

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Bispecific Antibodies specifically binding to PD1 and LAG3

<130> P34215-WO

<150> EP17165125.0

<151> 2017-04-05

<160> 169

<170> PatentIn version 3.5

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<220>

<223> heavy chain HVR-H1, PD1-0103

<400> 1

Gly Phe Ser Phe Ser Ser Tyr
1 5

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<223> heavy chain HVR-H2, PD1-0103

<400> 2

Gly Gly Arg
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<223> heavy chain HVR-H3, PD1-0103

<400> 3

Thr Gly Arg Val Tyr Phe Ala Leu Asp
1 5

<210> 4

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<220>

<223> light chain HVR-L1, PD1-0103

<400> 4

Ser Glu Ser Val Asp Thr Ser Asp Asn Ser Phe
1 5 10

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<223> light chain HVR-L2, PD1-0103

<400> 5

Arg Ser Ser

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<220>

<223> light chain HVR-L3, PD1-0103

<400> 6

Asn Tyr Asp Val Pro Trp

1

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<220>

<223> heavy chain variable domain VH, PD1-0103

<400> 7

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

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

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

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

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

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

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

Gly Thr Ser Val Thr Val Ser Ser
 115 120

<210> 8

<211> 111

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<213> Artificial Sequence

<220>

<223> light chain variable domain VL, PD1-0103

<400> 8

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

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro
 35 40 45

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

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

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

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

<210> 9

<211> 120

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<213> Artificial Sequence

<220>

<223> humanized variant -heavy chain variable domain VH of PD1-0103_01
 (PD1 0376)

<400> 9

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

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<220>

<223> humanized variant -light chain variable domain VL of PD1-0103_01
 (PD1 0376)

<400> 10

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

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
 35 40 45

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

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

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<220>

<223> humanized variant -light chain variable domain VL of PD1-0103_02

<400> 11

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

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro
 35 40 45

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

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

Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Asn Tyr
 85 90 95

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

<210> 12

<211> 111

<212> PRT

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<220>

<223> humanized variant -light chain variable domain VL of PD1-0103_03

<400> 12

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

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
 35 40 45

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

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

<210> 13

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<213> Artificial Sequence

<220>

<223> humanized variant -light chain variable domain VL of PD1-0103_04

<400> 13

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

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
 35 40 45

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

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

<210> 14

<211> 5

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<220>

<223> heavy chain HVR-H1, aLAG3(0414)

<400> 14

Asp Tyr Thr Met Asn
1 5

<210> 15
<211> 17
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<220>
<223> heavy chain HVR-H2, aLAG3(0414)

<400> 15

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

Gly

<210> 16
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain HVR-H3, aLAG3(0414)

<400> 16

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

<210> 17
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain HVR-L1, aLAG3(0414)

<400> 17

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

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

<220>
<223> light chain HVR-L2, aLAG3(0414)

<400> 18

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 19
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 <212> PRT
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<220>
 <223> light chain HVR-L3, aLAG3(0414)

<400> 19

Gln Gln Thr Tyr Ser Ser Pro Leu Thr
 1 5

<210> 20
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, aLAG3(0414)

<400> 20

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr
 20 25 30

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

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

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

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

Ala Lys Gly Leu Thr Asp Thr Thr Leu Tyr Gly Ser Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 21
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<220>
 <223> light chain variable domain VL, aLAG3(0414)

<400> 21

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

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

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

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

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

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

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

<210> 22

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H1, aLAG3(0403)

<400> 22

Asp	Tyr	Thr	Met	His
1				5

<210> 23

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H2, aLAG3(0403)

<400> 23

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

Gly

<210> 24

<211> 12
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<220>
 <223> heavy chain HVR-H3, aLAG3(0403)
 <400> 24

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

<210> 25
 <211> 11
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<220>
 <223> light chain HVR-L1, aLAG3(0403)
 <400> 25

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

<210> 26
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L2, aLAG3(0403)
 <400> 26

Ala Ala Ser Ser Leu Gln Ser
 1 5

<210> 27
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L3, aLAG3(0403)
 <400> 27

Gln Gln Thr Tyr Ser Thr Pro Leu Thr
 1 5

<210> 28
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, aLAG3(0403)
 <400> 28

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

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

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

Ser Leu Val Ser Trp Asp Gly Gly Gly Thr Tyr Tyr Thr Asn Ser Val
 50 55 60

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

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

Ala Lys Ala Ile Thr Asp Thr Ser Leu Tyr Gly Tyr Asp Tyr Trp Gly
 100 105 110

Gln Gly Ile Leu Val Thr Val Ser Ser
 115 120

<210> 29

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable domain VL, aLAG3(0403)

<400> 29

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Thr Pro Leu

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

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

<220>
 <223> heavy chain HVR-H1, aLAG3(0411)

<400> 30

Asp Tyr Thr Met Asn
 1 5

<210> 31
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H2, aLAG3(0411)

<400> 31

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

Gly

<210> 32
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H3, aLAG3(0411)

<400> 32

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

<210> 33
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L1, aLAG3(0411)

<400> 33

Arg Ala Ser Gln Ser Ile Val Ser Tyr Leu Asn

1 5 10

<210> 34
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L2, aLAG3(0411)

<400> 34

Ala Ser Ser Ser Leu Gln Ser
 1 5

<210> 35
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L3, aLAG3(0411)

<400> 35

Gln Gln Thr Tyr Ser Thr Pro Leu Thr
 1 5

<210> 36
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, aLAG3(0411)

<400> 36

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

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

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

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

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

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

Ala Lys Gly Leu Thr Asp Asp Thr Leu Tyr Gly Ser Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain variable domain VL, aLAG3(0411)

<400> 37

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

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

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

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

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

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

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

<210> 38
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H1, aLAG3(0417)

<400> 38

Asp Tyr Ala Met Ser
 1 5

<210> 39
 <211> 17
 <212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H2, aLAG3(0417)

<400> 39

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

Gly

<210> 40

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H3, aLAG3(0417)

<400> 40

Thr	His	Ser	Gly	Leu	Ile	Val	Asn	Asp	Ala	Phe	Asp	Ile
1				5					10			

<210> 41

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L1, aLAG3(0417)

<400> 41

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

<210> 42

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L2, aLAG3(0417)

<400> 42

Ala	Ala	Ser	Ser	Leu	Gln	Ser
1				5		

<210> 43

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L3, aLAG3(0417)

<400> 43

Gln Gln Thr Tyr Ser Thr Pro Leu Thr
1 5

<210> 44

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain variable domain VH, aLAG3(0417)

<400> 44

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

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

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

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

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

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

Thr Lys Thr His Ser Gly Leu Ile Val Asn Asp Ala Phe Asp Ile Trp
100 105 110

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

<210> 45

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable domain VL, aLAG3(0417)

<400> 45

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

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

20

25

30

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

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

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

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

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

<210> 46
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H1, aLAG3(0416)
 <400> 46

Asp Tyr Ala Met Ser
 1 5

<210> 47
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H2, aLAG3(0416)
 <400> 47

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

Gly

<210> 48
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H3, aLAG3(0416)
 <400> 48

Thr His Ser Gly Leu Ile Val Asn Asp Ala Phe Asp Ile
 1 5 10

<210> 49
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L1, aLAG3(0416)

<400> 49

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

<210> 50
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L2, aLAG3(0416)

<400> 50

Asp Ala Ser Ser Leu Glu Ser
 1 5

<210> 51
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L3, aLAG3(0416)

<400> 51

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
 1 5

<210> 52
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, aLAG3(0416)

<400> 52

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

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

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

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

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

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

Thr Lys Thr His Ser Gly Leu Ile Val Asn Asp Ala Phe Asp Ile Trp
 100 105 110

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

<210> 53

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable domain VL, aLAG3(0416)

<400> 53

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

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

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

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

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

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

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

<210> 54

<211> 120
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<220>
 <223> heavy chain variable domain VH, BMS-986016

<400> 54

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 Arg Gly Ser 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> 55
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain variable domain VL BMS-986016

<400> 55

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> 56
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H1, MDX25F7 (25F7)
 <400> 56

Asp Tyr Tyr Trp Asn
 1 5

<210> 57
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H2, MDX25F7 (25F7)
 <400> 57

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

<210> 58
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H3, MDX25F7 (25F7)
 <400> 58

Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe
 1 5 10

<210> 59
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain HVR-L1, MDX25F7 (25F7)

<400> 59

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

<210> 60

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L2, MDX25F7 (25F7)

<400> 60

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 61

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L3, MDX25F7 (25F7)

<400> 61

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 62

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain variable domain VH, MDX25F7 (25F7)

<400> 62

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> 63

$\langle 211 \rangle$	107
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<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> light chain variable domain VL, MDX25F7 (25F7)

<400> 63

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> 64

$\langle 211 \rangle$ 125

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> heavy chain variable domain VH, humanized BAP050 (LAG525)

<400> 64

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

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

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

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

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

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

Ala Arg Asn Pro Pro Tyr Tyr Tyr Gly Thr Asn Asn Ala Glu Ala Met
 100 105 110

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

<210> 65

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain variable domain VL, humanized BAP050 (LAG525)

<400> 65

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100

105

<210> 66
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, MDX26H10 (26H10)

<400> 66

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

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

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

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

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

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

<210> 67
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain variable domain VL, MDX26H10 (26H10)

<400> 67

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

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35

40

45

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 68

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> human kappa light chain constant region

<400> 68

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> 69

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> human lambda light chain constant region

<400> 69

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 Thr Pro Ser Lys Gln Ser Asn Asn Lys
 50 55 60

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

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

Lys Thr Val Ala Pro Thr Glu Cys Ser
 100 105

<210> 70

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> human heavy chain constant region derived from IgG1

<400> 70

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 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu 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 Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly
 325

<210> 71
 <211> 329
 <212> PRT

<213> Artificial Sequence

<220>

<223> human heavy chain constant region derived from IgG1 with mutations L234A, L235A and P329G

<400> 71

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 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 Gly 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 Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
325

<210> 72

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> human heavy chain constant region derived from IgG4

<400> 72

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 Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly
 325

<210> 73
 <211> 497
 <212> PRT
 <213> Homo sapiens
 <400> 73

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

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
 260 265 270

Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
 275 280 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
 290 295 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
 305 310 315 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
 325 330 335

Gly Lys Leu Leu Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe
 340 345 350

Val Trp Ser Ser Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro
 355 360 365

Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys
 370 375 380

Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr
 385 390 395 400

Glu Leu Ser Ser Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala
 405 410 415

Leu Pro Ala Gly His Leu Leu Leu Phe Leu Ile Leu Gly Val Leu Ser
 420 425 430

Leu Leu Leu Leu Val Thr Gly Ala Phe Gly Phe His Leu Trp Arg Arg
 435 440 445

Gln Trp Arg Pro Arg Arg Phe Ser Ala Leu Glu Gln Gly Ile His Pro
 450 455 460

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

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gln
 485 490 495

Leu

<210> 74
 <211> 422
 <212> PRT
 <213> Homo sapiens

<400> 74

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

Ser Pro Thr Ile Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly
 20 25 30

Val Thr Trp Gln His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro
 35 40 45

Gly His Pro Leu Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp
 50 55 60

Gly Pro Arg Pro Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly
 65 70 75 80

Leu Arg Ser Gly Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu
 85 90 95

Arg Gly Arg Gln Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg
 100 105 110

Arg Ala Asp Ala Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg
 115 120 125

Ala Leu Ser Cys Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr
 130 135 140

Ala Ser Pro Pro Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn
 145 150 155 160

Cys Ser Phe Ser Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg
 165 170 175

Asn Arg Gly Gln Gly Arg Val Pro Val Arg Glu Ser Pro His His His
 180 185 190

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

Gly Pro Trp Gly Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser
 210 215 220

Ile Met Tyr Asn Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu
 225 230 235 240

Thr Val Tyr Ala Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu
 245 250 255

Pro Ala Gly Val Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro
 260 265 270

Pro Gly Gly Gly Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe
 275 280 285

Thr Leu Arg Leu Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr
 290 295 300

Cys His Ile His Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu
 305 310 315 320

Ala Ile Ile Thr Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu
 325 330 335

Gly Lys Leu Leu Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe
 340 345 350

Val Trp Ser Ser Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro
 355 360 365

Trp Leu Glu Ala Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys
 370 375 380

Gln Leu Tyr Gln Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr
 385 390 395 400

Glu Leu Ser Ser Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala
 405 410 415

Leu Pro Ala Gly His Leu
 420

<210> 75
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 75

Lys Ile Glu Glu Leu Glu
 1 5

<210> 76

<211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer rbHC.up

<400> 76
 aagcttgcca ccatggagac tgggctgcgc tggcttc 37

<210> 77
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer rbHCf.do

<400> 77
 ccattggtga ggggtgccga g 21

<210> 78
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer BcPCR_FHLC_leader.fw

<400> 78
 atggacatga ggggtccccgc 20

<210> 79
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer BcPCR_huCkappa.rev

<400> 79
 gatttcaact gctcatcaga tggc 24

<210> 80
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain HVR-H1, PD1-0098

<400> 80

Gly Tyr Ser Ile Thr Ser Asp Tyr
 1 5

<210> 81
 <211> 3
 <212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H2, PD1-0098

<400> 81

Tyr Ser Gly

1

<210> 82

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H3, PD1-0098

<400> 82

His Gly Ser Ala Pro Trp Tyr Phe Asp

1

5

<210> 83

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L1, PD1-0098

<400> 83

Ser Gln Asn Ile Val His Ser Asp Gly Asn Thr Tyr

1

5

10

<210> 84

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L2, PD1-0098

<400> 84

Lys Val Ser

1

<210> 85

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L3, PD1-0098

<400> 85

Gly Ser His Phe Pro Leu

1

5

<210> 86
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain variable domain VH, PD1-0098

<400> 86

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

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

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

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

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

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

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

Gly Thr Thr Leu Thr Val Ser Ser
 115 120

<210> 87
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain variable domain VL, PD1-0098

<400> 87

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

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

Asp Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35

40

45

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

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

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

Ser His Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105 110

<210> 88

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H1, PD1-0069

<400> 88

Gly Tyr Thr Phe Thr Asp Tyr
 1 5

<210> 89

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H2, PD1-0069

<400> 89

Tyr Ser Gly
 1

<210> 90

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain HVR-H3, PD1-0069

<400> 90

Gly Ile Thr Thr Gly Phe Ala
 1 5

<210> 91

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L1, PD1-0069

<400> 91

Ser Lys Gly Val Ser Thr Ser Ser Tyr Ser Phe
1 5 10

<210> 92

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L2, PD1-0069

<400> 92

Tyr Ala Ser
1

<210> 93

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain HVR-L3, PD1-0069

<400> 93

Ser Arg Glu Phe Pro Trp
1 5

<210> 94

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain variable domain VH, PD1-0069

<400> 94

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

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

Ala Met His Trp Val Lys Gln Ser His Ala Arg Thr Leu Glu Trp Ile
35 40 45

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

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

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

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

Leu Val Thr Val Ser Ala
115

<210> 95
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable domain VL, PD1-0069

<400> 95

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

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

Ser Tyr Ser Phe Met His Trp Tyr Gln Gln Lys Pro Arg Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr 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 Asn Ile His
65 70 75 80

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

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

<210> 96
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain 1 of 1+1 PD1/LAG3 0799

<400> 96

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
340 345 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 97

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 2 of 1+1 PD1/LAG3 0799

<400> 97

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

Ser Leu Arg Leu Ala Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr

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

275

280

285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro Gly Lys
 450

<210> 98

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 1 of 1+1 PD1/LAG3 0799

<400> 98

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val
 115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
 145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
 165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
 180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
 210 215 220

Gly Glu Cys
 225

<210> 99
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> light chain 2 of 1+1 PD1/LAG3 0799

<400> 99

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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

<210> 100

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 2 of 1+1 PD1/LAG3 0927

<400> 100

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 101
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain 2 of 1+1 PD1/LAG3 0927

<400> 101

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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

<210> 102

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 1 of 1+1 PD1/LAG3 0222

<400> 102

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
340 345 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 103

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 2 of 1+1 PD1/LAG3 0222

<400> 103

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

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

275

280

285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 104

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 1 of 1+1 PD1/LAG3 0222

<400> 104

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

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

Ala Met His Trp Val Lys Gln Ser His Ala Arg Thr Leu Glu Trp Ile
 35 40 45

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

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

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

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

Leu Val Thr Val Ser Ala Ala Ser Val Ala Ala Pro Ser Val Phe Ile
 115 120 125

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 130 135 140

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 145 150 155 160

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 165 170 175

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 180 185 190

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 195 200 205

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 210 215 220

Cys
 225

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

<220>
 <223> light chain 2 of 1+1 PD1/LAG3 0222

<400> 105

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

<210> 106

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 1 of 1+1 PD1/LAG3 0224

<400> 106

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
340 345 350

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 107

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 1 of 1+1 PD1/LAG3 0224

<400> 107

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp

20

25

30

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

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

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

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

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

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val
 115 120 125

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 130 135 140

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
 145 150 155 160

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
 165 170 175

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
 180 185 190

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 195 200 205

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
 210 215 220

Gly Glu Cys
 225

<210> 108

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> aLAG3(0156) heavy chain (MDX25F7)

<400> 108

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	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	115	120	125	
Phe	Pro	Leu	Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	130	135	140	
Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	145	150	155	160
Trp	Asn	Ser	Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	165	170	175	
Arg	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	180	185	190	
Ser	Ser	Ser	Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	195	200	205	
Thr	Lys	Val	Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	210	215	220	
Cys	Pro	Pro	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	225	230	235	240
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	245	250	255	

Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr
260 265 270

Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg
275 280 285

Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile
290 295 300

Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His
305 310 315 320

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg
325 330 335

Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu
340 345 350

Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu
370 375 380

Asp Asn Tyr Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr
385 390 395 400

Phe Leu Tyr Asn Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly
405 410 415

Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
435 440

<210> 109

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> aLAG3(0156) light chain (MDX25F7)

<400> 109

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

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

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

Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu
 275 280 285

Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro
 290 295 300

Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val
 305 310 315 320

His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335

Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg
 340 345 350

Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly
 355 360 365

Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala
 370 375 380

Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly Ser
 385 390 395 400

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

Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His
 420 425 430

Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
 435 440

<210> 111

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> aLAG3(0414) light chain

<400> 111

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 112

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> aLAG3(0416) heavy chain

<400> 112

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

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

Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35					40					45					
Ser	Gly	Ile	Asp	Asn	Ser	Gly	Tyr	Tyr	Thr	Tyr	Tyr	Thr	Asp	Ser	Val		
	50					55					60						
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Val	Lys	Asn	Thr	Leu	Tyr		
65					70					75					80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Leu	Cys		
				85					90					95			
Thr	Lys	Thr	His	Ser	Gly	Leu	Ile	Val	Asn	Asp	Ala	Phe	Asp	Ile	Trp		
			100					105					110				
Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro		
		115					120					125					
Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr		
	130					135					140						
Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr		
145					150					155					160		
Val	Thr	Trp	Asn	Ser	Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro		
			165						170					175			
Ser	Val	Arg	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser		
			180					185					190				
Val	Thr	Ser	Ser	Ser	Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala		
		195					200					205					
Thr	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys		
	210					215					220						
Pro	Thr	Cys	Pro	Pro	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile		
225					230					235					240		
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu		
				245					250					255			
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln		
			260					265					270				
Phe	Thr	Trp	Tyr	Ile	Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro		
		275					280					285					

Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu
 290 295 300

Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys
 305 310 315 320

Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 325 330 335

Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro
 340 345 350

Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn
 355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys
 370 375 380

Ala Glu Asp Asn Tyr Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly
 385 390 395 400

Ser Tyr Phe Leu Tyr Asn Lys Leu Ser Val Pro Thr Ser Glu Trp Gln
 405 410 415

Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
 435 440 445

<210> 113

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> aLAG3(0416) light chain

<400> 113

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

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

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 114

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain of 2+2 PD1/LAG3 8970

<400> 114

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr
 20 25 30

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

Ala	Val	Ile	Ser	Trp	Asp	Gly	Gly	Gly	Thr	Tyr	Tyr	Thr	Asp	Ser	Val
50						55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Phe	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Gly	Leu	Thr	Asp	Thr	Thr	Leu	Tyr	Gly	Ser	Asp	Tyr	Trp	Gly
			100					105						110	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		115					120					125			
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
	130					135					140				
Ala	Leu	Gly	Cys	Leu	Val	Glu	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145					150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165					170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
			180					185					190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Glu	Lys	Val	Glu	Pro	Lys	Ser	Cys
	210					215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				245					250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				

Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	305	310	315	320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro	Ile	325	330	335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	340	345	350	
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	355	360	365	
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	370	375	380	
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	385	390	395	400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	405	410	415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	420	425	430	
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	435	440	445	
Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	450	455	460	
Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	465	470	475	480
Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	485	490	495	
Phe	Ser	Ser	Tyr	Thr	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	500	505	510	
Leu	Glu	Trp	Val	Ala	Thr	Ile	Ser	Gly	Gly	Gly	Arg	Asp	Ile	Tyr	Tyr	515	520	525	
Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	530	535	540	
Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	545	550	555	560

Val Tyr Tyr Cys Val Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu Asp
 565 570 575

Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala
 580 585 590

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 595 600 605

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 625 630 635 640

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 645 650 655

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 660 665 670

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 675 680 685

Ser Phe Asn Arg Gly Glu Cys
 690 695

<210> 115

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> light chain 1 of 2+2 PD1/LAG3 8970

<400> 115

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

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

Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
 35 40 45

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser

72																
65				70				75				80				
Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Asn	Tyr	
				85					90					95		
Asp	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Ser	
				100					105					110		
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	
				115					120					125		
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	
				130					135					140		
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	
145					150					155					160	
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	
				165					170					175		
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	
				180					185					190		
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	
				195					200					205		
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys									
				210					215							
<210> 116																
<211> 696																
<212> PRT																
<213> Artificial Sequence																
<220>																
<223> heavy chain of 2+2 PD1/LAG3 8984																
<400> 116																
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1					5					10					15	
Ser	Leu	Arg	Leu	Ala	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Tyr	
				20					25					30		
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
				35					40					45		
Ser	Gly	Ile	Asp	Asn	Ser	Gly	Tyr	Tyr	Thr	Tyr	Tyr	Thr	Asp	Ser	Val	
				50					55					60		

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Val	Lys	Asn	Thr	Leu	Tyr	65	70	75	80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Leu	Cys	85	90	95	
Thr	Lys	Thr	His	Ser	Gly	Leu	Ile	Val	Asn	Asp	Ala	Phe	Asp	Ile	Trp	100	105	110	
Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	115	120	125	
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	130	135	140	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Glu	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	145	150	155	160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	165	170	175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	180	185	190	
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	195	200	205	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Glu	Lys	Val	Glu	Pro	Lys	Ser	210	215	220	
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	225	230	235	240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	245	250	255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	260	265	270	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	275	280	285	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	290	295	300	
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	305	310	315	320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 325 330 335
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460
 Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480
 Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 485 490 495
 Ser Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510
 Gly Leu Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr
 515 520 525
 Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 530 535 540
 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 545 550 555 560
 Ala Val Tyr Tyr Cys Val Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu
 565 570 575

Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val
 580 585 590

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 595 600 605

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 610 615 620

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 625 630 635 640

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 645 650 655

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 660 665 670

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 675 680 685

Lys Ser Phe Asn Arg Gly Glu Cys
 690 695

<210> 117

<211> 694

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain of 2+2 PD1/LAG3 9010

<400> 117

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

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 Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

340

345

350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe
 485 490 495

Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 500 505 510

Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr Tyr Pro
 515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 545 550 555 560

Tyr Tyr Cys Val Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu Asp Ser
 565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala
 580 585 590

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

595

600

605

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 610 615 620

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 625 630 635 640

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 645 650 655

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 660 665 670

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 675 680 685

Phe Asn Arg Gly Glu Cys
 690

<210> 118

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 1 of 2+1 PD1/LAG3 8310

<400> 118

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr
 20 25 30

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

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

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

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

Ala Lys Gly Leu Thr Asp Thr Thr Leu Tyr Gly Ser Asp Tyr Trp Gly
 100 105 110

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser		
		115					120					125					
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala		
	130					135					140						
Ala	Leu	Gly	Cys	Leu	Val	Glu	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val		
145					150					155					160		
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala		
				165					170					175			
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
			180					185					190				
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
		195					200					205					
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Glu	Lys	Val	Glu	Pro	Lys	Ser	Cys		
	210					215					220						
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly		
225					230					235					240		
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met		
				245					250					255			
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His		
			260					265					270				
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val		
		275					280					285					
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr		
	290					295					300						
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly		
305					310					315					320		
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro	Ile		
				325					330					335			
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val		
			340					345					350				
Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser		
		355					360					365					

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 450 455 460

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
 465 470 475 480

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser
 485 490 495

Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
 500 505 510

Leu Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr Tyr
 515 520 525

Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 530 535 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 545 550 555 560

Val Tyr Tyr Cys Val Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu Asp
 565 570 575

Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala
 580 585 590

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 595 600 605

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
625 630 635 640

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
645 650 655

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
660 665 670

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
675 680 685

Ser Phe Asn Arg Gly Glu Cys
690 695

<210> 119

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 2 of 2+1 PD1/LAG3 8310

<400> 119

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr
20 25 30

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

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

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

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

Ala Lys Gly Leu Thr Asp Thr Thr Leu Tyr Gly Ser Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

130

135

140

Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

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385                      390                      395                      400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
      405                      410                      415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
      420                      425                      430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
      435                      440                      445

Pro Gly Lys
      450

<210> 120
<211> 696
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain 1of 2+1 PD1/LAG3 8311

<400> 120

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

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

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

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

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

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

Thr Lys Thr His Ser Gly Leu Ile Val Asn Asp Ala Phe Asp Ile Trp
      100     105     110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
      115     120     125

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

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Ala	Ala	Leu	Gly	Cys	Leu	Val	Glu	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145					150					155					160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
				165					170					175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			180					185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		195					200					205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Glu	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				245					250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			260					265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		275					280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	290					295					300				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
305					310					315					320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Gly	Ala	Pro
				325					330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			340					345					350		
Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
		355					360					365			
Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
	370					375					380				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
385					390					395					400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460
 Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480
 Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 485 490 495
 Ser Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510
 Gly Leu Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr
 515 520 525
 Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 530 535 540
 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 545 550 555 560
 Ala Val Tyr Tyr Cys Val Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu
 565 570 575
 Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val
 580 585 590
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 595 600 605
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 610 615 620
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 625 630 635 640
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 645 650 655

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 660 665 670

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 675 680 685

Lys Ser Phe Asn Arg Gly Glu Cys
 690 695

<210> 121

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 2 of 2+1 PD1/LAG3 8311

<400> 121

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

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

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

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

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

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

Thr Lys Thr His Ser Gly Leu Ile Val Asn Asp Ala Phe Asp Ile Trp
 100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

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

Ala Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro

165

170

175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 225 230 235 240

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

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

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe
 485 490 495

Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 500 505 510

Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr Tyr Pro
 515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 545 550 555 560

Tyr Tyr Cys Val Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu Asp Ser
 565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala
 580 585 590

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 595 600 605

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 610 615 620

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 625 630 635 640

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 645 650 655

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 660 665 670

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 675 680 685

Phe Asn Arg Gly Glu Cys
690

<210> 123
<211> 941
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain 1 of 2+1 PD1/LAG3 8312

<400> 123

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr
20 25 30

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

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

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

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

Ala Lys Gly Leu Thr Asp Thr Thr Leu Tyr Gly Ser Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His

195

200

205

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

450

455

460

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser
 465 470 475 480

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser
 485 490 495

Glu Ser Val Asp Thr Ser Asp Asn Ser Phe Ile His Trp Tyr Gln Gln
 500 505 510

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Arg Ser Ser Thr Leu
 515 520 525

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 530 535 540

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 545 550 555 560

Tyr Cys Gln Gln Asn Tyr Asp Val Pro Trp Thr Phe Gly Gln Gly Thr
 565 570 575

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 580 585 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 675 680 685

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 690 695 700

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val

705		710		715		720									
Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu
				725					730					735	
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ser	Ser	Tyr	Thr	Met
			740					745					750		
Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Thr
		755					760					765			
Ile	Ser	Gly	Gly	Gly	Arg	Asp	Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly
	770					775					780				
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
785					790					795					800
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Val	Leu
				805					810					815	
Leu	Thr	Gly	Arg	Val	Tyr	Phe	Ala	Leu	Asp	Ser	Trp	Gly	Gln	Gly	Thr
			820					825					830		
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
		835					840					845			
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
	850					855					860				
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
865					870					875					880
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
				885					890						895
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
			900					905					910		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
		915					920					925			
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys			
	930					935					940				

<210> 124

<211> 942

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 1of 2+1 PD1/LAG3 8313

<400> 124

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

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

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

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

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

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

Thr Lys Thr His Ser Gly Leu Ile Val Asn Asp Ala Phe Asp Ile Trp
 100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

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

Ala Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
 225 230 235 240

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 450 455 460

Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp
 465 470 475 480

Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala
 485 490 495

Ser Glu Ser Val Asp Thr Ser Asp Asn Ser Phe Ile His Trp Tyr Gln
 500 505 510

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Arg Ser Ser Thr
 515 520 525

Leu Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
 530 535 540

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
 545 550 555 560

Tyr Tyr Cys Gln Gln Asn Tyr Asp Val Pro Trp Thr Phe Gly Gln Gly
 565 570 575

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 580 585 590

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 595 600 605

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 610 615 620

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 625 630 635 640

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 645 650 655

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 660 665 670

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 675 680 685

Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 690 695 700

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 705 710 715 720

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 725 730 735

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr Thr
 740 745 750

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
755 760 765

Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr Tyr Pro Asp Ser Val Lys
770 775 780

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
785 790 795 800

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val
805 810 815

Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu Asp Ser Trp Gly Gln Gly
820 825 830

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
835 840 845

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
850 855 860

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
865 870 875 880

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
885 890 895

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
900 905 910

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
915 920 925

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
930 935 940

<210> 125

<211> 940

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 1of 2+1 PD1/LAG3 1088

<400> 125

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 Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

275

280

285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
 465 470 475 480

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Glu
 485 490 495

Ser Val Asp Thr Ser Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Lys
 500 505 510

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Arg Ser Ser Thr Leu Glu
 515 520 525

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe

530

535

540

Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr
 545 550 555 560

Cys Gln Gln Asn Tyr Asp Val Pro Trp Thr Phe Gly Gln Gly Thr Lys
 565 570 575

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 580 585 590

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 595 600 605

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 610 615 620

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 625 630 635 640

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 645 650 655

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 660 665 670

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly
 675 680 685

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 690 695 700

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 705 710 715 720

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 725 730 735

Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr Thr Met Ser
 740 745 750

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile
 755 760 765

Ser Gly Gly Gly Arg Asp Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg
 770 775 780

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met

785 790 795 800
 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Leu Leu
 805 810 815
 Thr Gly Arg Val Tyr Phe Ala Leu Asp Ser Trp Gly Gln Gly Thr Leu
 820 825 830
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 835 840 845
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 850 855 860
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 865 870 875 880
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 885 890 895
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 900 905 910
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 915 920 925
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 930 935 940

<210> 126
 <211> 589
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain 1of 2+1 PD1/LAG3 0918

<400> 126

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	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
	210					215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly
225					230					235					240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
				245					250					255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
			260					265						270	
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
		275					280					285			
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	290					295					300				
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
305					310					315					320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 485 490 495

Ser Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 500 505 510

Gly Leu Glu Trp Val Ala Thr Ile Ser Gly Gly Gly Arg Asp Ile Tyr
 515 520 525

Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 530 535 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 545 550 555 560

Ala Val Tyr Tyr Cys Val Leu Leu Thr Gly Arg Val Tyr Phe Ala Leu
 565 570 575

Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 580 585

<210> 127

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 2 of 2+1 PD1/LAG3 0918

<400> 127

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 Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys

195

200

205

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

450

455

460

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
 465 470 475 480

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Glu
 485 490 495

Ser Val Asp Thr Ser Asp Asn Ser Phe Ile His Trp Tyr Gln Gln Lys
 500 505 510

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Arg Ser Ser Thr Leu Glu
 515 520 525

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 530 535 540

Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr
 545 550 555 560

Cys Gln Gln Asn Tyr Asp Val Pro Trp Thr Phe Gly Gln Gly Thr Lys
 565 570 575

Val Glu Ile Lys
 580

<210> 128
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 128

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

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

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

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

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
 65 70 75 80

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

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Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
      100                      105                      110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
      115                      120                      125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
      130                      135                      140

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

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
      165                      170                      175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
      180                      185                      190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
      195                      200                      205

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

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
225                      230                      235                      240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
      245                      250                      255

Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
      260                      265                      270

Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
      275                      280                      285

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<210> 129

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker G4S

<400> 129

```

Gly Gly Gly Gly Ser
1          5

```

<210> 130
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker (G4S)2

<400> 130

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

<210> 131
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker (SG4)2

<400> 131

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

<210> 132
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker G4(SG4)2

<400> 132

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

<210> 133
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker

<400> 133

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

<210> 134
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker (G4S)3

<400> 134

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

<210> 135

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker (G4S)4

<400> 135

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

Gly Gly Gly Ser
20

<210> 136

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 136

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 137

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 137

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

<210> 138

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 138

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 139
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker

<400> 139

Gly Gly Ser Gly Ser Gly
 1 5

<210> 140
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker

<400> 140

Gly Gly Ser Gly
 1

<210> 141
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker

<400> 141

Gly Gly Ser Gly Asn Gly Ser Gly
 1 5

<210> 142
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker

<400> 142

Gly Gly Asn Gly Ser Gly Ser Gly
 1 5

<210> 143
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Peptide linker

<400> 143

Gly Gly Asn Gly Ser Gly
1 5

<210> 144

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain 2 of 1+1 PD1/LAG3 0725 (1+1 trans)

<400> 144

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

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 225 230 235 240

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 245 250 255

Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr Thr Met Asn
 260 265 270

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
 275 280 285

Ser Trp Asp Gly Gly Gly Thr Tyr Tyr Thr Asp Ser Val Lys Gly Arg
 290 295 300

Phe Thr Ile Ser Arg Asp Asp Phe Lys Asn Thr Leu Tyr Leu Gln Met
 305 310 315 320

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly
 325 330 335

Leu Thr Asp Thr Thr Leu Tyr Gly Ser Asp Tyr Trp Gly Gln Gly Thr
 340 345 350

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 370 375 380

Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 385 390 395 400

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 405 410 415

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 420 425 430

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 435 440 445

Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys
 450 455 460

<210> 145
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> heavy chain 2 of 2+1 PD1/LAG3 0750 (2+1 trans)

<400> 145

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr
 20 25 30

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

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

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

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

Ala Lys Gly Leu Thr Asp Thr Thr Leu Tyr Gly Ser Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

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

Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

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

Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 450 455 460

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 465 470 475 480

Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Asp Asp Tyr Thr Met Asn
 485 490 495

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile
 500 505 510

Ser Trp Asp Gly Gly Gly Thr Tyr Tyr Thr Asp Ser Val Lys Gly Arg
 515 520 525

Phe Thr Ile Ser Arg Asp Asp Phe Lys Asn Thr Leu Tyr Leu Gln Met
 530 535 540

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly
 545 550 555 560

Leu Thr Asp Thr Thr Leu Tyr Gly Ser Asp Tyr Trp Gly Gln Gly Thr
 565 570 575

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 580 585 590

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 595 600 605

Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 610 615 620

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

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 645 650 655

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 660 665 670

Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys
 675 680 685

<210> 146

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain CEA (CEA TCB)

<400> 146

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

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

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
 100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

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

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

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 147

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain CD3 (CEA TCB)

<400> 147

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

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

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

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

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

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

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Ser Ala
 100 105 110

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
 115 120 125

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
 180 185 190

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
 195 200 205

Val Glu Pro Lys Ser Cys
 210

<210> 148
 <211> 694
 <212> PRT
 <213> Artificial Sequence

<220>

<223> CEA CD3 crossfab VHck fc knob P329GLALA (CEA TCB)

<400> 148

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
 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 Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
 50 55 60

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220

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

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
485 490 495

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
500 505 510

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
515 520 525

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
530 535 540

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
545 550 555 560

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
565 570 575

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
580 585 590

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
595 600 605

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
610 615 620

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
625 630 635 640

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
645 650 655

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
660 665 670

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

Ser Leu Ser Pro Gly Lys
690

<210> 149

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA VHCH1 Fc hole P329GLALA (CEA TCB)

<400> 149

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
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 Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

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

<210> 150

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> CD3 VH-CL (CEACAM5 TCB)

<400> 150

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

<210> 151

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> CEACAM5 VH-CH1(EE)-Fc (hole, P329G LALA)

<400> 151

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

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

Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys
 210 215 220

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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                230                235                240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                250                255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
                260                265                270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                275                280                285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                290                295                300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                310                315                320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                330                335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
                340                345                350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                355                360                365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                370                375                380

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
                405                410                415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
                420                425                430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                435                440                445

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Pro

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<210> 152
<211> 674
<212> PRT
<213> Artificial Sequence

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<220>

<223> CEACAM5 VH-CH1(EE)-CD3 VL-CH1-Fc (knob, P329G LALA)

<400> 152

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

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

Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser Cys
 210 215 220

Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
 225 230 235 240

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

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
500 505 510

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
515 520 525

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
530 535 540

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
545 550 555 560

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
565 570 575

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
580 585 590

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
595 600 605

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
610 615 620

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
625 630 635 640

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
645 650 655

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
660 665 670

Ser Pro

<210> 153

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> CEACAM5 VL-CL(RK)

<400> 153

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

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

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

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg Ala Thr Gly Ile 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 Gln Thr Asn
 85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Arg Lys
 115 120 125

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 154

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-HCDR1

<400> 154

Glu Phe Gly Met Asn
 1 5

<210> 155
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-HCDR2

<400> 155

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

Gly

<210> 156
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-HCDR3

<400> 156

Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr
 1 5 10

<210> 157
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-LCDR1

<400> 157

Lys Ala Ser Ala Ala Val Gly Thr Tyr Val Ala
 1 5 10

<210> 158
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-LCDR2

<400> 158

Ser Ala Ser Tyr Arg Lys Arg
 1 5

<210> 159
 <211> 10

<212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-LCDR3

<400> 159

His Gln Tyr Tyr Thr Tyr Pro Leu Phe Thr
 1 5 10

<210> 160
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA VH

<400> 160

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 Glu Phe
 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 Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
 50 55 60

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 161
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA VL

<400> 161

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

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

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

<210> 162
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-HCDR1 (CEACAM5)

<400> 162

Asp Thr Tyr Met His
 1 5

<210> 163
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-HCDR2 (CEACAM5)

<400> 163

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

Gly

<210> 164
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>

<223> CEA-HCDR3 (CEACAM5)

<400> 164

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

<210> 165

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LCDR1 (CEACAM5)

<400> 165

Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly Phe Leu His
 1 5 10 15

<210> 166

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LCDR2 (CEACAM5)

<400> 166

Arg Ala Ser Asn Arg Ala Thr
 1 5

<210> 167

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LCDR3 (CEACAM5)

<400> 167

Gln Gln Thr Asn Glu Asp Pro Tyr Thr
 1 5

<210> 168

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA VH (CEACAM5)

<400> 168

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 169

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA VL (CEACAM5)

<400> 169

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 Gly Glu Ser Val Asp Ile Phe
 20 25 30

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

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg Ala Thr Gly Ile 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 Gln Thr Asn
 85 90 95

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