> PRT
 <213> Streptococcus dysgalactiae

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

<400> 25

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> 26
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant deimmunized Albumin Binding Domain

<400> 26

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> 27
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant Deimmunized Albumin Binding Domain

<400> 27

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> 28

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant deimmunized Albumin Binding Domain

<400> 28

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> 29

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Alternative Linker 2

<400> 29

Gly Gly Gly Ser
1

<210> 30
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Alternative Linker 2

<400> 30

Ala Ser Thr Lys Gly
1 5

<210> 31
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 31

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

<210> 32
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 32

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

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

<220>
<223> Alternative Linker 2

<400> 33

Leu Glu Pro Lys Ser Ser
1 5

<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Alternative Linker 2

<400> 34

Ala Pro Ser Ser Ser
1 5

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 35

Ala Pro Ser Ser Ser Pro Met Glu
1 5

<210> 36

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 36

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

<210> 37

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 37

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

<210> 38

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(525)

<223> Human LAG-3 (Signaling Sequence and Mature Protein)

<220>

<221> MISC_FEATURE

<222> (1)..(28)

<223> Signaling Sequence

<220>

<221> MISC_FEATURE

<222> (29)..(525)

<223> Mature Protein

<400> 38

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

Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
20 25 30

Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
35 40 45

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

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

Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
85 90 95

Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
100 105 110

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

Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
130 135 140

Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145 150 155 160

Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
165 170 175

Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
180 185 190

Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
195 200 205

Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
210 215 220

Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225 230 235 240

Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
245 250 255

Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
260 265 270

Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
275 280 285

Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
290 295 300

Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305 310 315 320

Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
325 330 335

Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
340 345 350

Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
355 360 365

Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
370 375 380

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

Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
405 410 415

Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
420 425 430

Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
435 440 445

His Leu Leu Leu Phe Leu Ile Leu Gly Val Leu Ser Leu Leu Leu Leu
450 455 460

Val Thr Gly Ala Phe Gly Phe His Leu Trp Arg Arg Gln Trp Arg Pro
465 470 475 480

Arg Arg Phe Ser Ala Leu Glu Gln Gly Ile His Pro Pro Gln Ala Gln
485 490 495

Ser Lys Ile Glu Glu Leu Glu Gln Glu Pro Glu Pro Glu Pro Glu Pro
500 505 510

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gln Leu
515 520 525

<210> 39
<211> 120
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(120)
<223> Heavy Chain Variable Domain of LAG-3 mAb A

<400> 39

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 Asp Tyr
20 25 30

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

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

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

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

Phe Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 40
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> Light Chain Variable Domain of LAG-3 mAb A

<400> 40

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 Ile 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 Leu
 85 90 95

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

<210> 41
 <211> 120
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)

<223> Heavy Chain Variable Domain of LAG-3 mAb 1

<400> 41

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 Tyr Thr Phe Arg Asn Tyr
20 25 30

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

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Ser Thr Tyr Ala Asp Asp Phe
50 55 60

Glu Gly Arg Phe Ala Phe Ser Leu Gly Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 42

<211> 6

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(6)

<223> CDRH1 of LAG-3 mAb 1

<400> 42

Arg Asn Tyr Gly Met Asn
1 5

<210> 43
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of LAG-3 mAb 1

<400> 43

Trp Ile Asn Thr Tyr Thr Gly Glu Ser Thr Tyr Ala Asp Asp Phe Glu
1 5 10 15

Gly

<210> 44
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRH3 of LAG-3 mAb 1

<400> 44

Glu Ser Leu Tyr Asp Tyr Tyr Ser Met Asp Tyr
1 5 10

<210> 45
<211> 112
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(112)
<223> VL Domain of LAG-3 mAb 1

<400> 45

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

Asp Arg Phe Thr 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 Trp Gln Gly
85 90 95

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

<210> 46
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> CDRL1 of LAG-3 mAb 1

<400> 46

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

<210> 47
<211> 7
<212> PRT
<213> Mus musculus

<220>

<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of LAG-3 mAb 1

<400> 47

Leu Val Ser Glu Leu Asp Ser
1 5

<210> 48
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDRL3 of LAG-3 mAb 1

<400> 48

Trp Gln Gly Thr His Phe Pro Tyr Thr
1 5

<210> 49
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of hLAG-3 mAb 1 VH1

<400> 49

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 Tyr Thr Gly Glu Ser Thr Tyr Ala Asp Asp Phe
50 55 60

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 50

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> VH Domain of hLAG-3 mAb 1 VH2

<400> 50

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 Tyr Thr Gly Glu Ser Thr Tyr Ala Asp Asp Phe
50 55 60

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

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

Ala Arg Glu Ser Leu Tyr Asp Tyr Tyr Ser Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 51

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> VH Domain of hLAG-3 mAb 1 VL1

<400> 51

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

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

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

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

<210> 52

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of hLAG-3 mAb 1 VL2

<400> 52

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

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

<210> 53

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of hLAG-3 mAb 1 VL3

<400> 53

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

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

<210> 54

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of hLAG-3 mAb 1 VL4

<400> 54

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

Thr His Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

110

<210> 55
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRL1 of the VL Domain of hLAG-3 mAb 1 VL4

<400> 55

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Ala Lys Thr Tyr Leu Asn
 1 5 10 15

<210> 56
 <211> 118
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(118)
 <223> VH Domain of LAG-3 mAb 6

<400> 56

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

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

Asn Met Asp Trp Val Lys Gln Ser His Gly Glu Ser Leu Glu Trp Ile
 35 40 45

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

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

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

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

Thr Leu Thr Val Ser Ser
115

<210> 57
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of LAG-3 mAb 6

<400> 57

Asp Tyr Asn Met Asp
1 5

<210> 58
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of LAG-3 mAb 6

<400> 58

Asp Ile Asn Pro Asp Asn Gly Val Thr Ile Tyr Asn Gln Lys Phe Glu
1 5 10 15

Gly

<210> 59
<211> 9
<212> PRT
<213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(9)
 <223> CDRH3 of LAG-3 mAb 6

<400> 59

Glu Ala Asp Tyr Phe Tyr Phe Asp Tyr
 1 5

<210> 60
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> VL Domain of LAG-3 mAb 6

<400> 60

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

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

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

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

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

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

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

<210> 61
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRL1 of LAG-3 mAb 6

<400> 61

Lys Ala Ser Gln Asp Val Ser Ser Val Val Ala
1 5 10

<210> 62
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of LAG-3 mAb 6

<400> 62

Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 63
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL3 of LAG-3 mAb 6

<400> 63

His Tyr Ser Thr Pro Trp Thr
1 5

<210> 64
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(113)
 <223> Heavy Chain Variable Domain of PD-1 mAb A

<400> 64

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

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

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

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

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

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

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

Ser

<210> 65
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> Light Chain Variable Domain of PD-1 mAb A

<400> 65

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 Ser Ser Asn Trp Pro Arg
 85 90 95

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

<210> 66
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(120)
 <223> Heavy Chain Variable Domain of PD-1 mAb B

<400> 66

Gln Val Gln Leu Val Gln Ser Gly Val 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

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 67
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(111)
 <223> Light Chain Variable Domain of PD-1 mAb B

<400> 67

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 Lys Gly Val Ser Thr Ser
 20 25 30

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

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

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

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

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

<210> 68
<211> 288
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(288)
<223> Human PD-1 Polypeptide (NCI Sequence NP 005009.2)

<220>
<221> MISC_FEATURE
<222> (1)..(20)
<223> Human PD-1 Signal Sequence

<400> 68

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1 5 10 15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20 25 30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50 55 60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala

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

275

280

285

<210> 69
 <211> 121
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(121)
 <223> VH Domain of PD-1 mAb 1

<400> 69

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

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

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

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

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

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

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

Gln Gly Thr Ser Val Thr Val Ser Ser
 115 120

<210> 70
 <211> 373
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(373)
 <223> Polynucleotide Encoding VH Domain of PD-1 mAb 1

<400> 70
 cagatccagt gatgtgcagc ttcaggagtc gggacctggc cgggtgaaac cttctcagtc 60
 tctgtccctc acctgcactg tcactggctt ctcaatcacc aatgattatg cctggaactg 120
 gatccgacag tttccaggaa acaaactgga gtggatgggc cacataacct acagtggcag 180
 cactagctac aacccatctc tcaaaagtcg aatctctatc actcgggaca catccaagaa 240
 ccacttcttc ctgcagttga gttctgtgac tcctgaggac acagccacat attactgtgc 300
 aagagattac ggtagtggct acccctatac tttggactac tgggggtcaag gtacctcagt 360
 caccgtctcc tcc 373

<210> 71
 <211> 6
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(6)

<400> 71

Asn Asp Tyr Ala Trp Asn
 1 5

<210> 72
 <211> 16
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(16)
 <223> CDRH2 of PD-1 mAb 1

<400> 72

His Ile Thr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys Ser
 1 5 10 15

<210> 73
 <211> 12
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(12)
 <223> CDRH3 of PD-1 mAb 1

<400> 73

Asp Tyr Gly Ser Gly Tyr Pro Tyr Thr Leu Asp Tyr
 1 5 10

<210> 74
 <211> 106
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(106)
 <223> VL Domain of PD-1 mAb 1

<400> 74

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

Glu Lys Val Thr Met Thr Cys Ser Ala Thr Ser Ile Val Ser Tyr Val
 20 25 30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
 65 70 75 80

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

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

<210> 75
<211> 318
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(318)
<223> Polynucleotide Encoding VL Domain of PD-1 mAb 1

<400> 75
caaattgttc tcacccagtc tccagcactc atgtctgcat ctccagggga gaaggtcacc 60
atgacctgca gtgccacctc aattgtaagt tacgtttact ggtaccagca gaagcctgga 120
tcctcccccc aaccctggat ttatctcaca tccaacctgg cttctggagt ccctgctcgc 180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagcat ggaggctgaa 240
gatgctgcca cttattactg ccagcagtgg agtgataacc cgtacacgtt cggagggggg 300
accaagctgg aaataaaa 318

<210> 76
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> CDRL1 of PD-1 mAb 1

<400> 76

Ser Ala Thr Ser Ile Val Ser Tyr Val Tyr
1 5 10

<210> 77
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of PD-1 mAb 1

<400> 77

Leu Thr Ser Asn Leu Ala Ser
1 5

<210> 78
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDRL3 of PD-1 mAb 1

<400> 78

Gln Gln Trp Ser Asp Asn Pro Tyr Thr
1 5

<210> 79
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of hPD-1 mAb 1 VH1

<400> 79

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

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

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

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

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

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 80
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hPD-1 mAb 1 VH1

<400> 80
gacgtacagc tccaggaaag tggcccaggt ctggtgaagc catcccagac actgagcctg 60
acttgaccg tgagtggctt ctccatctca aatgactacg cctggaattg gattaggcag 120
cctcccggta aagggctgga gtggatcggc cacatcacat acagcggctc cacatcatat 180
aatcccagtc tgaagagccg tcttaccatt actcgcgaca ctagtaagaa ccagtttgtt 240
ctgacatga ccaacatgga ccctgtggat actgcaacat actattgtgc tcgagattat 300
ggttctggtt acccttatac actcgactac tggggacagg gaaccactgt gaccgtgagc 360
tcc 363

<210> 81
<211> 106
<212> PRT
<213> Artificial Sequence

<220>

<223> VL Domain of hPD-1 mAb 1 VL1

<400> 81

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

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

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

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

Gly Ser Gly Thr Asp 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 Asp Asn Pro Tyr Thr
85 90 95

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

<210> 82

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide Encoding hPD-1 mAb 1 VL1

<400> 82

gaaatcggtc tgaccagag ccagcaacc ctgtctgtct ccccgagaga aaaggtcacc 60

attacttgct ctgtacttc tatcgtgtcc tacgtgtact ggtatcagca gaagcccggc 120

caggctcccc agccattgat atatctgacc agcaacctgg cttctggtat ccagctcgt 180

ttttccggta gcgggtccgg gactgatttc actttgacta tcagctctct ggaggcagaa 240

gacgccgcca cctattattg tcaacagtgg tcagacaatc catacacttt tggcgggtggc 300

accaaagtcg aaataaag

318

<210> 83
<211> 116
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(116)
<223> VH Domain of PD-1 mAb 2

<400> 83

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

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

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

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

Lys Gly Arg Phe Thr Val Thr Arg Asp Asn Ala Lys Asn Thr Leu Phe
65 70 75 80

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

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

Thr Val Ser Ser
115

<210> 84
<211> 348
<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(348)

<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 2

<400> 84

gatgtgcagc tcgtggagtc tgggggaggc ttagtgcagc ctggagggtc cgggaaactc 60

tcctgtgcag cctctggatt cgttttcagt agctttggaa tgcactgggt tcgtcaggct 120

ccagagaagg ggctggagtg ggtcgcatat atcagtagtg gcagtatgag catttcctat 180

gcagacacag tgaagggccg attcaccgtc accagagaca atgccaagaa caccctgttc 240

ctgcaaataa ccagtctaag gtctgaggac acggccattt attactgtgc atccctgagt 300

gactactttg actactgggg ccaaggcacc actctcacag tctcctcc 348

<210> 85

<211> 5

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<223> CDRH1 of PD-1 mAb 2

<400> 85

Ser Phe Gly Met His

1 5

<210> 86

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDRH2 of PD-1 mAb 2

<400> 86

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

Gly

<210> 87
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> CDRH3 of PD-1 mAb 2

<400> 87

Leu Ser Asp Tyr Phe Asp Tyr
 1 5

<210> 88
 <211> 112
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(112)
 <223> VL Domain of PD-1 mAb 2

<400> 88

Asp Val Val Met Ser 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

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

Pro Lys Leu Leu Ile Tyr Arg 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 Phe Phe Cys Ser Gln Thr
85 90 95

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

<210> 89
<211> 336
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(336)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 2

<400> 89
gatgttgatga tgtcccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gagccttggt cacagtactg gaaacaccta tttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatct acagggtttc taaccgattt 180
tctgggggtcc ccgacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agtagagtgg aggctgagga tctgggagtt tttttctgct ctcaaactac acatgttccg 300
tggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 90
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> CDRL1 of PD-1 mAb 2

<400> 90

Arg Ser Ser Gln Ser Leu Val His Ser Thr Gly Asn Thr Tyr Leu His
 1 5 10 15

<210> 91
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> CDRL2 of PD-1 mAb 2

<400> 91

Arg Val Ser Asn Arg Phe Ser
 1 5

<210> 92
 <211> 9
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(9)
 <223> CDRL3 of PD-1 mAb 2

<400> 92

Ser Gln Thr Thr His Val Pro Trp Thr
 1 5

<210> 93
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH Domain of hPD-1 mAb 2 VH1

<400> 93

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

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

Thr Val Ser Ser
115

<210> 94
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hPD-1 mAb 2 VH1

<400> 94
gaagtgcaat tggttgagag tgggtggtggc ctggtgcagc caggtggaag tctgcggttg 60
tcctgtgcag caagcggatt tgtgttcagc tcttttggga tgcattgggt gcgccaggct 120
cccggaagg gtctcgagtg ggtagcatac atctccagcg ggtccatgtc tattagttat 180
gccgacacag tgaaaggcag gtttactatc tcccgtgaca atgcaaaaaa cacactgtac 240
ctgcaaata atagcctgcg caccgaggac accgccttgt actactgcgc ttccctgtct 300
gattacttcg actactgggg tcagggcaca actgtgacag tttcttcc 348

<210> 95
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of hPD-1 mAb 2 VL1

<400> 95

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

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

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

Pro Gln Leu Leu Ile Tyr Arg 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 Val Gly Val Tyr Tyr Cys Ser Gln Thr
85 90 95

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

<210> 96
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hPD-1 mAb 2 VL1

<400> 96

gacgttgatga tgacacagtc accactgagt ctgccagtta ccctggggcca gccagccagt 60
atttcttgatc ggagttcaca gagtctggta cattccacag gaaatacata tctccattgg 120
tacctgcaaa aaccagggca gagccccag ctgctgattt atagagtgtc taatcgattt 180
tctggcgtgc cagatcgggt cagcggcagc gggctctggca ctgatttcac actgaaaatc 240

tctagggtgg aggcagagga cgtaggcgtt tactactgta gtcagaccac ccatgtaccc 300
 tggacttttg gccaaaggtag taagctggaa atcaag 336

<210> 97
 <211> 125
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(125)
 <223> VH Domain of PD-1 mAb 3

<400> 97

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

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

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

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

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

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

Thr Arg Glu Lys Ile Thr Thr Ile Val Glu Gly Thr Tyr Trp Tyr Phe
 100 105 110

Asp Val Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 98

<211> 375
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(375)
 <223> Polynucleotide Encoding the VH Domain of PD-1 mAb 3

<400> 98
 caggttcaac tgcaacagtc tggggctgag ctggtgaggc ctggggcttc agtgacgctg 60
 tcctgcaagg cttcgggcta cacatttact gactatgtaa tgcactgggt gaagcagaca 120
 cctgtgcatg gcctggaatg gattggaact attgacatctg aaactgggtgg tactgcctac 180
 aatcagaagt tcaagggcaa ggccatactg actgcagaca agtcctccaa cacagcctac 240
 atggagctcc gcagcctgac atctgaggac tctgccgtct attactttac aagagagaag 300
 attactacga tagtagaggg gacatactgg tacttcgatg tctggggcac agggaccacg 360
 gtcaccgtct cctca 375

<210> 99
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDRH1 of PD-1 mAb 3

<400> 99

Asp Tyr Val Met His
 1 5

<210> 100
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)

<223> CDRH2 of PD-1 mAb 3

<400> 100

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

Gly

<210> 101

<211> 16

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(16)

<223> CDRH3 of PD-1 mAb 3

<400> 101

Glu Lys Ile Thr Thr Ile Val Glu Gly Thr Tyr Trp Tyr Phe Asp Val
1 5 10 15

<210> 102

<211> 112

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(112)

<223> VL Domain of PD-1 mAb 3

<400> 102

Asp Val Leu Leu 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 Asn Ile Val His Ser
20 25 30

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

<210> 103
<211> 336
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(336)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 3

<400> 103
gatgttttgc tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gaacattgta catagtaatg gagacaccta tttggaatgg 120
tacctgcaga aaccaggcca gtctccaaag ctctgatct ataaagtttc caaccgattt 180
tctgggggtcc cagacagggt cagtggcagt gggtcaggga cagattttac actcaaaatc 240
agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatcttccg 300
tacacgttcg gagggggggac caagctggaa ataaaa 336

<210> 104
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)

<223> CDRL1 of PD-1 mAb 3

<400> 104

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asp Thr Tyr Leu Glu
1 5 10 15

<210> 105

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> CDRL2 of PD-1 mAb 3

<400> 105

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 106

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRL3 of PD-1 mAb 3

<400> 106

Phe Gln Gly Ser His Leu Pro Tyr Thr
1 5

<210> 107

<211> 116

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(116)

<223> VH Domain of PD-1 mAb 4

<400> 107

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

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

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

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

Lys Gly Arg Phe Thr Val Thr Arg Asp Asn Ala Lys Asn Thr Leu Phe
65 70 75 80

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

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

Thr Val Ser Ser
115

<210> 108
<211> 348
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(348)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 4

<400> 108
gatgtgcagc tcgtggagtc tgggggaggc ttagtgcagc ctggagggtc ccggaaactc 60
tcctgtgcag cctctggatt cgttttcagt agctttggaa tgcactgggt tcgtcaggct 120
ccagagaagg ggctggagtg ggtcgcata attagtagtg gcagtatgag tatttcctat 180

gcagacacag tgaagggccg attcacgctc accagagaca atgccaagaa caccctgttc 240
 ctgcaaatga ccagtctaag gtctgaggac acggccattt attactgtgc atccctgact 300
 gactactttg actactgggg ccaaggcacc actctcacag tctcctca 348

<210> 109
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDRH1 of PD-1 mAb 4

<400> 109

Ser Phe Gly Met His
 1 5

<210> 110
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDRH2 of PD-1 mAb 4

<400> 110

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

Gly

<210> 111
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> CDRH3 of PD-1 mAb 4

<400> 111

Leu Thr Asp Tyr Phe Asp Tyr
 1 5

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

<220>
 <221> MISC_FEATURE
 <222> (1)..(112)
 <223> VL Domain of PD-1 mAb 4

<400> 112

Asp Val Val Met Ser 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

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

Pro Lys Leu Leu Ile Tyr Arg 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 Thr
 85 90 95

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

<210> 113
 <211> 336
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(336)
 <223> Polynucleotide Encoding the VL Domain of PD-1 mAb

<400> 113
 gatgttgatga tgtcccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
 atctcctgca gatctagtca gaggcttggt cacagtactg gaaacaccta tttccattgg 120
 tacctgcaga agccaggcca gtctccaaag ctctgatct acagggtttc taaccgattt 180
 tctgggggtcc ccgacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaactac acatgttccg 300
 tggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 114
 <211> 16
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(16)
 <223> CDRL1 of PD-1 mAb 4

<400> 114

Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Thr	Gly	Asn	Thr	Tyr	Phe	His
1				5					10					15	

<210> 115
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> CDRL2 of PD-1 mAb 4

<400> 115

Arg Val Ser Asn Arg Phe Ser
1 5

<210> 116

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRL3 of PD-1 mAb 4

<400> 116

Ser Gln Thr Thr His Val Pro Trp Thr
1 5

<210> 117

<211> 119

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(119)

<223> VH Domain of PD-1 mAb 5

<400> 117

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

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

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

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

Ala Arg Glu His Tyr Gly Ser Ser Pro Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 118
<211> 357
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(357)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 5

<400> 118
caggtccaac tgcagcagcc tggggttgaa ctggtgaggc ctggagcttc agtgaagctg 60
tcctgcaagg cttctggcta ctccttcacc gcctactgga tgaactggat gaaacagagg 120
cctggacaag gccttgagtg gattggcgtg attcatcctt ccgatagtga aacttggtta 180
aatcagaagt tcaaggacaa ggccacattg actgtagaca aatcctccag cacagcctac 240
atgcaactca tcagcccgac atctgaggac tctgcggtct attactgtgc aagagagcac 300
tacggtagta gcccgtttgc ttactggggc caagggactc tggtcactgt ctctgca 357

<210> 119
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of PD-1 mAb 5

<400> 119

Ala Tyr Trp Met Asn
1 5

<210> 120
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of PD-1 mAb 5

<400> 120

Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 121
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> CDRH3 of PD-1 mAb 5

<400> 121

Glu His Tyr Gly Ser Ser Pro Phe Ala Tyr
1 5 10

<210> 122
<211> 111
<212> PRT
<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(111)

<223> VL Domain of PD-1 mAb 5

<400> 122

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

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

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 123

<211> 333

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(333)

<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 5

<400> 123

gacattgtgc tgaccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca gagccaacga aagtgttgat aattatggca tgagttttat gaactggttc 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa ccaaggatcc 180

ggggtccctg ccaggttttag tggcagtggg tctgggacag atttcagcct caacatccat 240
cctatggagg aggatgatac tgcaatgtat ttctgtcagc aaagtaagga ggttccgtac 300
acgttcggag gggggaccaa gctggaaata aaa 333

<210> 124
<211> 15
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> CDRL1 of PD-1 mAb 5

<400> 124

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

<210> 125
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of PD-1 mAb 5

<400> 125

Ala	Ala	Ser	Asn	Gln	Gly	Ser
1			5			

<210> 126
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDRL3 of PD-1 mAb 5

<400> 126

Gln Gln Ser Lys Glu Val Pro Tyr Thr
1 5

<210> 127

<211> 118

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(118)

<223> VH Domain of PD-1 mAb 6

<400> 127

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Asn 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 Glu Lys Arg Leu Glu Trp Val
35 40 45

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

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

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

Ala Arg Gln Lys Ala Thr Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Thr
115

<210> 128

<211> 333
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(333)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 6

<400> 128
gaaatcgtac tcacccagtc acctgcaacc ctttctctga gccccggtga acgtgccact 60
ctcagctgca gagcaagtga gagtgtggac aattacggca tgtccttcat gaactggttt 120
cagcagaagc ctgggcagcc acctaagctg ctcatccacg ccgcctctaa ccgcggatct 180
ggggtgcctt cacgtttttc tggatcagga agtggcactg acttcaccct tacaatcagc 240
tctctggagc cagaggactt tgccgtctat ttctgccagc aatctaaaga ggtgccctat 300
acttttggtg gcgggaccaa ggttgagatc aaa 333

<210> 129
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of PD-1 mAb 6

<400> 129

Ser Tyr Gly Met Ser
1 5

<210> 130
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of PD-1 mAb 6

<400> 130

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

Gly

<210> 131

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRH3 of PD-1 mAb 6

<400> 131

Gln Lys Ala Thr Thr Trp Phe Ala Tyr
1 5

<210> 132

<211> 111

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(111)

<223> VL Domain of PD-1 mAb 6

<400> 132

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

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

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 133
<211> 333
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(333)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 6

<400> 133
gacattgtgc tgaccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca gagccagcga aagtgttgat aattatggca ttagttttat gaactggttc 120
caacagaaac caggacagcc acccaaactc ctcatctatc ctgcatccaa ccaaggatcc 180
ggggtccctg ccaggttttag tggcagtgagg tctgggacag acttcagcct caacatccat 240
cctatggagg aggatgatgc tgcaatgtat ttctgtcagc aaagtaagga ggttccgtgg 300
acgttcggtg gaggcaccaa gctggaaatc aaa 333

<210> 134
<211> 15
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> CDRL1 of PD-1 mAb 6

<400> 134

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

<210> 135

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> CDRL2 of PD-1 mAb 6

<400> 135

Pro Ala Ser Asn Gln Gly Ser
1 5

<210> 136

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRL3 of PD-1 mAb 6

<400> 136

Gln Gln Ser Lys Glu Val Pro Trp Thr
1 5

<210> 137

<211> 119

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(119)

<223> VH Domain of PD-1 mAb 7

<400> 137

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 Ser Phe Thr Ser Tyr
 20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
 50 55 60

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

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

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

Thr Leu Val Thr Val Ser Ser
 115

<210> 138
 <211> 357
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(357)
 <223> Polynucleotide Encoding the VH Domain of PD-1 mAb 7

<400> 138
 gaggtccaac tgcagcagcc tggggctgaa ctggtgaggc ctggagcttc agtgaagctg 60
 tcctgcaagg cttctggcta ctccttcacc agctactgga tgaactgggt gaagcagagg 120
 cctggacaag gccttgagtg gattggcgtg attcatcctt ccgatagtga aacttggtta 180
 gatcagaagt tcaaggacaa ggccacattg actgtagaca aatcctccac cacagcctac 240

atgcaactca tcagcccgac atctgaggac tctgcggtct attactgtgc aagggagcac 300
 tacggtacta gcccgtttgc ttactggggc caagggactc tggtcactgt gtctttcc 357

<210> 139
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDRH1 of PD-1 mAb 7

<400> 139

Ser Tyr Trp Met Asn
 1 5

<210> 140
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDRH2 of PD-1 mAb 7

<400> 140

Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe Lys
 1 5 10 15

Asp

<210> 141
 <211> 10
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE

<222> (1)..(10)

<223> CDRH3 of PD-1 mAb 7

<400> 141

Glu His Tyr Gly Thr Ser Pro Phe Ala Tyr
1 5 10

<210> 142

<211> 111

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(111)

<223> VL Domain of PD-1 mAb 7

<400> 142

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

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

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ala
50 55 60

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

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

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

<210> 143

<211> 333

<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(333)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 7

<400> 143
gacattgtgc tgaccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60
atctcctgca gagccaacga aagtgttgat aattatggca tgagttttat gaactggttc 120
caacagaaac caggacagcc acccaaactc ctcatccatg ctgcatccaa ccaaggatcc 180
ggggtccctg ccaggtttag tggcagtggg tttgggacag acttcagcct caacatccat 240
cctatggagg aggatgatgc tgcaatgtat ttctgtcagc aaagtaagga ggttccgtac 300
acgttcggag gggggaccaa gctggaaata aaa 333

<210> 144
<211> 15
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> CDRL1 of PD-1 mAb 7

<400> 144

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

<210> 145
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of PD-1 mAb 7

<400> 145

Ala Ala Ser Asn Gln Gly Ser
1 5

<210> 146
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDRL3 of PD-1 mAb 7

<400> 146

Gln Gln Ser Lys Glu Val Pro Tyr Thr
1 5

<210> 147
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of hPD-1 mAb 7 VH1

<400> 147

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 Ser Phe Thr Ser Tyr
20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
50 55 60

Lys Asp 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 Glu His Tyr Gly Thr Ser Pro Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 148
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hPD-1 mAb 7 VH1

<400> 148
caagttcaat tgggtacagag cggggcagag gtgaagaaac ccggcgccag tgttaaggtg 60
tcctgcaaag ccagcgggta cagctttaca agctattgga tgaattgggt gcgtcaagca 120
ccagggcagg gtctggaatg gattgggggtg atacatcctt ctgacagcga aacatggttg 180
gaccagaaat ttaaagatcg tgtgacaatt acagtcgata agtccacaag cactgcttac 240
atggaactct ccagcttgcg gtccgaggac accgctgtgt attattgcgc cagagagcac 300
tacggcacat caccttttgc atactggggc cagggaactc tcgtaaccgt atcctcc 357

<210> 149
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of hPD-1 mAb 7 VH2

<400> 149

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 Ser Phe Thr Ser Tyr
20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
 50 55 60

Lys Asp 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 Glu His Tyr Gly Thr Ser Pro Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 150
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hPD-1 mAb 7 VH2

<400> 150
 caagttcaat tggtagagag cggggcagag gtgaagaaac ccggcgccag tgttaaggtg 60
 tcctgcaaag ccagcggta cagctttaca agctattgga tgaattgggt gcgtcaagca 120
 ccagggcagg gtctggaatg ggctggggtg atacatcctt ctgacagcga aacatggttg 180
 gaccagaaat ttaaagatcg tgtgacaatt acagtcgata agtccacaag cactgcttac 240
 atggaactct ccagcttgcg gtccgaggac accgctgtgt attattgcgc cagagagcac 300
 tacggcacat caccttttgc atactggggc cagggaactc tcgtaaccgt atcctcc 357

<210> 151
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>

<223> VL Domain of hPD-1 mAb 7 VL1

<400> 151

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 Asn Glu Ser Val Asp Asn Tyr
20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

<210> 152

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide Encoding hPD-1 mAb 7 VL1

<400> 152

gaaatcgtagc tcaccagtc acctgcaacc ctttctctga gccccggtga acgtgccact 60
ctcagctgca gagcaaatga gagtgtggac aattacggca tgtccttcat gaactggttt 120
cagcagaagc ctgggcagcc acctaagctg ctcatccacg ccgcctctaa ccagggatct 180
ggggtgcctt cacgtttttc tggatcagga agtggcactg acttcaccct tacaatcagc 240
tctctggagc cagaggactt tgccgtctat ttctgccagc aatctaaaga ggtgccttat 300
acttttggtg gcgggaccaa gggtgagatc aaa 333

<210> 153
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL Domain of hPD-1 mAb 7 VL2

<400> 153

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 Glu Ser Val Asp Asn Tyr
 20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
 50 55 60

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

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

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

<210> 154
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hPD-1 mAb 7 VL2

<400> 154

gaaatcgtac tcaccagtc acctgcaacc ctttctctga gccccggtga acgtgccact 60

ctcagctgca gagcaagtga gagtgtggac aattacggca tgtccttcac gaactggttt 120

cagcagaagc ctgggcagcc acctaagctg ctcatccacg cgcctctaa ccagggatct 180
 ggggtgcctt cacgtttttc tggatcagga agtggcactg acttcaccct tacaatcagc 240
 tctctggagc cagaggactt tgccgtctat ttctgccagc aatctaaaga ggtgccttat 300
 acttttggtg gcgggaccaa ggttgagatc aaa 333

<210> 155
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VL Domain of hPD-1 mAb 7 VL3

<400> 155

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 Glu Ser Val Asp Asn Tyr
 20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Arg Gly Ser Gly Val Pro Ser
 50 55 60

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

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

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

<210> 156
 <211> 333
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Polynucleotide Encoding hPD-1 mAb 7 VL3

<400> 156

gaaatcgtac tcaccagtc acctgcaacc ctttctctga gccccggtga acgtgccact 60

ctcagctgca gagcaagtga gagtgtggac aattacggca tgtccttcat gaactggttt 120

cagcagaagc ctgggcagcc acctaagctg ctcattccacg ccgcctctaa ccgcggatct 180

ggggtgcctt cacgtttttc tggatcagga agtggcactg acttcaccct tacaatcagc 240

tctctggagc cagaggactt tgccgtctat ttctgccagc aatctaaaga ggtgccctat 300

acttttggtg gcgggaccaa ggttgagatc aaa 333

<210> 157

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRL1 of the VL Domain of hPD-1 mAb 7 VL2 and hPD-1 mAb 7 VL3

<400> 157

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

<210> 158

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRL2 of the VL Domain of hPD-1 mAb 7 VL3

<400> 158

Ala Ala Ser Asn Arg Gly Ser
1 5

<210> 159

<211> 113

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(113)

<223> VH Domain of PD-1 mAb 8

<400> 159

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

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

Tyr Met Asn Trp Val Lys Gln Asn His Gly Lys Ser Leu Glu Trp Ile
35 40 45

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

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

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

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

Ser

<210> 160

<211> 339

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(339)

<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 8

<400> 160

gagggccagc tgcaacaatc tggacctgag ctggtgaagc ctggggcttc agtgaagata

60

tcctgtaagg cttctggata cacgttcact gactactaca tgaactgggt gaagcagaac	120
catggaaaga gccttgagt gattggagat attaatccta aaaatgggtga cactcactac	180
aaccagaagt tcaagggcga ggccacattg actgtagaca agtcctccac cacagcctac	240
atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc gagcgatttt	300
gactactggg gccaaaggcac cactctcaca gtctcctcc	339

<210> 161
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDRH1 of PD-1 mAb 8

<400> 161

Asp Tyr Tyr Met Asn
1 5

<210> 162
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDRH2 of PD-1 mAb 8

<400> 162

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

Gly

<210> 163
 <211> 4

<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(4)
<223> CDRH3 of PD-1 mAb 8

<400> 163

Asp Phe Asp Tyr
1

<210> 164
<211> 112
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(112)
<223> VL Domain of PD-1 mAb 8

<400> 164

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

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

Asn Gly Asn Thr Tyr Leu Asn Trp Phe 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 Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 165
<211> 336
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(336)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 8

<400> 165
gatgttgtga tgacccaaac tccactctcc ctgcctgtcg gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gacccttgta tatagtaatg gaaacaccta tttaaattgg 120
ttcctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
tctgggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttcca 300
ttcacgttcg gtcgggggac aaagttggaa ataaaa 336

<210> 166
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> CDRL1 of PD-1 mAb 8

<400> 166

Arg Ser Ser Gln Thr Leu Val Tyr Ser Asn Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 167
<211> 7
<212> PRT
<213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> CDRL2 of PD-1 mAb 8

<400> 167

Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 168
 <211> 9
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(9)
 <223> CDRL3 of PD-1 mAb 8

<400> 168

Ser Gln Ser Thr His Val Pro Phe Thr
 1 5

<210> 169
 <211> 119
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(119)
 <223> VH Domain of PD-1 mAb 9

<400> 169

Glu Val Met Leu Val Glu Ser Gly Gly Gly 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

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 170
<211> 357
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(357)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 9

<400> 170
gaagtgatgc tgggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60
tcctgtgcag cctctggatt cactttcagt agttatcttg tgtcttgggt tcgccagact 120
ccggagaaga ggctggagtg ggtcgcaacc attagtgggtg gtggtggtaa cacctactat 180
tcagacagtg tgaagggtcg attcaccatc tccagagaca atgccaagaa caccctgtac 240
ctgcaaata gtagtctgag gtctgaggac acggccttgt attactgtgc aaggtatggt 300
ttcgacggcg cctggtttgc ttactggggc caagggactc tggtcactgt ctcttcc 357

<210> 171
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of PD-1 mAb 9

<400> 171

Ser Tyr Leu Val Ser
1 5

<210> 172
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of PD-1 mAb 9

<400> 172

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

Gly

<210> 173
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> CDRH3 of PD-1 mAb 9

<400> 173

Tyr Gly Phe Asp Gly Ala Trp Phe Ala Tyr
1 5 10

<210> 174
<211> 107
<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(107)

<223> VL Domain of PD-1 mAb 9

<400> 174

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

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

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

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

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

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

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

<210> 175

<211> 321

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(321)

<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 9

<400> 175

gacatccaga tgactcagtc tccagcctcc ctatctgcat ctgtgggaga tattgtcacc

60

atcacatgtc gagcaagtga gaatatttac agttatttag catggtatca gcagaaacag 120
gaaaaatctc ctgagctcct ggtctataat gcaaaaacct tggcagcagg tgtgccatca 180
aggttcagtg gcagtggatc aggcacacag ttttctctga ccatcaacag cctgcagcct 240
gaagattttg ggaattatta ctgtcagcat cattatgctg ttccgtggac gttcgggtgga 300
ggcaccagac tggaaatcac a 321

<210> 176
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRL1 of PD-1 mAb 9

<400> 176

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

<210> 177
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of PD-1 mAb 9

<400> 177

Asn Ala Lys Thr Leu Ala Ala
1 5

<210> 178
<211> 9
<212> PRT
<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRL3 of PD-1 mAb 9

<400> 178

Gln His His Tyr Ala Val Pro Trp Thr
1 5

<210> 179

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> VH Domain of hPD-1 mAb 9 VH1

<400> 179

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg 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

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

Ala Thr Ile Ser Gly Gly Gly Gly Asn Thr Tyr Tyr Ser Asp Ser 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 Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

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

Thr Leu Val Thr Val Ser Ser
115

<210> 180
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hPD-1 mAb 9 VH1

<400> 180
 gaggtgcagc tgggtggaaag tggggggcggc ctggtgacgac ccgggggaag tctgaaactg 60
 tcctgtgcag catcaggatt tactttttca tcttatctcg tgtcttgggt aagacaagca 120
 cccggaaaag gcttggaatg ggtggccact atctccggtg gaggtggcaa cacctactat 180
 agcgacagtg tcaagggaag atttaccatc agtcgacgaca acgctaagaa tagcctgtac 240
 ctccagatga actccctgcg cgccgaggac accgccacct attactgtgc acgctatgga 300
 tttgacggcg catggtttgc ctactgggga cagggcacat tggtaaccgt tagctcc 357

<210> 181
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH Domain of hPD-1 mAb 9 VH2

<400> 181

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Arg 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

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

Ala Thr Ile Ser Gly Gly Gly Gly Asn Thr Tyr Tyr Ser Asp Ser 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 Ala Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

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

Thr Leu Val Thr Val Ser Ser
115

<210> 182
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hPD-1 mAb 9 VH2

<400> 182
gaggtgcagc tgggtggaaag tgggggcggc ctggcgcgac ccgggggaag tctgaaactg 60
tcctgtgcag catcaggatt tactttttca tcttatctcg tgggctgggt aagacaagca 120
cccggaaaag gcttggaatg gacggccact atctccggtg gaggtggcaa cacctactat 180
agcgacagtg tcaagggaag atttaccatc agtcgcgaca acgctaagaa tagcctgtac 240
ctccagatga actccgcacg cgccgaggac accgccacct attactgtgc acgctatgga 300
tttgacggcg catggtttgc ctactgggga cagggcacat tggttaaccgt tagctcc 357

<210> 183
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1 of the VH Domain of hPD-1 mAb 9 VH2 Having a Serine to Glycine Amino Acid Substitution

<400> 183

Ser Tyr Leu Val Gly
1 5

<210> 184
<211> 107
<212> PRT

<213> Artificial Sequence

<220>

<223> VL Domain of hPD-1 mAb 9 VL1

<400> 184

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

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

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

Tyr Asn Ala Lys Thr Leu Ala Ala 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 Ala Val Pro Trp
85 90 95

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

<210> 185

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide Encoding hPD-1 mAb 9 VL1

<400> 185

gacattcaga tgactcagtc tcccagcagt ctgtccgcat ccgtggggga tcgggtcacc 60

atcacctgcc gtgcctcaga aaacatctat tcatacctcg cctggtatca acagaaacct 120

ggtaaagccc caaaattgct catttacaac gccaaagacc tcgcagctgg cgtgccaagt 180

aggttctcag gcagcggctc agggacagat ttcaccctca ccatatcctc actgcagccc 240

gaggattttg ccacttacta ctgccagcat cattacgcag tgccctggac cttcggacaa 300
ggcactaagc tcgagatcaa a 321

<210> 186
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of hPD-1 mAb 9 VL2

<400> 186

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

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

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

Tyr Asp Ala Lys Thr Leu Ala Ala 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 Ala Val Pro Trp
85 90 95

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

<210> 187
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hPD-1 mAb 9 VL2

<400> 187

gacattcaga tgactcagtc tcccagcagt ctgtccgcat ccgtggggga tcgggtcacc 60
 atcacctgcc gtgcctcaga aaacatctat aactacctcg cctgggtatca acagaaacct 120
 ggtaaagccc caaaattgct catttacgac gccaaagacc tcgcagctgg cgtgccaagt 180
 aggttctcag gcagcggctc agggacagat ttcaccctca ccatatcctc actgcagccc 240
 gaggattttg ccacttacta ctgccagcat cattacgcag tgccctggac cttcggacaa 300
 ggcactaagc tcgagatcaa a 321

<210> 188
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRL1 of the VL Domain of hPD-1 mAb 9 VL2
 <400> 188

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

<210> 189
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRL2 of the VL Domain of hPD-1 mAb 9 VL2
 <400> 189

Asp Ala Lys Thr Leu Ala Ala
 1 5

<210> 190
 <211> 116
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(116)
 <223> VH Domain of PD-1 mAb 10

<400> 190

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

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

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

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

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

Thr Val Ser Ser
115

<210> 191

<211> 348

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(348)

<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 10

<400> 191

gaagtgatac tgggtggagtc tggggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt aactatctca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaagt attagtgggt gtggtagtaa tatctactat 180

ccagacagtg tgaagggtcg attcaccata tccagggaca atgccaagaa caccctgtac 240
 ctgcaaataga acagtctgag gtctgaggac acggccttgt attactgtgc aagacaagaa 300
 ctggcttttg actactggggg ccaaggcacc actctcacag tctcctcc 348

<210> 192
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDRH1 of PD-1 mAb 10

<400> 192

Asn Tyr Leu Met Ser
 1 5

<210> 193
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDRH2 of PD-1 mAb 10

<400> 193

Ser Ile Ser Gly Gly Gly Ser Asn Ile Tyr Tyr Pro Asp Ser Val Lys
 1 5 10 15

Gly

<210> 194
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>

<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRH3 of PD-1 mAb 10

<400> 194

Gln Glu Leu Ala Phe Asp Tyr
1 5

<210> 195
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(107)
<223> VL Domain of PD-1 mAb 10

<400> 195

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 Thr Ser Gln Asp Ile Ser Asn Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Ile 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 Ser Thr Leu Pro Trp
85 90 95

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

<210> 196

<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(321)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 10

<400> 196
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc 60
atcagttgca ggacaagtca ggacattagc aatttttttaa actggtatca gcagaaacca 120
gatggaacta ttaaactcct gatctactac acatcaagat tacactcagg agtcccatca 180
aggttcagtg gcagtggggtc tggaacagat tattctctca ccattagcaa cctggagcaa 240
gaagatatcg ccacttactt ttgccaacag ggtagtacgc ttccgtggac gttcgggtgga 300
ggcaccaagc tggaaatcat a 321

<210> 197
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRL1 of PD-1 mAb 10

<400> 197

Arg Thr Ser Gln Asp Ile Ser Asn Phe Leu Asn
1 5 10

<210> 198
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of PD-1 mAb 10

<400> 198

Tyr Thr Ser Arg Leu His Ser
1 5

<210> 199

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (19)..()

<223> CDRL3 of PD-1 mAb 10

<400> 199

Gln Gln Gly Ser Thr Leu Pro Trp Thr
1 5

<210> 200

<211> 117

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(117)

<223> VH Domain of PD-1 mAb 11

<400> 200

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

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

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Lys Trp Met
35 40 45

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

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

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

Thr Thr Gly Thr Tyr Ser Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 201
<211> 351
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(351)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 11

<400> 201
gaggttcagc tccagcagtc tgggactgtg ctggcaaggc ctggggcttc agtgaagatg 60
tcctgcaaga cttctggcta cacatttacc ggctactgga tgcactgggt aaaacagagg 120
cctggacagg gtctgaaatg gatgggggct atttatacctg gaaatagtga tactcactac 180
aaccagaagt tcaagggcaa ggccaaactg actgcagtca catccgccag cactgcctac 240
atggagctca gcagcctgac aaatgaggac tctgcgatct attactgtac tactgggacc 300
tactcgtact tcgatgtctg gggcacaggg accacggtca ccgtctcctc a 351

<210> 202
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of PD-1 mAb 11

<400> 202

Gly Tyr Trp Met His
1 5

<210> 203

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDRH2 of PD-1 mAb 11

<400> 203

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

Gly

<210> 204

<211> 8

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(8)

<223> CDRH3 of PD-1 mAb 11

<400> 204

Gly Thr Tyr Ser Tyr Phe Asp Val
1 5

<210> 205

<211> 106

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(106)

<223> VL Domain of PD-1 mAb 11

<400> 205

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

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Ser
20 25 30

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

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 206

<211> 318

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(318)

<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 11

<400> 206

gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gagcattggc acaagcatac actggtatca gcacagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatctctgg gatcccttcc 180

aggtttagtg gcagtggatc agggactgat ttactctta gcatcaacag tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa agtaatagct ggctcacgtt cggtgctggg 300
 accaagctgg agctgaaa 318

<210> 207
 <211> 11
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(11)
 <223> CDRL1 of PD-1 mAb 11

<400> 207

Arg Ala Ser Gln Ser Ile Gly Thr Ser Ile His
 1 5 10

<210> 208
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> CDRL2 of PD-1 mAb 11

<400> 208

Tyr Ala Ser Glu Ser Ile Ser
 1 5

<210> 209
 <211> 8
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(8)
 <223> CDRL3 of PD-1 mAb 11

<400> 209

Gln Gln Ser Asn Ser Trp Leu Thr
1 5

<210> 210
<211> 125
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(125)
<223> VH Domain of PD-1 mAb 12

<400> 210

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

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

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

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

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

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

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

Asp Val Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 211
<211> 375

<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(375)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 12

<400> 211
cagggtcacc tgcagcagtc tggggctgag ctggtgaggc ctggggcttc agtgacgctg 60
tcctgcaagg cttcgggctt cacatttact gactatgaga tgcactgggt gaaacagaca 120
cctgtgcatg gcctggaatg gattgggact attgatacctg aaactgggtg tactgcctac 180
aatcagaagt tcaagggcaa ggccatactg acagtagaca aatcttccac tacaacctac 240
atggagctcc gcagcctgac atctgaggac tctgccgtct tttattgttc aagagagagg 300
attactacgg ttgttgaggg ggccatactg tacttcgatg tctggggcac agggaccacg 360
gtcaccgtct cctca 375

<210> 212
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of PD-1 mAb 12

<400> 212

Asp Tyr Glu Met His
1 5

<210> 213
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of PD-1 mAb 12

<400> 213

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

Gly

<210> 214

<211> 16

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(16)

<223> CDRH3 of PD-1 mAb 12

<400> 214

Glu Arg Ile Thr Thr Val Val Glu Gly Ala Tyr Trp Tyr Phe Asp Val
1 5 10 15

<210> 215

<211> 112

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(112)

<223> VL Domain of PD-1 mAb 4

<400> 215

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 Asn Ile Val His 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 Cys Lys Val Ser Thr 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 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 216
<211> 336
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(336)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 12

<400> 216
gatgttttga tgaccagac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gaacattgta catagtaatg gaaacaccta tttagaatgg 120
tacctgcaga aaccaggcca gtctccaaag ctctgatct gcaaagtttc caccgattt 180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tattattgct ttcaaggttc acatgttccg 300
tacacgttcg gaggggggac caagctggaa ataaaa 336

<210> 217
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> CDRL1 of PD-1 mAb 12

<400> 217

Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 218

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> CDRL2 of PD-1 mAb 12

<400> 218

Lys Val Ser Thr Arg Phe Ser
1 5

<210> 219

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRL3 of PD-1 mAb 12

<400> 219

Phe Gln Gly Ser His Val Pro Tyr Thr
1 5

<210> 220

<211> 121

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(121)

<223> VH Domain of PD-1 mAb 13

<400> 220

Glu Val Met Leu Val Glu Ser Gly Gly Gly 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 His
20 25 30

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

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

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

Thr Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 221

<211> 363

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)..(363)

<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 13

<400> 221

gaagtgatgc tgggtggagtc tggggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt agccatacca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtgggt gtggttctaa tatctactat 180

ccagacagtg tgaagggtcg attcaccatc tccagagaca atgccaagaa caccctgtac 240
 ctgcaaata gtagtctgag gtctgaggac acggccttgt attactgtgc aagacaagct 300
 tactacggta attactggta cttcgatgtc tggggcacag ggaccacggt caccgtctcc 360
 tcc 363

<210> 222
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(5)
 <223> CDRH1 of PD-1 mAb 13

<400> 222

Ser His Thr Met Ser
 1 5

<210> 223
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> CDRH2 of PD-1 mAb 13

<400> 223

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

Gly

<210> 224
 <211> 12
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(12)
 <223> CDRH3 of PD-1 mAb 13

<400> 224

Gln Ala Tyr Tyr Gly Asn Tyr Trp Tyr Phe Asp Val
 1 5 10

<210> 225
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> VL Domain of PD-1 mAb 13

<400> 225

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

Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
 20 25 30

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

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

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

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

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

<210> 226
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(321)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 13

<400> 226
gacattcaga tgaccagtc tcctgccacc cagtctgcat ctctgggaga aagtgtcacc 60
atcacgtgcc tggcaagtca gaccattggg acatgggttag catgggtatca gcagaaacca 120
gggaaatctc ctgagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 180
aggttcagtg gtagtggatc tggcacaaaa ttttctttca agatcagcag cctacaggct 240
gaagattttg taagttatta ctgtcaacaa cttgacagta ttccgtggac gttcgggtgga 300
ggcaccaagc tggaaatcaa a 321

<210> 227
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRL1 of PD-1 mAb 13

<400> 227

Leu Ala Ser Gln Thr Ile Gly Thr Trp Leu Ala
1 5 10

<210> 228
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)

<223> CDRL2 of PD-1 mAb 13

<400> 228

Ala Ala Thr Ser Leu Ala Asp
1 5

<210> 229

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRL3 of PD-1 mAb 13

<400> 229

Gln Gln Leu Asp Ser Ile Pro Trp Thr
1 5

<210> 230

<211> 117

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(117)

<223> VH Domain of PD-1 mAb 14

<400> 230

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 Asn Phe Ile Ser Tyr
20 25 30

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

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

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

Val Thr Val Ser Ser
115

<210> 231
<211> 351
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(351)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 14

<400> 231
caggtccaac tgcagcagcc tggggctgag cttgtgaagc ctggggcttc agtgaagatg 60
tcctgcaagg cttctggcta caacttcatac agctactgga taacctgggt gaaacagagg 120
cctggacaag gccttcagtg gattggaaat atttatcctg gtactgatgg tactacctac 180
aatgagaagt tcaagagcaa ggccacactg actgtagaca catcctccag cacagcctac 240
atgcaccta gtcgcctgac atctgaggac tctgcggtct attactgtgc aactgggcta 300
cactggtact tcgatgtctg gggcacaggg accacggtca ccgtctcctc c 351

<210> 232
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)

<223> CDRH1 of PD-1 mAb 14

<400> 232

Ser Tyr Trp Ile Thr
1 5

<210> 233

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> CDRH2 of PD-1 mAb 14

<400> 233

Asn Ile Tyr Pro Gly Thr Asp Gly Thr Thr Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 234

<211> 8

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(8)

<223> CDRH3 of PD-1 mAb 14

<400> 234

Gly Leu His Trp Tyr Phe Asp Val
1 5

<210> 235

<211> 107

<212> PRT

<213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> VL Domain of PD-1 mAb 14

<400> 235

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

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

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

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

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

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

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

<210> 236
 <211> 321
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)..(321)
 <223> Polynucleotide Encoding the VL Domain of PD-1 mAb 14

<400> 236

gacattgtga tgaccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagt 60
 gtcacctgca aggccagtc gagtgtgggt actaatgtag cctggatatca acagaagccc 120
 ggtcaatctc ctaaagcact gatttactcg gcacccctccc gattcagtggt cgtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcagtaa tgtgcagtct 240
gaagacttgg cagagtatatt ctgtcagcaa tataacagct atccgtacac gttcggaggg 300
gggaccaagc tggaaataaa a 321

<210> 237
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRL1 of PD-1 mAb 14

<400> 237

Lys Ala Ser Gln Ser Val Gly Thr Asn Val Ala
1 5 10

<210> 238
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDRL2 of PD-1 mAb 14

<400> 238

Ser Ala Ser Ser Arg Phe Ser
1 5

<210> 239
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDRL3 of PD-1 mAb 14

<400> 239

Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr
1 5

<210> 240

<211> 117

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(117)

<223> VH Domain of PD-1 mAb 15

<400> 240

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
20 25 30

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

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

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

Val Thr Val Ser Ser
115

<210> 241
<211> 351
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(351)
<223> Polynucleotide Encoding the VH Domain of PD-1 mAb 15

<400> 241
gaagtgatgc tgggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60
tcctgtgcag cctctggatt cattttcagt agctatctca tctcttgggt tcgccagact 120
ccggagaaga ggctggagtg ggtcgctgcc attagtgggtg gtggtgctga cacctactat 180
gccgacagtg tgaagggtcg attcaccatc tccagagaca atgccaagaa caccctgtat 240
ctgcaaatga gcagtctgag gtctgaggac acggccttat attactgtac aagacgaggg 300
acctatgcta tggactactg ggggtcaagga acctcagtca ccgtctcctc c 351

<210> 242
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> CDRH1 of PD-1 mAb 15

<400> 242

Ser Tyr Leu Ile Ser
1 5

<210> 243
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDRH2 of PD-1 mAb 15

<400> 243

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

Gly

<210> 244

<211> 8

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(8)

<223> CDRH3 of PD-1 mAb 15

<400> 244

Arg Gly Thr Tyr Ala Met Asp Tyr
1 5

<210> 245

<211> 107

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(107)

<223> VL Domain of PD-1 mAb 15

<400> 245

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

Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
20 25 30

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

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

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

Glu Asp Phe Val Asn Tyr Tyr Cys Gln Gln Leu Tyr Ser Ile Pro Trp
85 90 95

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

<210> 246
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(321)
<223> Polynucleotide Encoding the VL Domain of PD-1 mAb 15

<400> 246
gacattcaga tgaccagtc tccgcctcc cagtctgcat ctctgggaga aagtgtcacc 60
atcacatgcc tggcaagtca gaccattggt acatgggttag catggtatca gcagaaacca 120
gggaaatctc ctgagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 180
aggttcagtg gtagtggatc tggcacaaaa ttttctttca agatcagcag cctacaggct 240
gaagattttg taaattatta ctgtcaacaa ctttacagta ttccgtggac gttcgggtgga 300
ggcaccaagc tggaaatcaa a 321

<210> 247
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDRL1 of PD-1 mAb 15

<400> 247

Leu Ala Ser Gln Thr Ile Gly Thr Trp Leu Ala
1 5 10

<210> 248

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> CDRL2 of PD-1 mAb 15

<400> 248

Ala Ala Thr Ser Leu Ala Asp
1 5

<210> 249

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> CDRL3 of PD-1 mAb 15

<400> 249

Gln Gln Leu Tyr Ser Ile Pro Trp Thr
1 5

<210> 250

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> VH Domain of hPD-1 mAb 15 VH1

<400> 250

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
	20		
Ser	Cys	Ala	Ala
		25	
Ser	Gly	Phe	Thr
			30
Ser	Ser	Tyr	
Leu	Ile	Ser	Trp
	35		
Val	Arg	Gln	Ala
		40	
Pro	Gly	Lys	Gly
			45
Leu	Glu	Trp	Val
Ala	Ala	Ile	Ser
	50		
Gly	Gly	Gly	Ala
		55	
Asp	Thr	Tyr	Tyr
			60
Ala	Asp	Ser	Val
Lys	Gly	Arg	Phe
	65		
Thr	Ile	Ser	Arg
	70		
Asp	Asn	Ala	Lys
		75	
Asn	Ser	Leu	Tyr
			80
Leu	Gln	Met	Asn
Ser	Leu	Arg	Ala
	85		
Glu	Asp	Thr	Ala
		90	
Thr	Tyr	Tyr	Cys
			95
Ala	Arg	Arg	Gly
			100
Thr	Tyr	Ala	Met
Asp	Tyr	Trp	Gly
			105
Gln	Gly	Thr	Leu
			110
Val	Thr	Val	Ser
Ser			
	115		

<210> 251
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hPD-1 mAb 15 VH1

<400> 251	
gaagtgaac tggttgaaag tggcggcgagg ctggtgcggc caggtggttc actcagactg	60
tcttgtgcag cttcaggctt tacattctcc tcttatctta tctcttggtt gcgccaagcc	120
ccaggtaagg gccttgaatg ggtcgccgcc attagtgggg gtggtgccga tacatattat	180
gccgacagcg tcaagggacg tttcaccatc agcagggaca acgccaagaa tagcctttac	240
ctgcagatga actcacttag agctgaagac accgctactt attactgtgc ccggcgcgagg	300
acttacgcta tggactattg gggccagggc accttggtca ctgtctcatc c	351

<210> 252
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH Domain of hPD-1 mAb 15 VL1

<400> 252

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 Leu Ala Ser Gln Thr Ile Gly Thr Trp
 20 25 30

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

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

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

<210> 253
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide encoding hPD-1 mAb 15 VL1

<400> 253

gatatccaga tgaccagtc tcccagctct ctcagtgcaa gcgtaggcga ccgtgtgacc 60

atcacctgtc tggccagtca gaccattgga acctggctcg cctggtatca gcagaaacct 120

ggcaaggccc ctaagctgct gatttacgcc gccacctccc tcgcagatgg agtgccctcc 180
 cgatttagcg ggtccggggtc cggcaccgac ttcacattca caatcagcag cctccagccc 240
 gaggatttcg ctacatacta ctgtcaacag ctctactcca ttccatggac ctttggtcag 300
 ggtactaaac tggagatcaa a 321

<210> 254
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(98)
 <223> Human IgG4 CH1 Domain

<400> 254

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

<210> 255
 <211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1 Humanized Antibody Heavy Chain

<400> 255

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly
325

<210> 256

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG4 Humanized Antibody Heavy Chain with Stabilized Hinge Region

<400> 256

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly
 325

<210> 257
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(98)
 <223> Human IgG2 CH1 Domain

<400> 257

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> 258
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1 Sequence for the CH2 and CH3 Domains

<220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa is a lysine (K) or is absent

<400> 258

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> 259
 <211> 217
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> IgG4 Sequence for the CH2 and CH3 Domains

 <220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa is a lysine (K) or is absent

<400> 259

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> 260

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild-type and Variant Human IgG1 CH2 and CH3 Domains

<220>

<221> MISC_FEATURE

<222> (4)..(5)

<223> Xaa4 and Xaa5 are both L (wild type), or are both A (decreased FcgammaR binding)

<220>

<221> MISC_FEATURE

<222> (22)..(26)

<223> Xaa22, Xaa24 and Xaa26 respectively are M, S and T (wild type), or are Y, T and E (extended half-life)

<220>

<221> MISC_FEATURE

<222> (136)..(177)

<223> Xaa136, Xaa138, and Xaa177 respectively are: T, L and Y (wild type), or are W, L and Y (knob), or S, A and V (hole)

<220>

<221> MISC_FEATURE

<222> (204)..(205)

<223> Xaa204 and Xaa205 respectively are N and H (wild type), or are N and R (no protein A binding), or A and K (no protein A binding)

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> Xaa217 is K or is absent

<400> 260

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

Pro Lys Asp Thr Leu Xaa Ile Xaa Arg Xaa 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 Xaa Cys Xaa 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

Xaa 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 Xaa Xaa Tyr Thr Gln
 195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
 210 215

<210> 261

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

<220>
<223> Alternative Linker 2

<400> 261

Leu Gly Gly Gly Ser Gly
1 5

<210> 262
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 3

<400> 262

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

<210> 263
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 3

<400> 263

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

<210> 264
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain of a Humanized PD-1 Antibody (hPD-1 mAb 7(1.2))

<400> 264

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

210

215

<210> 265

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain of a Humanized Antibody ((hPD-1 mAb 7(1.2))

<400> 265

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 Ser Phe Thr Ser Tyr
20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
50 55 60

Lys Asp 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 Glu His Tyr Gly Thr Ser Pro Phe Ala 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 Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 266

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain of a Humanized Antibody ((hPD-1 mAb 7(1.2))

<400> 266

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 Ser Phe Thr Ser Tyr
20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
50 55 60

Lys Asp 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 Glu His Tyr Gly Thr Ser Pro Phe Ala 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
 210 215 220

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

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val

290

295

300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

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

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

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440 445

<210> 267

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> First and Third Polypeptide Chains of DART A

<220>

<221> MISC_FEATURE

<222> (34)..(34)

<223> Xaa34 is A or G

<220>
 <221> MISC_FEATURE
 <222> (307)..(307)
 <223> Xaa307 is Y or M

<220>
 <221> MISC_FEATURE
 <222> (309)..(309)
 <223> Xaa309 is T or S

<220>
 <221> MISC_FEATURE
 <222> (311)..(311)
 <223> Xaa311 is E or T

<400> 267

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

Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser
			20					25					30		

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

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

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

Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly
			115				120					125			

Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala
	130					135					140				

Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala
145 150 155 160

Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser
165 170 175

Glu Thr Trp Leu Asp Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val
180 185 190

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

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu His Tyr Gly Thr Ser
210 215 220

Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
225 230 235 240

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

Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu
260 265 270

Lys Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
275 280 285

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

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

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

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

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

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

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

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

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

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
450 455 460

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

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

Ser Leu Ser Leu Gly
500

<210> 268
<211> 273
<212> PRT
<213> Artificial Sequence

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

<400> 268

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 Glu Ser Val Asp Asn Tyr
 20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
 50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
 130 135 140

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

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

Ser Thr Tyr Ala Asp Asp Phe Glu Gly Arg Phe Val Phe Ser Met Asp
 180 185 190

Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu
 195 200 205

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ser Leu Tyr Asp Tyr Tyr
210 215 220

Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
225 230 235 240

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

Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys
260 265 270

Glu

<210> 269
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> First and Third Polypeptide Chains of DART D

<400> 269

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140

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

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

Ser Thr Tyr Ala Asp Asp Phe Glu Gly Arg Phe Val Phe Ser Met Asp
180 185 190

Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu
195 200 205

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ser Leu Tyr Asp Tyr Tyr
210 215 220

Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Leu
225 230 235 240

Gly Gly Gly Ser Gly Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
245 250 255

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
260 265 270

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

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

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
305 310 315 320

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
325 330 335

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
340 345 350

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
355 360 365

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
370 375 380

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
385 390 395 400

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
420 425 430

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
435 440 445

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
450 455 460

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
465 470 475 480

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

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
500 505 510

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
515 520 525

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
530 535 540

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
545 550 555 560

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
565 570

<210> 270
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fourth Polypeptide Chains of DART D

<400> 270

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly
115 120 125

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
130 135 140

Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala
145 150 155 160

Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser
165 170 175

Glu Thr Trp Leu Asp Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val
180 185 190

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

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu His Tyr Gly Thr Ser
210 215 220

Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu
225 230 235 240

Gly Gly Gly Ser Gly Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
245 250 255

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
260 265 270

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
275 280 285

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
290 295 300

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 305 310 315 320

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 325 330 335

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 340 345 350

<210> 271
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> First and Third Polypeptide Chains of DART E

<400> 271

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly
 115 120 125

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
130 135 140

Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala
145 150 155 160

Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser
165 170 175

Glu Thr Trp Leu Asp Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val
180 185 190

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

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu His Tyr Gly Thr Ser
210 215 220

Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Leu
225 230 235 240

Gly Gly Gly Ser Gly Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
245 250 255

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
260 265 270

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

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

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
305 310 315 320

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
325 330 335

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
340 345 350

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
355 360 365

Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val
370 375 380

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
385 390 395 400

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
420 425 430

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
435 440 445

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
450 455 460

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
465 470 475 480

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

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
500 505 510

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
515 520 525

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
530 535 540

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 545 550 555 560

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 565 570

<210> 272
 <211> 352
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Second and Fourth Polypeptide Chains of DART E

<400> 272

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 Glu Ser Val Asp Asn Tyr
 20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
 50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
 130 135 140

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

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

Ser Thr Tyr Ala Asp Asp Phe Glu Gly Arg Phe Val Phe Ser Met Asp
 180 185 190

Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu
 195 200 205

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ser Leu Tyr Asp Tyr Tyr
 210 215 220

Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Leu
 225 230 235 240

Gly Gly Gly Ser Gly Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 245 250 255

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 260 265 270

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 275 280 285

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 290 295 300

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 305 310 315 320

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 325 330 335

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
340 345 350

<210> 273
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> First Polypeptide Chain of DART F

<400> 273

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 Ser Phe Thr Ser Tyr
20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
50 55 60

Lys Asp 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 Glu His Tyr Gly Thr Ser Pro Phe Ala 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 Tyr Ile Thr
245 250 255

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

<210> 274

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Second and Fifth Polypeptide Chains of DART F

<400> 274

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 275
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<223> Third Polypeptide Chain of DART F

<400> 275

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 Ser Phe Thr Ser Tyr
20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
50 55 60

Lys Asp 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 Glu His Tyr Gly Thr Ser Pro Phe Ala 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 Tyr Ile Thr
245 250 255

Arg Glu 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 Val Met Thr
450 455 460

Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile
465 470 475 480

Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser Asp Ala Lys Thr Tyr
485 490 495

Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro Pro Glu Arg Leu Ile
500 505 510

Tyr Leu Val Ser Glu Leu Asp Ser Gly Val Pro Asp Arg Phe Ser Gly
515 520 525

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
530 535 540

Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Tyr
545 550 555 560

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
565 570 575

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
580 585 590

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
595 600 605

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
610 615 620

Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp
625 630 635 640

Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val Asp Lys Ser Thr Ser
645 650 655

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
660 665 670

Tyr Tyr Cys Ala Arg Glu His Tyr Gly Thr Ser Pro Phe Ala Tyr Trp
675 680 685

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
690 695 700

Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
705 710 715 720

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
725 730

<210> 276
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Fourth Polypeptide Chain of DART F

<400> 276

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140

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

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

Ser Thr Tyr Ala Asp Asp Phe Glu Gly Arg Phe Val Phe Ser Met Asp
180 185 190

Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu
195 200 205

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ser Leu Tyr Asp Tyr Tyr
210 215 220

Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
225 230 235 240

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

Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys
260 265 270

Glu

<210> 277
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> First Polypeptide Chain of DART G

<400> 277

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 Tyr Thr Gly Glu Ser Thr Tyr Ala Asp Asp Phe
 50 55 60

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

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

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

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225 230 235 240

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

Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Ala Lys Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly

<210> 278
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Second and Fifth Polypeptide Chain of DART G

<400> 278

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

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

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

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

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 279
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<223> Third Polypeptide Chain of DART G

<400> 279

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 Tyr Thr Gly Glu Ser Thr Tyr Ala Asp Asp Phe
50 55 60

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

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

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

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225 230 235 240

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

Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Glu Ile Val Leu
450 455 460

Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
465 470 475 480

Leu Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr Gly Met Ser Phe
485 490 495

Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
500 505 510

His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser Arg Phe Ser Gly
515 520 525

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
530 535 540

Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Ser Lys Glu Val Pro Tyr
545 550 555 560

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Ser Gly
565 570 575

Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
580 585 590

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
595 600 605

Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
610 615 620

Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp
625 630 635 640

Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val Asp Lys Ser Thr Ser
645 650 655

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
660 665 670

Tyr Tyr Cys Ala Arg Glu His Tyr Gly Thr Ser Pro Phe Ala Tyr Trp
675 680 685

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly Gly
690 695 700

Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
705 710 715 720

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
725 730

<210> 280
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> Fourth Polypeptide Chain of DART G

<400> 280

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140

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

Gly Gln Gly Leu Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser Glu
165 170 175

Thr Trp Leu Asp Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val Asp
180 185 190

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
195 200 205

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu His Tyr Gly Thr Ser Pro
210 215 220

Phe Ala Tyr Trp Gly Gln Gly Thr Leu 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
260 265 270

<210> 281
<211> 503
<212> PRT
<213> Artificial Sequence

<220>

<223> First Polypeptide Chain of DART H

<400> 281

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140

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

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

Ser Thr Tyr Ala Asp Asp Phe Glu Gly Arg Phe Val Phe Ser Met Asp
180 185 190

Thr Ser Ala Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu
195 200 205

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ser Leu Tyr Asp Tyr Tyr
210 215 220

Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
225 230 235 240

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

Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu
260 265 270

Lys Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
275 280 285

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

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
420 425 430

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
500

<210> 282
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> Second Polypeptide Chain of DART H

<400> 282

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly
115 120 125

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
130 135 140

Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Met Asn Trp Val Arg Gln Ala
145 150 155 160

Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser
165 170 175

Glu Thr Trp Leu Asp Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val
180 185 190

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

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu His Tyr Gly Thr Ser
210 215 220

Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
225 230 235 240

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

Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys
260 265 270

Glu

<210> 283
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Third Polypeptide Chain of DART H

<400> 283

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

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
 180 185 190

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

His Glu Ala Leu His Asn Arg Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro Gly Lys
 225

<210> 284
 <211> 563
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> First and Third Polypeptide Chains of DART 1

<400> 284

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 Ile 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 Leu
85 90 95

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

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

Pro Gly Arg Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe
130 135 140

Ser Asn Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
145 150 155 160

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala
165 170 175

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

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

Tyr Tyr Cys Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val
210 215 220

Thr Val Ser Ser Leu Gly Gly Gly Ser Gly Ala Ser Thr Lys Gly Pro
225 230 235 240

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
245 250 255

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
260 265 270

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
275 280 285

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
290 295 300

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
305 310 315 320

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
325 330 335

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
340 345 350

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
355 360 365

Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser
370 375 380

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
385 390 395 400

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
405 410 415

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
420 425 430

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
450 455 460

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
465 470 475 480

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
485 490 495

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
500 505 510

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
515 520 525

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
530 535 540

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
545 550 555 560

Ser Pro Gly

<210> 285

<211> 348

<212> PRT

<213> Artificial Sequence

<220>

<223> Second and Fourth Polypeptide Chains of DART 1

<400> 285

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 Ser Ser Asn Trp Pro Arg
85 90 95

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

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

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

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

Glu Trp Ile Gly Glu Ile Asn His Asn Gly Asn Thr Asn Ser Asn Pro
165 170 175

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

Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
195 200 205

Tyr Cys Ala Phe Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe Asp Pro
210 215 220

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

Gly Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
245 250 255

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
260 265 270

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
275 280 285

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 290 295 300

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 305 310 315 320

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 325 330 335

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 340 345

<210> 286
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> First Polypeptide Chain of BSAB A

<400> 286

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 Ser Phe Thr Ser Tyr
 20 25 30

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

Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp Gln Lys Phe
 50 55 60

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

Thr His Thr Cys Pro Glu 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 Thr
 355 360 365

Cys Glu 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

<210> 287
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Second Polypeptide Chain of BSAB A

<400> 287

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 Glu Ser Val Asp Asn Tyr
 20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 288

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Third Polypeptide Chain of BSAB A

<400> 288

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 Tyr Thr Gly Glu Ser Thr Tyr Ala Asp Asp Phe
50 55 60

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

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

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

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Arg
210 215 220

Lys Thr His Thr Cys Pro Arg Cys Pro Ala Pro Glu Ala Ala Gly Gly
225 230 235 240

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly

<210> 289
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fourth Polypeptide Chain of BSAB A

<400> 289

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

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

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

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

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 290
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> First and Third Polypeptide Chains of DART I

<400> 290

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 Ser Ser Val
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 His Tyr Ser Thr Pro Trp
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 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 Ser Phe
130 135 140

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

Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp
165 170 175

Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val 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 Ala Arg Glu His Tyr Gly Thr Ser Pro Phe Ala 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 Glu Ser Lys Tyr
260 265 270

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr
290 295 300

Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
305 310 315 320

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
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 Arg Leu Thr Val Asp Lys
 450 455 460

Ser Arg Trp Gln Glu 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 Leu Gly
 485 490 495

<210> 291
 <211> 271
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Second and Fourth Polypeptide Chains of DART I

<400> 291

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 Glu Ser Val Asp Asn Tyr
 20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
 50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
 130 135 140

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

Gly Gln Gly Leu Glu Trp Met Gly Asp Ile Asn Pro Asp Asn Gly Val
 165 170 175

Thr Ile Tyr Asn Gln Lys Phe Glu Gly Arg Val Thr Met Thr Thr Asp
 180 185 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ala Asp Tyr Phe Tyr Phe
 210 215 220

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Cys
 225 230 235 240

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

Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
 260 265 270

<210> 292
 <211> 566
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> First and Third Polypeptide Chains of DART J

<400> 292

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 Ser Ser Val
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 His Tyr Ser Thr Pro Trp
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 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 Ser Phe
130 135 140

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

Glu Trp Ile Gly Val Ile His Pro Ser Asp Ser Glu Thr Trp Leu Asp
165 170 175

Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Val 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 Ala Arg Glu His Tyr Gly Thr Ser Pro Phe Ala Tyr Trp
210 215 220

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

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

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
260 265 270

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
275 280 285

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
290 295 300

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
305 310 315 320

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
325 330 335

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
340 345 350

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
355 360 365

Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val
370 375 380

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
385 390 395 400

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
405 410 415

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
420 425 430

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
435 440 445

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
465 470 475 480

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
485 490 495

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
500 505 510

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
515 520 525

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
530 535 540

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
545 550 555 560

Leu Ser Leu Ser Leu Gly
565

<210> 293
<211> 350
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fourth Polypeptide Chains of DART J

<400> 293

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 Glu Ser Val Asp Asn Tyr
20 25 30

Gly Met Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile His Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ser
50 55 60

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

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

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

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

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
130 135 140

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

Gly Gln Gly Leu Glu Trp Met Gly Asp Ile Asn Pro Asp Asn Gly Val
165 170 175

Thr Ile Tyr Asn Gln Lys Phe Glu Gly Arg Val Thr Met Thr Thr Asp
180 185 190

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

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ala Asp Tyr Phe Tyr Phe
210 215 220

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Leu Gly Gly
225 230 235 240

Gly Ser Gly Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
245 250 255

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
260 265 270

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
275 280 285

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
290 295 300

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
305 310 315 320

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
325 330 335

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
340 345 350

<210> 294
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of hLAG-3 mAb 6 VH1

<400> 294

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

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

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

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

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

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

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

Thr Leu Thr Val Ser Ser
115

<210> 295
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> VH Domain of hLAG-3 mAb 6 VH2

<400> 295

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 Asp Tyr
20 25 30

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

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

Glu 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 Glu Ala Asp Tyr Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 296
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL Domain of hLAG-3 mAb 6 VL1

<400> 296

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 Ser Ser Val
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 His Tyr Ser Thr Pro Trp
85 90 95

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

<210> 297
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> VL Domain of hLAG-3 mAb 6 VL2

<400> 297

Asp Ile Val 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 Ser Ser Val
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 Asp 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 Val Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
85 90 95

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

<210> 298

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRL1 of the VL Domain of hLAG-3 mAb 6 VL1 and VL2

<400> 298

Arg Ala Ser Gln Asp Val Ser Ser Val Val Ala
1 5 10