

1301_0121PCT_Sequence_Listing_ST25
SEQUENCE LISTING

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

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

<130> 1301.0121PCT

<150> US 62/255,094

<151> 2015-11-13

<150> US 62/172,277

<151> 2015-06-08

<160> 140

<170> PatentIn version 3.5

<210> 1

<211> 217

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(217)

<223> IgG1 Fc Region

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> X is Lysine (K) or 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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25
215

210

<210> 2
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(216)
<223> IgG2 Fc Region

<220>
<221> MISC_FEATURE
<222> (216)..(216)
<223> X is Lysine (K) or 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

1301_0121PCT_Sequence_Listing_ST25

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>
 <221> MISC_FEATURE
 <222> (1)..(217)
 <223> IgG3 Fc

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

<400> 3

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

1301_0121PCT_Sequence_Listing_ST25

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	Gln
			45
Phe	Lys	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
	65		
Thr	Phe	Arg	Val
	70		
Val	Val	Ser	Val
		75	
Leu	Thr	Val	Leu
			80
His	Gln	Asp	Trp
			85
Leu	Asn	Gly	Lys
			90
Glu	Tyr	Lys	Cys
			95
Lys	Val	Ser	Asn
			100
Lys	Gly	Gln	Ala
			105
Thr	Ile	Ser	Lys
			110
Thr	Lys	Glu	Pro
			115
Glu	Pro	Gln	Val
			120
Tyr	Thr	Leu	Pro
			125
Ser	Arg	Glu	Glu
			130
Met	Thr	Lys	Gly
			135
Phe	Tyr	Pro	Asn
			140
Asn	Gln	Pro	Glu
			145
Asn	Ser	Gly	Gln
			150
Trp	Glu	Ser	Ser
			155
Leu	Thr	Val	Asp
			160
Lys	Arg	Trp	Gln
			165
Gln	Gln	Gly	Asn
			170
Ile	Thr	Phe	Phe
			175
Leu	Ser	Asp	Ser
			180
Leu	Thr	Val	Asp
			185
Lys	Ser	Arg	Trp
			190
Gln	Gln	Gly	Asn
			195
Ile	Thr	Phe	Arg
			200
Gln	Thr	Phe	Arg
			205
Gln	Thr	Phe	Arg
			210
Gln	Thr	Phe	Arg
			215
Gln	Thr	Phe	Arg
			220
Gln	Thr	Phe	Arg
			225
Gln	Thr	Phe	Arg
			230
Gln	Thr	Phe	Arg
			235
Gln	Thr	Phe	Arg
			240
Gln	Thr	Phe	Arg
			245
Gln	Thr	Phe	Arg
			250
Gln	Thr	Phe	Arg
			255
Gln	Thr	Phe	Arg
			260
Gln	Thr	Phe	Arg
			265
Gln	Thr	Phe	Arg
			270
Gln	Thr	Phe	Arg
			275
Gln	Thr	Phe	Arg
			280
Gln	Thr	Phe	Arg
			285
Gln	Thr	Phe	Arg
			290
Gln	Thr	Phe	Arg
			295
Gln	Thr	Phe	Arg
			300
Gln	Thr	Phe	Arg
			305
Gln	Thr	Phe	Arg
			310
Gln	Thr	Phe	Arg
			315
Gln	Thr	Phe	Arg
			320
Gln	Thr	Phe	Arg
			325
Gln	Thr	Phe	Arg
			330
Gln	Thr	Phe	Arg
			335
Gln	Thr	Phe	Arg
			340
Gln	Thr	Phe	Arg
			345
Gln	Thr	Phe	Arg
			350
Gln	Thr	Phe	Arg
			355
Gln	Thr	Phe	Arg
			360
Gln	Thr	Phe	Arg
			365
Gln	Thr	Phe	Arg
			370
Gln	Thr	Phe	Arg
			375
Gln	Thr	Phe	Arg
			380
Gln	Thr	Phe	Arg
			385
Gln	Thr	Phe	Arg
			390
Gln	Thr	Phe	Arg
			395
Gln	Thr	Phe	Arg
			400
Gln	Thr	Phe	Arg
			405
Gln	Thr	Phe	Arg
			410
Gln	Thr	Phe	Arg
			415
Gln	Thr	Phe	Arg
			420
Gln	Thr	Phe	Arg
			425
Gln	Thr	Phe	Arg
			430
Gln	Thr	Phe	Arg
			435
Gln	Thr	Phe	Arg
			440
Gln	Thr	Phe	Arg
			445
Gln	Thr	Phe	Arg
			450
Gln	Thr	Phe	Arg
			455
Gln	Thr	Phe	Arg
			460
Gln	Thr	Phe	Arg
			465
Gln	Thr	Phe	Arg
			470
Gln	Thr	Phe	Arg
			475
Gln	Thr	Phe	Arg
			480
Gln	Thr	Phe	Arg
			485
Gln	Thr	Phe	Arg
			490
Gln	Thr	Phe	Arg
			495
Gln	Thr	Phe	Arg
			500
Gln	Thr	Phe	Arg
			505
Gln	Thr	Phe	Arg
			510
Gln	Thr	Phe	Arg
			515
Gln	Thr	Phe	Arg
			520
Gln	Thr	Phe	Arg
			525
Gln	Thr	Phe	Arg
			530
Gln	Thr	Phe	Arg
			535
Gln	Thr	Phe	Arg
			540
Gln	Thr	Phe	Arg
			545
Gln	Thr	Phe	Arg
			550
Gln	Thr	Phe	Arg
			555
Gln	Thr	Phe	Arg
			560
Gln	Thr	Phe	Arg
			565
Gln	Thr	Phe	Arg
			570
Gln	Thr	Phe	Arg
			575
Gln	Thr	Phe	Arg
			580
Gln	Thr	Phe	Arg
			585
Gln	Thr	Phe	Arg
			590
Gln	Thr	Phe	Arg
			595
Gln	Thr	Phe	Arg
			600
Gln	Thr	Phe	Arg
			605
Gln	Thr	Phe	Arg
			610
Gln	Thr	Phe	Arg
			615
Gln	Thr	Phe	Arg
			620
Gln	Thr	Phe	Arg
			625
Gln	Thr	Phe	Arg
			630
Gln	Thr	Phe	Arg
			635
Gln	Thr	Phe	Arg
			640
Gln	Thr	Phe	Arg
			645
Gln	Thr	Phe	Arg
			650
Gln	Thr	Phe	Arg
			655
Gln	Thr	Phe	Arg
			660
Gln	Thr	Phe	Arg
			665
Gln	Thr	Phe	Arg
			670
Gln	Thr	Phe	Arg
			675
Gln	Thr	Phe	Arg
			680
Gln	Thr	Phe	Arg
			685
Gln	Thr	Phe	Arg
			690
Gln	Thr	Phe	Arg
			695
Gln	Thr	Phe	Arg
			700
Gln	Thr	Phe	Arg
			705
Gln	Thr	Phe	Arg
			710
Gln	Thr	Phe	Arg
			715
Gln	Thr	Phe	Arg
			720
Gln	Thr	Phe	Arg
			725
Gln	Thr	Phe	Arg
			730
Gln	Thr	Phe	Arg
			735
Gln	Thr	Phe	Arg
			740
Gln	Thr	Phe	Arg
			745
Gln	Thr	Phe	Arg
			750
Gln	Thr	Phe	Arg
			755
Gln	Thr	Phe	Arg
			760
Gln	Thr	Phe	Arg
			765
Gln	Thr	Phe	Arg
			770
Gln	Thr	Phe	Arg
			775
Gln	Thr	Phe	Arg
			780
Gln	Thr	Phe	Arg
			785
Gln	Thr	Phe	Arg
			790
Gln	Thr	Phe	Arg
			795
Gln	Thr	Phe	Arg
			800
Gln	Thr	Phe	Arg
			805
Gln	Thr	Phe	Arg
			810
Gln	Thr	Phe	Arg
			815
Gln	Thr	Phe	Arg
			820
Gln	Thr	Phe	Arg
			825
Gln	Thr	Phe	Arg
			830
Gln	Thr	Phe	Arg
			835
Gln	Thr	Phe	Arg
			840
Gln	Thr	Phe	Arg
			845
Gln	Thr	Phe	Arg
			850
Gln	Thr	Phe	Arg
			855
Gln	Thr	Phe	Arg
			860
Gln	Thr	Phe	Arg
			865
Gln	Thr	Phe	Arg
			870
Gln	Thr	Phe	Arg
			875
Gln	Thr	Phe	Arg
			880
Gln	Thr	Phe	Arg
			885
Gln	Thr	Phe	Arg
			890
Gln	Thr	Phe	Arg
			895
Gln	Thr	Phe	Arg
			900
Gln	Thr	Phe	Arg
			905
Gln	Thr	Phe	Arg
			910
Gln	Thr	Phe	Arg
			915
Gln	Thr	Phe	Arg
			920
Gln	Thr	Phe	Arg
			925
Gln	Thr	Phe	Arg
			930
Gln	Thr	Phe	Arg
			935

1301_0121PCT_Sequence_Listing_ST25

195

200

205

Lys Ser Leu Ser Leu Ser Pro Gly Xaa
210 215

<210> 4
<211> 217
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(217)
<223> IgG4 Fc Region

<220>
<221> MISC_FEATURE
<222> (217)..(217)
<223> X is Lysine (K) or 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

1301_0121PCT_Sequence_Listing_ST25

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> 525
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(525)
 <223> LAG-3

<400> 5

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

1301_0121PCT_Sequence_Listing_ST25

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	

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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

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

<400> 6

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

1301_0121PCT_Sequence_Listing_ST25

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
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

<400> 7	
cagatccagt tggatgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc	60
tcctgcaagg cttctgggta taccttcaga aactatggaa tgaactgggt gaagcaggct	120
ccaggaaagg ttttaaagtg gatgggctgg ataaacacct aactggaga gtcaacatat	180

1301_0121PCT_Sequence_Listing_ST25

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

<220>
 <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

<400> 9

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

1301_0121PCT_Sequence_Listing_ST25

<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
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

1301_0121PCT_Sequence_Listing_ST25

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
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Polynucleotide Encoding LAG-3 mAb 1 VL

<400> 12
gatgttgtgg tgacccagac tccactcact ttgtcgggta ccattggaca accagcctcc 60
atctcttgca agtcaagtca gagcctctta catagtgatg gaaagacata tttgaattgg 120
ttgttacaga ggccaggcca gtctccagag cgcctaattct atctgggtgtc tgaactggac 180
tctggagtcc ctgacagggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240
agcagagtgg aggctgagga tttgggagtt tattattgct ggcaagggtac acattttccg 300
tacacgttcg gagggggggac caagctggaa ataaaa 336

<210> 13
<211> 16
<212> PRT
<213> Mus musculus

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

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

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> PRT
<213> Artificial Sequence

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

<400> 17

Cys Ala Gly Gly Thr Gly Cys Ala Ala Cys Thr Gly Gly Thr Thr Cys
1 5 10 15

Ala Ala Thr Cys Cys Gly Gly Cys Gly Cys Cys Gly Ala Gly Gly Thr
20 25 30

Gly Ala Ala Ala Ala Ala Gly Cys Cys Thr Gly Gly Cys Gly Cys Cys
35 40 45

1301_0121PCT_Sequence_Listing_ST25

Thr	Cys	Cys	Gly	Thr	Gly	Ala	Ala	Ala	Gly	Thr	Gly	Thr	Cys	Cys	Thr	50	55	60	
Gly	Thr	Ala	Ala	Gly	Gly	Cys	Ala	Thr	Cys	Thr	Gly	Gly	Gly	Thr	Ala	65	70	75	80
Thr	Ala	Cys	Gly	Thr	Thr	Cys	Ala	Cys	Ala	Ala	Ala	Thr	Thr	Ala	Thr	85	90	95	
Gly	Gly	Thr	Ala	Thr	Gly	Ala	Ala	Cys	Thr	Gly	Gly	Gly	Thr	Gly	Cys	100	105	110	
Gly	Ala	Cys	Ala	Gly	Gly	Cys	Ala	Cys	Cys	Ala	Gly	Gly	Gly	Cys	Ala	115	120	125	
Gly	Gly	Gly	Ala	Cys	Thr	Gly	Gly	Ala	Ala	Thr	Gly	Gly	Ala	Thr	Gly	130	135	140	
Gly	Gly	Gly	Thr	Gly	Gly	Ala	Thr	Cys	Ala	Ala	Thr	Ala	Cys	Thr	Thr	145	150	155	160
Ala	Thr	Ala	Cys	Ala	Gly	Gly	Cys	Gly	Ala	Gly	Ala	Gly	Thr	Ala	Cys	165	170	175	
Thr	Thr	Ala	Thr	Gly	Cys	Thr	Gly	Ala	Cys	Gly	Ala	Thr	Thr	Thr	Cys	180	185	190	
Gly	Ala	Gly	Gly	Gly	Cys	Ala	Gly	Ala	Thr	Thr	Thr	Gly	Thr	Cys	Thr	195	200	205	
Thr	Cys	Thr	Cys	Cys	Ala	Thr	Gly	Gly	Ala	Cys	Ala	Cys	Cys	Ala	Gly	210	215	220	
Cys	Gly	Cys	Thr	Ala	Gly	Thr	Ala	Cys	Cys	Gly	Cys	Thr	Thr	Ala	Thr	225	230	235	240

1301_0121PCT_Sequence_Listing_ST25

Cys Thr Cys Cys Ala Gly Ala Thr Thr Ala Gly Thr Thr Cys Thr Cys
245 250 255

Thr Cys Ala Ala Gly Gly Cys Gly Gly Ala Gly Gly Ala Cys Ala Cys
260 265 270

Ala Gly Cys Thr Gly Thr Thr Thr Ala Thr Thr Ala Thr Thr Gly Thr
275 280 285

Gly Cys Cys Cys Gly Cys Gly Ala Gly Ala Gly Thr Thr Thr Gly Thr
290 295 300

Ala Thr Gly Ala Cys Thr Ala Cys Thr Ala Thr Ala Gly Cys Ala Thr
305 310 315 320

Gly Gly Ala Thr Thr Ala Cys Thr Gly Gly Gly Gly Ala Cys Ala Ala
325 330 335

Gly Gly Thr Ala Cys Ala Ala Cys Cys Gly Thr Gly Ala Cys Ala Gly
340 345 350

Thr Gly Ala Gly Thr Thr Cys Cys
355 360

<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

1301_0121PCT_Sequence_Listing_ST25

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

<400> 19
caggtgcaac tgggtcaatc 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 atttctgtgc ccgcgagagt 300
ttgtatgact actatagcat ggattactgg ggacaaggta caaccgtgac agtgagttcc 360

1301_0121PCT_Sequence_Listing_ST25

<210> 20
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hLAG-3 mAb 1 VL1

<400> 20

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> 21
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide Encoding hLAG-3 mAb 1 VL1

1301_0121PCT_Sequence_Listing_ST25

<400> 21
gatatcgta tgactcagac accactgtca ctgagtgtga ccccgagtca gcccgctagt 60
atttcctgta aatcatccca gtccctcctg catagcgatg gaaagaccta tttgaactgg 120
cttctgcaga aaccaggcca aagtccagag agattgatct acctcgtttc agaactcgac 180
agtggagtgc ccgatcgctt ctcagggtcc ggctctggga ctgattttac tctcaagatc 240
tcaagagtgg aggccgagga cgtcgggggtt tactactgtt ggcagggtac 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

1301_0121PCT_Sequence_Listing_ST25

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
 gatatcgtaa tgactcagac accactgtca ctgagtgtga cccaggtca gcccgctagt 60
 atttcctgta aatcatccca gtccctcctg catagcgatg gaaagaccta tttgaactgg 120
 cttctgcaga gaccaggcca aagtccagag agattgatct acctcgtttc agaactcgac 180
 agtggagtgcc ccgatcgctt ctcagggtcc ggctctggga ctgattttac tctcaagatc 240
 tcaagagtgg aggccgagga cgtcgggggtt tactactgtt ggcagggtac 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

1301_0121PCT_Sequence_Listing_ST25

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
gatatcgtta tgactcagac accactgtca ctgagtgtga ccccagggtca gcccgcctagt 60
atttcctgta aatcatccca gtccctcctg catagcgatg gaaagaccta tttgaactgg 120
cttctgcaga aaccaggcca accgccagag agattgatct acctcgtttc agaactcgac 180
agtggagtgc ccgatcgctt ctcagggtcc ggctctggga ctgattttac tctcaagatc 240
tcaagagtgg aggccgagga cgtcgggggtt tactactgtt 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

1301_0121PCT_Sequence_Listing_ST25

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
gatatcgtta tgactcagac accactgtca ctgagtgtga ccccaggtca gcccgctagt 60
atttcctgta aatcatccca gtccctcctg catagcgatg caaagaccta tttgaactgg 120
cttctgcaga aaccaggcca accgccagag agattgatct acctcgtttc agaactcgac 180
agtggagtgc ccgatcgctt ctcagggtcc ggctctggga ctgattttac tctcaagatc 240
tcaagagtgg aggccgagga cgtcgggggtt tactactgtt ggcagggtac ccacttcctt 300
tatacatttg gcggaggcac aaaagtggag attaaa 336

1301_0121PCT_Sequence_Listing_ST25

<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>
 <221> MISC_FEATURE
 <222> (1)..(121)
 <223> LAG-3 mAb 2 VH

<400> 29

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

1301_0121PCT_Sequence_Listing_ST25

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
 <211> 363
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <223> Polynucleotide Encoding LAG-3 mAb 2 VH

<400> 30
 gaggtccagc ttcagcagtc aggacctgag ctggtgaaac ctggggcctc agtgaagatt 60
 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 tttactgtgc aagatggcac 300
 aggaactact ttggcccctg gtttgcttac tggggccaag ggactccggt cactgtctct 360
 gca 363

<210> 31
 <211> 5
 <212> PRT
 <213> Mus musculus

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

1301_0121PCT_Sequence_Listing_ST25

<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
1 5 10

<210> 34

<211> 111

1301_0121PCT_Sequence_Listing_ST25

<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> LAG-3 mAb 2 VL

<400> 34

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

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

1301_0121PCT_Sequence_Listing_ST25

```

<400> 35
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc      60
atctcctgca aggccagcca aagtgttgat tatgatgggtg aaagttatat gaactgggtac    120
caacagaaac caggacagcc acccaaactc ctcatTTatg ttgtatccaa tctagaatct      180
gggatcccag ccaggtttag 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

```

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

65	70	75	80
Met Glu Leu Arg Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys			
	85	90	95
Thr Arg Trp Ser 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> 40
 <211> 363
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <223> Polynucleotide Encoding LAG-3 mAb 3 VH

<400> 40	
gagggtccggc ttcagcagtc aggacctgag ctggtgaaac ctggggcctc agtgaagata	60
tcctgcaagg cttctggata cacattcact gactacaaca ttcactgggt gaggcagagc	120
catggacaga gccttgagtg gattggatat atttatcctt ataatggtga tactggctac	180
aaccagaagt tcaagaccaa ggccacattg actgtagaca attcctccaa cacagcctac	240
atggaactcc gcagcctggc atctgaagac tctgcagtct attactgtac aagatggagc	300
aggaactact ttggcccctg gtttgcttac tggggccaag ggactctggt cactgtctct	360
gca	363

<210> 41
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>

1301_0121PCT_Sequence_Listing_ST25

<221> MISC_FEATURE
 <222> (1)..(5)
 <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
 1 5 10 15

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

1301_0121PCT_Sequence_Listing_ST25

<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>

1301_0121PCT_Sequence_Listing_ST25

<221> misc_feature

<223> Polynucleotide Encoding LAG-3 mAb 3 VL

<400> 45

gacattgtgc tgacccaatc tccaacttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatgggtg atagttatat gaactgggtat 120

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

<210> 46

<211> 15

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<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>

<221> MISC_FEATURE

<222> (1)..(7)

<223> LAG-3 mAb 3 VL CDR2

<400> 47

Ala Ala Ser Asn Leu Glu Ser

1301_0121PCT_Sequence_Listing_ST25

1 5

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

<220>
<221> MISC_FEATURE
<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

1301_0121PCT_Sequence_Listing_ST25

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>
<221> misc_feature
<223> Polynucleotide Encoding LAG-3 mAb 4 VH

<400> 50
gaggtccagc ttcaccagtc aggacctgag ctggtgaaac ctggggcctc agtgaagata 60
tcctgcaaga cttctggata cactttcact gactacaaca tacactgggt gaagcagagc 120
catggaaaga gccttgagtg gattggatat atttatcctt acaatgggtga 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

1301_0121PCT_Sequence_Listing_ST25

<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>
 <221> MISC_FEATURE
 <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
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (1)..(12)
 <223> LAG-3 mAb 4 VH CDR3

<400> 53

Trp Asn Met Asn Tyr Phe Gly Pro Trp Phe Ala Tyr
 1 5 10

1301_0121PCT_Sequence_Listing_ST25

<210> 54
 <211> 111
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <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
 <211> 333
 <212> DNA
 <213> Mus musculus

1301_0121PCT_Sequence_Listing_ST25

<220>

<221> misc_feature

<223> Polynucleotide Encoding LAG-3 mAb 4 VL

<400> 55

gacattgtgc tgaccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatgggtg ttacttatat caactgggtac 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

<211> 15

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<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

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> LAG-3 mAb 4 VL CDR2

<400> 57

1301_0121PCT_Sequence_Listing_ST25

Ala Ala Ser Asn Leu Glu Ser
1 5

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

<220>
<221> MISC_FEATURE
<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>
<221> MISC_FEATURE
<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
35 40 45

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

1301_0121PCT_Sequence_Listing_ST25

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
<211> 363
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Polynucleotide Encoding LAG-3 mAb 5 VH

<400> 60
gaggtccagc ttcagcagtc aggacctgag ctggtgaaac ctggggcctc agtgaagatt 60
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

<210> 61
<211> 5
<212> PRT

1301_0121PCT_Sequence_Listing_ST25

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(5)

<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>

<221> MISC_FEATURE

<222> (1)..(17)

<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>

<221> MISC_FEATURE

<222> (1)..(12)

<223> LAG-3 mAb 5 VH CDR3

<400> 63

1301_0121PCT_Sequence_Listing_ST25

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

<210> 64
<211> 111
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> LAG-3 mAb 5 VL

<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

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> 65
<211> 333
<212> DNA

1301_0121PCT_Sequence_Listing_ST25

<213> Mus musculus

<220>

<221> misc_feature

<223> Polynucleotide Encoding LAG-3 mAb 5 VL

<400> 65

```

gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc      60
atctcctgca aggccagcca aagtgttgat tatgatgggtg aaagttatat gaactgggtac    120
caacagaaac caggacagcc acccaaactc ctcatTTatg ttgtttccaa tctagaatct      180
gggatcccag ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat      240
cctgtggagg aggaggatgc tgcaacctat tactgtcagc aaagtagtga ggatccgctc     300
acgttcggtg ctgggaccaa gctggagctg aaa                                  333

```

<210> 66

<211> 15

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(15)

<223> LAG-3 mAb 5 VL CDR1

<400> 66

```

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

```

<210> 67

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> LAG-3 mAb 5 VL CDR2

1301_0121PCT_Sequence_Listing_ST25

<400> 67

Val Val Ser Asn Leu Glu Ser
1 5

<210> 68

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<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

<220>

<221> MISC_FEATURE

<222> (1)..(118)

<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

1301_0121PCT_Sequence_Listing_ST25

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> 70
<211> 354
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> Polynucleotide Encoding LAG-3 mAb 6 VH

<400> 70
gaggctctgc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc agtgaagata 60
ccctgcaagg cttctggata cacattcact gactacaaca tggactgggt gaagcagagc 120
catggagaga gccttgagt gattggagat attaatcctg acaatgggtg tactatctac 180
aaccagaagt ttgagggcaa ggccacactg actgtagaca agtcctccag tacagcctac 240
atggagctcc gcagcctgac atctgaggac actgcagtct attactgtgc aagagaggcg 300
gattacttct actttgacta ctggggccaa ggcaccactc tcacagtctc ctca 354

<210> 71
<211> 5
<212> PRT

1301_0121PCT_Sequence_Listing_ST25

<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>

<221> MISC_FEATURE

<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>

<221> MISC_FEATURE

<222> (1)..(9)

<223> LAG-3 mAb 6 VH CDR3

<400> 73

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

<213> Mus musculus

<220>

<221> misc_feature

<223> Polynucleotide Encoding LAG-3 mAb 6 VL

<400> 75

```

gacattgtga tgacccagtc tcacagattc atgtccacat cagttggaga cagggtcagc      60
atcacctgca aggccagtca ggatgtgagt tctgtttag cctggatatca acagaaacca      120
ggacaatctc ctaaattact gattttttcg gcatcctacc ggtacactgg agtccctgat      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>

<221> MISC_FEATURE

<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

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> LAG-3 mAb 6 VL CDR2

1301_0121PCT_Sequence_Listing_ST25

<400> 77

Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 78

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> MISC_FEATURE

<222> (1)..(7)

<223> LAG-3 mAb 6 VL CDR3

<400> 78

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

1301_0121PCT_Sequence_Listing_ST25

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

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

<400> 80
caggtccagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggcgcaag cgtgaagggtg 60
tcctgcaagg ccagcggcta caccttcacc gactacaaca tggactgggt ccgacaggcc 120
ccaggacagg gcctggaatg gatgggacgac 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

1301_0121PCT_Sequence_Listing_ST25

<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 tggcggcgga ctggtcaagc ctggcggcag cctgagactg 60

agctgcgctg ccagcggcctt caccttcagc gactacaaca tggactgggt cgcacaggcc 120

cctggcaagg gcctggaatg ggtgtccgac atcaaccccg acaacggcgt gaccatctac 180

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 84

```

gacatccaga tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc      60
atcacctgtc gggccagcca ggatgtgtcc agcgtggtgg cctggatatca gcagaagccc      120
ggcaaggccc ccaagctgct gatctacagc gccagctacc ggtacacagg cgtgcccagc      180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc      240
gaggacttcg ccacctacta ctgccagcag cactacagca ccccctggac cttcggcgga      300
ggcaccaagc tggaaatcaa 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

```

1301_0121PCT_Sequence_Listing_ST25

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 tgacccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca ggatgtgtcc agcgtggtgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacagc gccagctacc ggtacacagg cgtgcccgat 180
agattcagcg gcagcggctc cggcaccgac ttcaccttca ccatcagcag cctgcagccc 240
gaggacatcg ccgtttacta ctgccagcag cactacagca ccccttgac 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

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

<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>

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

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>

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

<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
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)

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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

Arg Val

```

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

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

<400> 123

```

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

1301_0121PCT_Sequence_Listing_ST25

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)

1301_0121PCT_Sequence_Listing_ST25

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> wherein, X 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

1301_0121PCT_Sequence_Listing_ST25

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> wherein, X 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

1301_0121PCT_Sequence_Listing_ST25

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>

1301_0121PCT_Sequence_Listing_ST25

<221> MISC_FEATURE

<222> (1)..(217)

<223> Knob Fc domain

<220>

<221> MISC_FEATURE

<222> (217)..(217)

<223> wherein, X 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 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> wherein, X 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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(217)

<223> IgG1 Fc universal

<220>

<221> MISC_FEATURE

<222> (1)..(217)

<223> (a) X1 and X2 are both L (wild type), or are both A (decreased FcγR binding);

(b) X3, X4, and X5 are respectively M, S and T (wild type), or Y, T and E (extended half-life),

<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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

<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>

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

<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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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> wherein, X 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

1301_0121PCT_Sequence_Listing_ST25

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

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> wherein, X is a lysine (K) or is absent

```

$\langle 400 \rangle$ 140

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

1301_0121PCT_Sequence_Listing_ST25

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

1301_0121PCT_Sequence_Listing_ST25

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