

SEQUENCE LISTING

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<120> LAG-3-Binding Molecules and Methods of Use Thereof

<130> 1301.0121PCT

<150> US 62/255,094
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<160> 140

<170> PatentIn version 3.5

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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

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 <213> Homo sapiens

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 <223> IgG2 Fc Region

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 <223> Xaa216 is Lysine (K) or Absent

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

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<213> Homo sapiens

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<223> IgG3 Fc

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<400> 3

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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
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55

60

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

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

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

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

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

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

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

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<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

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<223> LAG-3

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Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
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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> 6
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 <213> Mus musculus

<220>
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 <223> LAG-3 mAb 1 VH

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Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
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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> 7

<211> 360

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<223> Polynucleotide Encoding LAG-3 mAb 1 VH

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tcctgcaagg cttctgggta taccttcaga aactatggaa tgaactgggt gaagcaggct 120

ccaggaaagg ttttaaagtg gatgggctgg ataaacacct aactggaga gtcaacatat 180

gctgatgact tcgagggacg gtttgccttc tctttgggaa cctctgccag cactgcctat 240

ttgcagatca acatcctcaa aaatgaggac acggctacat atttctgtgc aagagaatcc 300

ctctatgatt actattctat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360

<210> 8

<211> 5

<212> PRT

<213> Mus musculus

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<221> MISC_FEATURE

<222> (1)..(5)

<223> LAG-3 mAb 1 VH CDR 1

<400> 8

Asn Tyr Gly Met Asn
1 5

<210> 9

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> LAG-3 mAb 1 VH CDR2

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

Gly

<210> 10

<211> 11

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(11)

<223> LAG-3 mAb 1 VH CDR3

<400> 10

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

<210> 11

<211> 112

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(112)

<223> LAG-3 mAb 1 VL

<400> 11

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
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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> 12
 <211> 336
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<220>
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 ttgttacaga ggccaggcca gtctccagag cgcctaattct atctgggtgtc tgaactggac 180
 tctggagtcc ctgacaggtt cactggcagt ggatcagggg cagatttcac actgaaaatc 240
 agcagagtgg aggctgagga tttgggagtt tattattgct ggcaagggtac acattttccg 300
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<210> 13
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 <212> PRT
 <213> Mus musculus

<220>
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 <223> LAG-3 mAb 1 VL CDR1

<400> 13
 Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn
 1 5 10 15

<210> 14
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE

<222> (1)..(7)
<223> LAG-3 mAb 1 VL CDR2

<400> 14

Leu Val Ser Glu Leu Asp Ser
1 5

<210> 15
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> LAG-3 mAb 1 VL CDR3

<400> 15

Trp Gln Gly Thr His Phe Pro Tyr Thr
1 5

<210> 16
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> hLAG-3 mAb 1 VH1

<400> 16

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> 17
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hLAG-3 mAb 1 VH1

<400> 17
 caggtgcaac tggttcaatc cggcgccgag gtgaaaaagc ctggcgccctc cgtgaaagtg 60
 tcctgtaagg catctgggta tacgttcaca aattatggta tgaactgggt gcgacaggca 120
 ccagggcagg gactggaatg gatgggggtg atcaatactt atacaggcga gagtacttat 180
 gctgacgatt tcgagggcag atttgtcttc tccatggaca ccagcgctag taccgcttat 240
 ctccagatta gttctctcaa ggcggaggac acagctgttt attattgtgc ccgcgagagt 300
 ttgtatgact actatagcat ggattactgg ggacaaggta caaccgtgac agtgagttcc 360

<210> 18
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hLAG-3 mAb 1 VH2

<400> 18
 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> 19
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Polynucleotide Encoding hLAG-3 mAb 1 VH2

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tcctgtaagg catctgggta tacgttcaca aattatggta tgaactgggt gcgacaggca      120
ccagggcagg gactggaatg gatgggggtg atcaatactt atacaggcga gagtacttat      180
gctgacgatt tcgagggcag atttgtcttc tccatggaca ccagcgctag taccgcttat      240
ctccagatta gttctctcaa ggcggaggac acagctgttt atttctgtgc ccgcgagagt      300
ttgtatgact actatagcat ggattactgg ggacaaggta caaccgtgac agtgagttcc      360
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<210> 20

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> hLAG-3 mAb 1 VL1

<400> 20

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1           5           10          15
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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
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Thr His Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105          110
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<210> 21

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide Encoding hLAG-3 mAb 1 VL1

<400> 21

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gatatcgta tgactcagac accactgtca ctgagtgtga cccaggtca gcccgctagt      60
atttcctgta aatcatccca gtcctcctg catagcgatg gaaagaccta tttgaactgg      120
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cttctgcaga aaccaggcca aagtccagag agattgatct acctcgtttc agaactcgac	180
agtggagtgc ccgatcgctt ctcaggggtcc ggctctggga ctgattttac tctcaagatc	240
tcaagagtgg aggccgagga cgtcgggggtt tactactggtt ggcaggggtac ccacttcctt	300
tatacatttg gcggaggcac aaaagtggag attaaa	336

<210> 22
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hLAG-3 mAb 1 VL2

<400> 22

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> 23
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hLAG-3 mAb 1 VL2

<400> 23

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atttcctgta aatcatccca gtccctcctg catagcgatg gaaagacctt tttgaactgg	120
cttctgcaga gaccaggcca aagtccagag agattgatct acctcgtttc agaactcgac	180
agtggagtgc ccgatcgctt ctcaggggtcc ggctctggga ctgattttac tctcaagatc	240
tcaagagtgg aggccgagga cgtcgggggtt tactactggtt ggcaggggtac ccacttcctt	300
tatacatttg gcggaggcac aaaagtggag attaaa	336

<210> 24
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hLAG-3 mAb 1 VL3

<400> 24

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> 25
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hLAG-3 mAb 1 VL3

<400> 25

gatatcgtaa tgactcagac accactgtca ctgagtgtga ccccagggtca gcccgctagt	60
atttcctgta aatcatccca gtcctcctctg catagcgatg gaaagaccta tttgaactgg	120
cttctgcaga aaccaggcca accgccagag agattgatct acctcgtttc agaactcgac	180
agtggagtgc ccgatcgctt ctgagggtcc ggctctggga ctgattttac tctcaagatc	240
tcaagagtgg aggccgagga cgtcgggggtt tactactggtt ggcagggtac ccacttcctt	300
tatacatttg gcggaggcac aaaagtggag attaaa	336

<210> 26
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>

<223> hLAG-3 mAb 1 VL4

<400> 26

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> 27

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide Encoding hLAG-3 mAb 1 VL4

<400> 27

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atttcctgta aatcatccca gtccctcctg catagcgatg caaagacctt tttgaactgg	120
cttctgcaga aaccaggcca accgccagag agattgatct acctcgtttc agaactcgac	180
agtggagtgc ccgatcgctt ctcaggggtcc ggctctggga ctgattttac tctcaagatc	240
tcaagagtgg aggccgagga cgtcgggggt tactactggt ggcaggggtac ccacttcctt	300
tatacatttg gcggaggcac aaaagtgag attaaa	336

<210> 28

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> hLAG-3 mAb 1 VL4 CDR1

<400> 28

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

<210> 29
 <211> 121
 <212> PRT
 <213> Mus musculus

<220>
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 <222> (1)..(121)
 <223> LAG-3 mAb 2 VH

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Glu Val 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 Thr Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Asn Ile His Trp Leu Arg Gln Ser His Gly Glu Ser Leu Glu Trp Ile
 35 40 45

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

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

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

Ala Arg Trp His Arg Asn Tyr Phe Gly Pro Trp Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Pro Val Thr Val Ser Ala
 115 120

<210> 30
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 <212> DNA
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<220>
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 tcctgcaaga cttctggata cacatttact gactacaaca tacactgggtt gaggcagagc 120
 catggagaga gccttgagtg gattggatat atttatcctt acagtgggtga tattggatac 180
 aaccagaagt tcaagaacag ggccacattg actgtagaca attcctccag cacagcctac 240
 atggatctcc gcagcctgac atctgaagac tctgcagtct ttactgtgc aagatggcac 300
 aggaactact ttggcccctg gtttgcttac tggggccaag ggactccggt cactgtctct 360

<210> 31
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<212> PRT
<213> Mus musculus

<220>
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<223> LAG-3 mAb 2 VH CDR 1

<400> 31

Asp Tyr Asn Ile His
1 5

<210> 32
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> LAG-3 mAb 2 VH CDR2

<400> 32

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

Asn

<210> 33
<211> 12
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(12)
<223> LAG-3 mAb 2 VH CDR3

<400> 33

Trp His Arg Asn Tyr Phe Gly Pro Trp Phe Ala Tyr
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<210> 34
<211> 111
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<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> LAG-3 mAb 2 VL

<400> 34

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1 5 10 15

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

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

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

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

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

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

<210> 35

<211> 333

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<223> Polynucleotide Encoding LAG-3 mAb 2 VL

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caacagaaac caggacagcc acccaaactc ctcatattatg ttgtatccaa tctagaatct	180
gggatcccag ccaggttttag tggcagtggg tctgggacag acttcaccct caacatccat	240
cctgtggagg aggaggatgc tgcaacctat tactgtcagc aaagtagtga ggatccgctc	300
acgttcggtg ctgggaccaa gctggagctg aaa	333

<210> 36

<211> 15

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(15)

<223> LAG-3 mAb 2 VL CDR1

<400> 36

Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Glu Ser Tyr Met Asn
1 5 10 15

<210> 37
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> LAG-3 mAb 2 VL CDR2

<400> 37

Val Val Ser Asn Leu Glu Ser
1 5

<210> 38
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> LAG-3 mAb 2 VL CDR3

<400> 38

Gln Gln Ser Ser Glu Asp Pro Leu Thr
1 5

<210> 39
<211> 121
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(121)
<223> LAG-3 mAb 3 VH

<400> 39

Glu Val Arg 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

Asn Ile His Trp Val Arg Gln Ser His Gly Gln Ser Leu Glu Trp Ile
35 40 45

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

Lys Thr Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Asn Thr Ala Tyr
Page 20

65		70		75		80
Met	Glu	Leu	Arg	Ser	Leu	Ala
				85		
					90	
						95
Thr	Arg	Trp	Ser	Arg	Asn	Tyr
			100			
					105	
						110
Gln	Gly	Thr	Leu	Val	Thr	Val
		115				
					120	

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<220>
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catggacaga gccttgagtg gattggatat atttattcctt ataatggtga tactggctac	180
aaccagaagt tcaagaccaa ggccacattg actgtagaca attcctccaa cacagcctac	240
atggaactcc gcagcctggc atctgaagac tctgcagtct attactgtac aagatggagc	300
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gca	363

<210> 41
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 <213> Mus musculus

<220>
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 <223> LAG-3 mAb 3 VH CDR 1

<400> 41

Asp	Tyr	Asn	Ile	His
1				5

<210> 42
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(17)
 <223> LAG-3 mAb 3 VH CDR2

<400> 42

Tyr Ile Tyr Pro Tyr Asn Gly Asp Thr Gly Tyr Asn Gln Lys Phe Lys
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Thr

<210> 43

<211> 12

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(12)

<223> LAG-3 mAb 3 VH CDR3

<400> 43

Trp Ser Arg Asn Tyr Phe Gly Pro Trp Phe Ala Tyr
1 5 10

<210> 44

<211> 111

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(111)

<223> LAG-3 mAb 3 VL

<400> 44

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

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

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

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

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

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

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

<210> 45
<211> 333
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
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caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa tctagaatct 180
gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatgc tgcaacctat tactgtcagc aaagtagtga ggatccgctc 300
acgttcggtg ctgggaccaa gctggagctg aaa 333

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<212> PRT
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<222> (1)..(15)
<223> LAG-3 mAb 3 VL CDR1

<400> 46
Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
1 5 10 15

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

<220>
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<222> (1)..(7)
<223> LAG-3 mAb 3 VL CDR2

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Ala Ala Ser Asn Leu Glu Ser
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<210> 48
<211> 9
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<220>
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<222> (1)..(9)

<223> LAG-3 mAb 3 VL CDR3

<400> 48

Gln Gln Ser Ser Glu Asp Pro Leu Thr
1 5

<210> 49

<211> 121

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(121)

<223> LAG-3 mAb 4 VH

<400> 49

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 50

<211> 363

<212> DNA

<213> Mus musculus

<220>

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<223> Polynucleotide Encoding LAG-3 mAb 4 VH

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tcctgcaaga cttctggata cactttcact gactacaaca tacactgggt gaagcagagc 120

catggaaaga gccttgagtg gattggatat atttatacctt acaatggtga tgctggctac 180
aaccagaact tcaagaccaa ggccacattg actgtagaca attcctccag cacagcctac 240
atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagatggaac 300
atgaactact ttggcccctg gtttgcttac tggggccaag ggactctggt cactgtctct 360
gcg 363

<210> 51
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> LAG-3 mAb 4 VH CDR 1

<400> 51

Asp Tyr Asn Ile His
1 5

<210> 52
<211> 17
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(17)
<223> LAG-3 mAb 4 VH CDR2

<400> 52

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

Thr

<210> 53
<211> 12
<212> PRT
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<220>
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<222> (1)..(12)
<223> LAG-3 mAb 4 VH CDR3

<400> 53

Trp Asn Met Asn Tyr Phe Gly Pro Trp Phe Ala Tyr
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<210> 54
<211> 111

<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(111)
<223> LAG-3 mAb 4 VL

<400> 54

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 Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

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

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

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

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

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

<210> 55
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atctcctgca aggccagcca aagtgttgat tatgatggtg ttacttatat caactggtac 120
caacagaaac caggacagcc acccaaactc ctcatctttg ctgcatccaa tctagaatct 180
gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240
cctgtggagg aggaggatgc tgcaacctat tactgtcagc aaagtaatga ggatccgctc 300
acgttcggtg ctgggaccaa gctggagctg aaa 333

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

<220>
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<222> (1)..(15)
<223> LAG-3 mAb 4 VL CDR1

<400> 56

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

<210> 57
<211> 7
<212> PRT
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<222> (1)..(7)
<223> LAG-3 mAb 4 VL CDR2

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Ala Ala Ser Asn Leu Glu Ser
1 5

<210> 58
<211> 9
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(9)
<223> LAG-3 mAb 4 VL CDR3

<400> 58

Gln Gln Ser Asn Glu Asp Pro Leu Thr
1 5

<210> 59
<211> 121
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(121)
<223> LAG-3 mAb 5 VH

<400> 59

Glu Val 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

Asn Ile His Trp Val Lys Gln Ser Pro Gly Lys Ser Leu Glu Trp Ile
Page 27

35

40

45

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

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

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

Ala Arg Trp His Arg Asn Tyr Phe Gly Pro Trp Phe Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala
 115 120

<210> 60
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 <212> DNA
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 tcctgcaaag cttctggata cacatttact gactacaaca tacactgggt gaagcagagc 120
 cctggaaaga gccttgaatg gattggatat atttatcctt acagtgggtga ttttggatac 180
 aaccagaagt tcaagagcaa ggccacattg actgtagaca attcctccag cacagcctac 240
 atggatctcc gcagcctgac atctgaggac tctgcagtct tttactgtgc aagatggcac 300
 aggaactact ttggcccctg gtttgcttac tggggccaag ggactctggt cactgtctct 360
 gca 363

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 <213> Mus musculus

<220>
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 <223> LAG-3 mAb 5 VH CDR 1

<400> 61

Asp Tyr Asn Ile His
 1 5

<210> 62
 <211> 17

<212> PRT
<213> Mus musculus

<220>
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<223> LAG-3 mAb 5 VH CDR2

<400> 62

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

Ser

<210> 63
<211> 12
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(12)
<223> LAG-3 mAb 5 VH CDR3

<400> 63

Trp His Arg Asn Tyr Phe Gly Pro Trp Phe Ala Tyr
1 5 10

<210> 64
<211> 111
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<213> Mus musculus

<220>
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<222> (1)..(111)
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<400> 64

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 Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

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

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

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

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<220>
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<222> (1)..(9)
<223> LAG-3 mAb 5 VL CDR3

<400> 68

Gln Gln Ser Ser Glu Asp Pro Leu Thr
1 5

<210> 69
<211> 118
<212> PRT
<213> Mus musculus

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<223> LAG-3 mAb 6 VH

<400> 69

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

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<212> DNA
<213> Mus musculus

<220>

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 catggagaga gccttgagtg gattggagat attaatcctg acaatgggtgt tactatctac 180
 aaccagaagt ttgagggcaa ggccacactg actgtagaca agtcctccag tacagcctac 240
 atggagctcc gcagcctgac atctgaggac actgcagtct attactgtgc aagagaggcg 300
 gattacttct actttgacta ctggggccaa ggcaccactc tcacagtctc ctca 354

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 <212> PRT
 <213> Mus musculus

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

<400> 71

Asp Tyr Asn Met Asp
 1 5

<210> 72
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
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 <222> (1)..(17)
 <223> LAG-3 mAb 6 VH CDR2

<400> 72

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

Gly

<210> 73
 <211> 9
 <212> PRT
 <213> Mus musculus

<220>
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 <222> (1)..(9)
 <223> LAG-3 mAb 6 VH CDR3

<400> 73

Glu Ala Asp Tyr Phe Tyr Phe Asp Tyr
1 5

<210> 74
<211> 107
<212> PRT
<213> Mus musculus

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

<400> 74

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> 75
<211> 321
<212> DNA
<213> Mus musculus

<220>
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atcacctgca aggccagtca ggatgtgagt tctgttgtag cctggtatca acagaaacca	120
ggacaatctc ctaaattact gattttttcg gcacacctacc ggtacactgg agtcacctgat	180
cgcttcactg gcagtggatc tgggacggat ttcactttca ccatcagcag tgtgcaggct	240
gcagacctgg cagtttatta ctgtcagcaa cattatagta ctccgtggac gttcggtgga	300
ggcaccaagc tggaaatcaa a	321

<210> 76
<211> 11
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(11)
<223> LAG-3 mAb 6 VL CDR1

<400> 76

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

<210> 77
<211> 7
<212> PRT
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<220>
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<223> LAG-3 mAb 6 VL CDR2

<400> 77

Ser Ala Ser Tyr Arg Tyr Thr
1 5

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

<220>
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<222> (1)..(9)
<223> LAG-3 mAb 6 VL CDR3

<400> 78

Gln Gln His Tyr Ser Thr Pro Trp Thr
1 5

<210> 79
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> hLAG-3 mAb 6 VH-1

<400> 79

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> 80
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<212> DNA
<213> Artificial Sequence

<220>
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tcctgcaagg ccagcggcta caccttcacc gactacaaca tggactgggt ccgacaggcc 120
ccaggacagg gcctggaatg gatggggcgac atcaaccccg acaacggcgt gaccatctac 180
aaccagaaat tcgagggcag agtgaccatg accaccgaca ccagcaccag caccgcctac 240
atggaactgc ggtccctgcg gagcgacgac accgccgtgt actactgcgc cagagaggcc 300
gactacttct acttcgacta ctggggccag ggcaccaccc tgaccgtgtc ctcc 354

<210> 81
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> hLAG-3 mAb 6 VH-2

<400> 81

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> 82
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hLAG-3 mAb 6 VH-2

<400> 82
gaggtccagc tgggtggaatc tggcgggcgga ctggtcaagc ctggcggcag cctgagactg 60
agctgcgctg ccagcggctt caccttcagc gactacaaca tggactgggt ccgacaggcc 120
cctggcaagg gcctggaatg ggtgtccgac atcaaccccg acaacggcgt gaccatctac 180
aaccagaagt tcgagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagagaggcc 300
gactacttct acttcgacta ctggggccag ggcaccaccc tgaccgtgtc ctcc 354

<210> 83
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> hLAG-3 mAb 6 VL-1

<400> 83

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> 84
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hLAG-3 mAb 6 VL-1

<400> 84
gacatccaga tgaccagag cccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca ggatgtgtcc agcgtggtgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacagc gccagctacc ggtacacagg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag cactacagca ccccttgac cttcggcgga 300
ggcaccaagc tggaatcaa g 321

<210> 85
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> hLAG-3 mAb 6 VL-2

<400> 85

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> 86
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hLAG-3 mAb 6 VL-2

<400> 86
gacatcgtga tgaccagag cccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca ggatgtgtcc agcgtggtgg cctggatatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacagc gccagctacc ggtacacagg cgtgcccgat 180
agattcagcg gcagcggctc cggcaccgac ttcaccttca ccatcagcag cctgcagccc 240
gaggacatcg ccgtttacta ctgccagcag cactacagca cccctggac cttcggcgga 300
ggcaccaagc tggaaatcaa g 321

<210> 87
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hLAG-3 mAb 6 VL-1/VL-2 CDRL1

<400> 87
Arg Ala Ser Gln Asp Val Ser Ser Val Val Ala
1 5 10

<210> 88
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 1

<400> 88
Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 89
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Cys Linker 2

<400> 89
Gly Gly Cys Gly Gly Gly
1 5

<210> 90
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD Linker

<400> 90

Gly Gly Gly Ser
1

<210> 91
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 91

Leu Gly Gly Gly Ser Gly
1 5

<210> 92
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 92

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

<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 93

Ala Ser Thr Lys Gly
1 5

<210> 94
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 94

Leu Glu Pro Lys Ser Ser
1 5

<210> 95
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 95

Ala Pro Ser Ser Ser
1 5

<210> 96
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting Domain

<400> 96

Gly Val Glu Pro Lys Ser Cys
1 5

<210> 97
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting Domain

<400> 97

Val Glu Pro Lys Ser Cys
1 5

<210> 98
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting Domain

<400> 98

Ala Glu Pro Lys Ser Cys
1 5

<210> 99
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Heterodimer-Promoting Domain

<400> 99

Gly Phe Asn Arg Gly Glu Cys
1 5

<210> 100

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Heterodimer-Promoting Domain

<400> 100

Phe Asn Arg Gly Glu Cys
1 5

<210> 101

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> E-Coil

<400> 101

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> 102

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> K-Coil

<400> 102

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> 103

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> modified E-Coil

<400> 103

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> 104
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> modified K-Coil

<400> 104

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> 105
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> ABD

<400> 105

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> 106
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> deimm ABD

<400> 106

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> 107
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> deimm ABD

<400> 107

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> 108
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> deimm ABD

<400> 108

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> 109
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge Linker

<400> 109

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

<210> 110
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 110

Ala Pro Ser Ser Ser Pro Met Glu
1 5

<210> 111
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Cys Linker

<400> 111

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

<210> 112
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 112

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

<210> 113
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 113

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

<210> 114
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> IgG1 Hinge

<400> 114

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

<210> 115
<211> 12
<212> PRT
<213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(12)
 <223> IgG2 Hinge
 <400> 115
 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
 1 5 10

<210> 116
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(12)
 <223> IgG4 Hinge
 <400> 116
 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
 1 5 10

<210> 117
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(12)
 <223> IgG4 Hinge (S228P)
 <400> 117
 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
 1 5 10

<210> 118
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(107)
 <223> LC kappa
 <400> 118
 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
 Page 45

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> 119
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(104)
 <223> LC lambda

<400> 119

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> 120
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

<222> (1)..(98)

<223> IgG1 CH1

<400> 120

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

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

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

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

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

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

Lys Val

<210> 121

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(98)

<223> IgG2 CH1

<400> 121

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> 122
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(98)
<223> IgG4 CH1

<400> 122

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> 123
<211> 217
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(217)
<223> IgG1 (AA)

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> Xaa217 is a lysine (K) or is absent

<400> 123

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> 124
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(217)
 <223> IgG1 Fc (AA/YTE)

<220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa217 is a lysine (K) or is absent

<400> 124

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> 125

<211> 217

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(217)

<223> IgG4 Fc (YTE)

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> Xaa217 is a lysine (K) or is absent

<400> 125

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> 126

<211> 217

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(217)

<223> Knob Fc domain

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> Xaa217 is a lysine (K) or is absent

<400> 126

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Xaa

210

215

<210> 127
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(217)
 <223> Hole Fc

<220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa217 is a lysine (K) or is absent

<400> 127

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> 128
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(217)
 <223> IgG1 Fc universal

<220>
 <221> MISC_FEATURE
 <222> (4)..(5)
 <223> Xaa4(X1) and Xaa5(X2) are both L (wild type), or are both A (decreased FcR binding)

<220>
 <221> MISC_FEATURE
 <222> (22)..(26)
 <223> Xaa22(X3), Xaa24(X4), and Xaa26(X5) are respectively M, S and T (wild type), or Y, T and E (extended half-life)

<220>
 <221> MISC_FEATURE
 <222> (136)..(138)
 <223> Xaa136(X6), and Xaa138(X7) are respectively T and L (wild type) or W and L (knob), or are S and A (hole)

<220>
 <221> MISC_FEATURE
 <222> (177)..(177)
 <223> Xaa177(X8) is Y (wild type) when Xaa136(X6) is T and Xaa138(X7) is L; Xaa177(X8) is Y (knob) when Xaa136(X6) is W and Xaa138(X7) is L; Xaa177 (X8) is V (hole) when Xaa136(X6) is S and Xaa138(X7) is A

<220>
 <221> MISC_FEATURE
 <222> (204)..(205)
 <223> Xaa204(X9) and Xaa205(X10) respectively are N and H (wild type), or are N and R (no protein A binding), or are A and K (no protein A binding)

<220>
 <221> MISC_FEATURE
 <222> (217)..(217)
 <223> Xaa217(X11) is K or is absent

<400> 128

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> 129
<211> 120
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(120)
<223> LAG-3 mAb A VH

<400> 129

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> 130
<211> 107
<212> PRT
<213> Mus musculus

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

<400> 130

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> 131

<211> 113
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(113)
 <223> PD-1 mAb 1 VH

<400> 131

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> 132
 <211> 107
 <212> PRT
 <213> Mus musculus

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

<400> 132

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> 133
<211> 120
<212> PRT
<213> Mus musculus

<400> 133

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> 134
<211> 111
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> PD-1 mAb 2 VL

<400> 134

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> 135
<211> 121
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(121)
<223> PD-1 mAb 3 VH

<400> 135

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

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

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

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

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

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

Ala Arg Trp Arg Asp Ser Ser Gly Tyr His Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 136
<211> 111
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> PD-1 mAb 3 VL

<400> 136

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

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

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 137
<211> 117
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(117)
<223> PD-1 mAb 4 VH

<400> 137

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

Ser Val Lys Ile 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 Gln Trp Met
35 40 45

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

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

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

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

Val Thr Val Ser Ser
115

<210> 138
<211> 106
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(106)
<223> PD-1 mAb 4 VL

<400> 138

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

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

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

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

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

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

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

<210> 139
<211> 330
<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(330)

<223> IgG1 entire constant region (AA)

<220>

<221> MISC_FEATURE

<222> (330)..(330)

<223> Xaa330 is a lysine (K) or is absent

<400> 139

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
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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 Xaa
 325 330

<210> 140
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(327)
 <223> IgG4 entire constant region (P)

<220>
 <221> MISC_FEATURE
 <222> (327)..(327)
 <223> Xaa327 is a lysine (K) or is absent

<400> 140

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 Xaa
 325