

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG
Hoffmann-La Roche Inc.

<120> Anti-HLA-G antibodies and use thereof

<130> Case P36618-WO

<150> EP20214951.4

<151> 2020-12-17

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<151> 2021-10-18

<160> 96

<170> PatentIn version 3.5

<210> 1

<211> 7

<212> PRT

<213> Homo sapiens

<400> 1

Ser Asn Arg Ala Ala Trp Asn
1 5

<210> 2

<211> 18

<212> PRT

<213> Homo sapiens

<400> 2

Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala Val Ser Val
1 5 10 15

Gln Gly

<210> 3

<211> 9

<212> PRT

<213> Homo sapiens

<400> 3

Val Arg Ala Val Ala Pro Phe Asp Tyr
1 5

<210> 4
<211> 17
<212> PRT
<213> Homo sapiens

<400> 4

Lys Ser Ser Gln Ser Val Leu Asn Ser Ser Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 5
<211> 7
<212> PRT
<213> Homo sapiens

<400> 5

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6

Gln Gln Tyr Tyr Arg Thr Pro Trp Thr
1 5

<210> 7
<211> 121
<212> PRT
<213> Homo sapiens

<400> 7

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Phe Ser Leu Arg Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Gln Gly Val Leu Val Thr Val Ser Ser
115 120

<210> 8
<211> 113
<212> PRT
<213> Homo sapiens

<400> 8

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 Ser Ser Gln Ser Val Leu Asn Ser
20 25 30

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

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

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

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

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

Lys

<210> 9
<211> 17
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L1, HLA-G-0090-VL-N31D

<400> 9

Lys Ser Ser Gln Ser Val Leu Asp Ser Ser Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 10
<211> 113
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, HLA-G-0090-VL-N31D

<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 Ser Ser Gln Ser Val Leu Asp Ser
20 25 30

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

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65		70		75		80									
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Phe	Cys	Gln	Gln
			85						90					95	

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

Lys

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

<220>
 <223> light chain CDR-L1, HLA-G-0090-VL-N31L

<400> 11

Lys	Ser	Ser	Gln	Ser	Val	Leu	Leu	Ser	Ser	Asn	Asn	Lys	Asn	Asn	Leu
1				5					10					15	

Ala

<210> 12
 <211> 113
 <212> PRT
 <213> Artificial

<220>
 <223> light chain variable domain VL, HLA-G-0090-VL-N31L

<400> 12

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	Ser	Ser	Gln	Ser	Val	Leu	Leu	Ser
			20					25					30		

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

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

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

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

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

Lys

<210> 13
<211> 17
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L1, HLA-G-0090-VL-N31Q

<400> 13

Lys Ser Ser Gln Ser Val Leu Gln Ser Ser Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 14
<211> 113
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, HLA-G-0090-VL-N31Q

<400> 14

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 Ser Ser Gln Ser Val Leu Gln Ser

20

25

30

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

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

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

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

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

Lys

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

<220>
 <223> light chain CDR-L1, HLA-G-0090-VL-N31S

<400> 15

Lys Ser Ser Gln Ser Val Leu Ser Ser Ser Asn Asn Lys Asn Asn Leu
 1 5 10 15

Ala

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

<220>
 <223> light chain variable domain VL, HLA-G-0090-VL-N31S

<400> 16

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 Ser Ser Gln Ser Val Leu Ser Ser
20 25 30

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

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

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

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

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

Lys

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

<220>
<223> light chain CDR-L1, HLA-G-0090-VL-N31T

<400> 17

Lys Ser Ser Gln Ser Val Leu Thr Ser Ser Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 18
<211> 113
<212> PRT

<213> Artificial

<220>

<223> light chain variable domain VL, HLA-G-0090-VL-N31T

<400> 18

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 Ser Ser Gln Ser Val Leu Thr Ser
20 25 30

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

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

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

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

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

Lys

<210> 19

<211> 17

<212> PRT

<213> Artificial

<220>

<223> light chain CDR-L1, HLA-G-0090-VL-N31Y

<400> 19

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 20
<211> 113
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, HLA-G-0090-VL-N31Y

<400> 20

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 Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

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

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

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

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

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

Lys

<210> 21
<211> 17
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L1, HLA-G-0090-VL-N31Y-N38Y

<400> 21

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 22
<211> 113
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, HLA-G-0090-VL-N31Y-N38Y

<400> 22

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 Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

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

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

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

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

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

Lys

<210> 23
<211> 17
<212> PRT

<213> Artificial

<220>

<223> light chain CDR-L1, HLA-G-0090-VL-S32P

<400> 23

Lys Ser Ser Gln Ser Val Leu Asn Pro Ser Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 24

<211> 113

<212> PRT

<213> Artificial

<220>

<223> light chain variable domain VL, HLA-G-0090-VL-S32P

<400> 24

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 Ser Ser Gln Ser Val Leu Asn Pro
20 25 30

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

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

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

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

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

Lys

<210> 25
<211> 17
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L1, HLA-G-0090-VL-S33A

<400> 25

Lys Ser Ser Gln Ser Val Leu Asn Ser Ala Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 26
<211> 113
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, HLA-G-0090-VL-S33A

<400> 26

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 Ser Ser Gln Ser Val Leu Asn Ser
20 25 30

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

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

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

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

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

Lys

<210> 27
<211> 17
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L1, HLA-G-0090-VL-S33D

<400> 27

Lys Ser Ser Gln Ser Val Leu Asn Ser Asp Asn Asn Lys Asn Asn Leu
1 5 10 15

Ala

<210> 28
<211> 113
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, HLA-G-0090-VL-S33D

<400> 28

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 Ser Ser Gln Ser Val Leu Asn Ser
20 25 30

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

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65		70		75		80									
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Phe	Cys	Gln	Gln
			85						90					95	

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

Lys

<210> 29
 <211> 17
 <212> PRT
 <213> Artificial

<220>
 <223> light chain CDR-L1, HLA-G-0090-VL-S33P

<400> 29

Lys	Ser	Ser	Gln	Ser	Val	Leu	Asn	Ser	Pro	Asn	Asn	Lys	Asn	Asn	Leu
1				5					10						15

Ala

<210> 30
 <211> 113
 <212> PRT
 <213> Artificial

<220>
 <223> light chain variable domain VL, HLA-G-0090-VL-S33P

<400> 30

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	Ser	Ser	Gln	Ser	Val	Leu	Asn	Ser
			20					25					30		

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

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

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

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

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

Lys

<210> 31
<211> 314
<212> PRT
<213> homo sapiens

<400> 31

Gly Ser His Ser Met Arg Tyr Phe Ser Ala Ala Val Ser Arg Pro Gly
1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Met Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ser Ala Cys Pro Arg Met Glu Pro Arg
35 40 45

Ala Pro Trp Val Glu Gln Glu Gly Pro Glu Tyr Trp Glu Glu Glu Thr
50 55 60

Arg Asn Thr Lys Ala His Ala Gln Thr Asp Arg Met Asn Leu Gln Thr
65 70 75 80

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

Trp Met Ile Gly Cys Asp Leu Gly Ser Asp Gly Arg Leu Leu Arg Gly
100 105 110

Tyr Glu Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Leu Ala Leu Asn Glu
115 120 125

Asp Leu Arg Ser Trp Thr Ala Ala Asp Thr Ala Ala Gln Ile Ser Lys
130 135 140

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

Glu Gly Thr Cys Val Glu Trp Leu His Arg Tyr Leu Glu Asn Gly Lys
165 170 175

Glu Met Leu Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His
180 185 190

Pro Val Phe Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe
195 200 205

Tyr Pro Ala Glu Ile Ile Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln
210 215 220

Thr Gln Asp Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg
245 250 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Glu Pro Leu Met Leu
260 265 270

Arg Trp Lys Gln Ser Ser Leu Pro Thr Ile Pro Ile Met Gly Ile Val
275 280 285

Ala Gly Leu Val Val Leu Ala Ala Val Val Thr Gly Ala Ala Val Ala
290 295 300

Ala Val Leu Trp Arg Lys Lys Ser Ser Asp
305 310

<210> 32
<211> 274
<212> PRT
<213> homo sapiens

<400> 32

Gly Ser His Ser Met Arg Tyr Phe Ser Ala Ala Val Ser Arg Pro Gly
1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Met Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ser Ala Cys Pro Arg Met Glu Pro Arg
35 40 45

Ala Pro Trp Val Glu Gln Glu Gly Pro Glu Tyr Trp Glu Glu Glu Thr
50 55 60

Arg Asn Thr Lys Ala His Ala Gln Thr Asp Arg Met Asn Leu Gln Thr
65 70 75 80

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

Trp Met Ile Gly Cys Asp Leu Gly Ser Asp Gly Arg Leu Leu Arg Gly
100 105 110

Tyr Glu Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Leu Ala Leu Asn Glu
115 120 125

Asp Leu Arg Ser Trp Thr Ala Ala Asp Thr Ala Ala Gln Ile Ser Lys
130 135 140

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

Glu Gly Thr Cys Val Glu Trp Leu His Arg Tyr Leu Glu Asn Gly Lys
165 170 175

Glu Met Leu Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His
180 185 190

Pro Val Phe Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe
195 200 205

Tyr Pro Ala Glu Ile Ile Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln
210 215 220

Thr Gln Asp Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg
245 250 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Glu Pro Leu Met Leu
260 265 270

Arg Trp

<210> 33
<211> 99
<212> PRT
<213> homo sapiens

<400> 33

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu
1 5 10 15

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro
20 25 30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys
35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu
50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys
65 70 75 80

Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp
85 90 95

Arg Asp Met

<210> 34
<211> 275
<212> PRT
<213> Artificial

<220>
<223> modified human HLA-G (wherein the HLA-G specific amino acids have
been replaced by HLA-A consensus amino acids (= degrafted HLA-G)
ECD

<400> 34

Gly Ser His Ser Met Arg Tyr Phe Ser Ala Ala Val Ser Arg Pro Gly
1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Met Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Pro Arg Met Glu Pro Arg
35 40 45

Ala Pro Trp Val Glu Gln Glu Gly Pro Glu Tyr Trp Asp Glu Glu Thr
50 55 60

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

Leu Arg Gly Cys Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln
85 90 95

Trp Met Ile Gly Cys Asp Val Gly Ser Asp Gly Arg Leu Leu Arg Gly
100 105 110

Tyr Glu Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Leu Ala Leu Asn Glu
115 120 125

Asp Leu Arg Ser Trp Thr Ala Ala Asp Thr Ala Ala Gln Ile Ser Lys
130 135 140

Arg Lys Cys Glu Ala Ala His Val Ala Glu Gln Arg Arg Ala Tyr Leu
145 150 155 160

Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys
165 170 175

Glu Thr Leu Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His
180 185 190

Pro Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe
195 200 205

Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln
210 215 220

Thr Gln Asp Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg
245 250 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Glu Pro Leu Thr Leu
260 265 270

Arg Trp Lys
275

<210> 35
<211> 341
<212> PRT
<213> homo sapiens

<400> 35

Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly
1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg
35 40 45

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

Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr
65 70 75 80

Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln
85 90 95

Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly
100 105 110

Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu
115 120 125

Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys
130 135 140

His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu
145 150 155 160

Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys
165 170 175

Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His
180 185 190

Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe
195 200 205

Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln
210 215 220

Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg
245 250 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu

260

265

270

Arg Trp Glu Pro Ser Ser Gln Pro Thr Ile Pro Ile Val Gly Ile Ile
 275 280 285

Ala Gly Leu Val Leu Phe Gly Ala Val Ile Thr Gly Ala Val Val Ala
 290 295 300

Ala Val Met Trp Arg Arg Lys Ser Ser Asp Arg Lys Gly Gly Ser Tyr
 305 310 315 320

Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser Asp Val Ser Leu
 325 330 335

Thr Ala Cys Lys Val
 340

<210> 36
 <211> 275
 <212> PRT
 <213> homo sapiens

<400> 36

Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly
 1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln
 20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg
 35 40 45

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

Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr
 65 70 75 80

Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln
 85 90 95

Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly
100 105 110

Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu
115 120 125

Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys
130 135 140

His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu
145 150 155 160

Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys
165 170 175

Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His
180 185 190

Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe
195 200 205

Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln
210 215 220

Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg
245 250 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu
260 265 270

Arg Trp Glu
275

<210> 37

<211> 275

<212> PRT

<213> mus musculus

<400> 37

Gly Pro His Ser Leu Arg Tyr Phe Val Thr Ala Val Ser Arg Pro Gly
1 5 10 15

Leu Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln
20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Asp Asn Pro Arg Phe Glu Pro Arg
35 40 45

Ala Pro Trp Met Glu Gln Glu Gly Pro Glu Tyr Trp Glu Glu Gln Thr
50 55 60

Gln Arg Ala Lys Ser Asp Glu Gln Trp Phe Arg Val Ser Leu Arg Thr
65 70 75 80

Ala Gln Arg Cys Tyr Asn Gln Ser Lys Gly Gly Ser His Thr Phe Gln
85 90 95

Arg Met Phe Gly Cys Asp Val Gly Ser Asp Trp Arg Leu Leu Arg Gly
100 105 110

Tyr Gln Gln Phe Ala Tyr Asp Gly Arg Asp Tyr Ile Ala Leu Asn Glu
115 120 125

Asp Leu Lys Thr Trp Thr Ala Ala Asp Thr Ala Ala Leu Ile Thr Arg
130 135 140

Arg Lys Trp Glu Gln Ala Gly Asp Ala Glu Tyr Tyr Arg Ala Tyr Leu
145 150 155 160

Glu Gly Glu Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Leu Gly Asn
165 170 175

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

Pro Arg Ser Gln Val Asp Val Thr Leu Arg Cys Trp Ala Leu Gly Phe
195 200 205

Tyr Pro Ala Asp Ile Thr Leu Thr Trp Gln Leu Asn Gly Glu Asp Leu

210

215

220

Thr Gln Asp Met Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
 225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Leu Gly Lys Glu Gln Asn
 245 250 255

Tyr Thr Cys His Val His His Lys Gly Leu Pro Glu Pro Leu Thr Leu
 260 265 270

Arg Trp Lys
 275

<210> 38

<211> 274

<212> PRT

<213> rat

<400> 38

Gly Ser His Ser Leu Arg Tyr Phe Tyr Thr Ala Val Ser Arg Pro Gly
 1 5 10 15

Leu Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Glu
 20 25 30

Phe Val Arg Phe Asp Ser Asp Ala Glu Asn Pro Arg Met Glu Pro Arg
 35 40 45

Ala Arg Trp Met Glu Arg Glu Gly Pro Glu Tyr Trp Glu Gln Gln Thr
 50 55 60

Arg Ile Ala Lys Glu Trp Glu Gln Ile Tyr Arg Val Asp Leu Arg Thr
 65 70 75 80

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

Glu Met Tyr Gly Cys Asp Val Gly Ser Asp Gly Ser Leu Leu Arg Gly
 100 105 110

Tyr Arg Gln Asp Ala Tyr Asp Gly Arg Asp Tyr Ile Ala Leu Asn Glu
115 120 125

Asp Leu Lys Thr Trp Thr Ala Ala Asp Phe Ala Ala Gln Ile Thr Arg
130 135 140

Asn Lys Trp Glu Arg Ala Arg Tyr Ala Glu Arg Leu Arg Ala Tyr Leu
145 150 155 160

Glu Gly Thr Cys Val Glu Trp Leu Ser Arg Tyr Leu Glu Leu Gly Lys
165 170 175

Glu Thr Leu Leu Arg Ser Asp Pro Pro Glu Ala His Val Thr Leu His
180 185 190

Pro Arg Pro Glu Gly Asp Val Thr Leu Arg Cys Trp Ala Leu Gly Phe
195 200 205

Tyr Pro Ala Asp Ile Thr Leu Thr Trp Gln Leu Asn Gly Glu Asp Leu
210 215 220

Thr Gln Asp Met Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr
225 230 235 240

Phe Gln Lys Trp Ala Ser Val Val Val Pro Leu Gly Lys Glu Gln Asn
245 250 255

Tyr Thr Cys Arg Val Glu His Glu Gly Leu Pro Lys Pro Leu Ser Gln
260 265 270

Arg Trp

<210> 39
<211> 440
<212> PRT
<213> homo sapiens

<400> 39

Arg Ile Ile Pro Arg His Leu Gln Leu Gly Cys Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Arg Thr Pro Lys Ile Gln
20 25 30

Val Tyr Ser Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn
35 40 45

Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu
50 55 60

Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe
65 70 75 80

Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro
85 90 95

Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser
100 105 110

Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Ser His Ser Met Arg Tyr Phe Ser Ala Ala Val Ser Arg Pro Gly Arg
145 150 155 160

Gly Glu Pro Arg Phe Ile Ala Met Gly Tyr Val Asp Asp Thr Gln Phe
165 170 175

Val Arg Phe Asp Ser Asp Ser Ala Cys Pro Arg Met Glu Pro Arg Ala
180 185 190

Pro Trp Val Glu Gln Glu Gly Pro Glu Tyr Trp Glu Glu Glu Thr Arg
195 200 205

Asn Thr Lys Ala His Ala Gln Thr Asp Arg Met Asn Leu Gln Thr Leu
210 215 220

Arg Gly Cys Tyr Asn Gln Ser Glu Ala Ser Ser His Thr Leu Gln Trp

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

<210> 40
<211> 441
<212> PRT
<213> Artificial

<220>

<223> exemplary modified human HLA-G β 2M MHC class I complex (wherein the HLA-G specific amino acids have been replaced by HLA-A consensus amino acids (= degrafted HLA-G))

<400> 40

Arg Ile Ile Pro Arg His Leu Gln Leu Gly Cys Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Arg Thr Pro Lys Ile Gln
20 25 30

Val Tyr Ser Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn
35 40 45

Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu
50 55 60

Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe
65 70 75 80

Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro
85 90 95

Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser
100 105 110

Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Ser His Ser Met Arg Tyr Phe Ser Ala Ala Val Ser Arg Pro Gly Arg
145 150 155 160

Gly Glu Pro Arg Phe Ile Ala Met Gly Tyr Val Asp Asp Thr Gln Phe

165

170

175

Val Arg Phe Asp Ser Asp Ala Ala Ser Pro Arg Met Glu Pro Arg Ala
 180 185 190

Pro Trp Val Glu Gln Glu Gly Pro Glu Tyr Trp Asp Glu Glu Thr Arg
 195 200 205

Asn Thr Lys Ala His Ala Gln Thr Asp Arg Val Asn Leu Gly Thr Leu
 210 215 220

Arg Gly Cys Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln Trp
 225 230 235 240

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

Glu Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Leu Ala Leu Asn Glu Asp
 260 265 270

Leu Arg Ser Trp Thr Ala Ala Asp Thr Ala Ala Gln Ile Ser Lys Arg
 275 280 285

Lys Cys Glu Ala Ala His Val Ala Glu Gln Arg Arg Ala Tyr Leu Glu
 290 295 300

Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu
 305 310 315 320

Thr Leu Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr His His Pro
 325 330 335

Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr
 340 345 350

Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr
 355 360 365

Gln Asp Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe
 370 375 380

Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr
385 390 395 400

Thr Cys His Val Gln His Glu Gly Leu Pro Glu Pro Leu Thr Leu Arg
405 410 415

Trp Lys Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
420 425 430

Trp His Glu His His His His His His
435 440

<210> 41
<211> 441
<212> PRT
<213> mus musculus

<400> 41

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

Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Lys Thr Pro Gln Ile Gln
20 25 30

Val Tyr Ser Arg His Pro Pro Glu Asn Gly Lys Pro Asn Ile Leu Asn
35 40 45

Cys Tyr Val Thr Gln Phe His Pro Pro His Ile Glu Ile Gln Met Leu
50 55 60

Lys Asn Gly Lys Lys Ile Pro Lys Val Glu Met Ser Asp Met Ser Phe
65 70 75 80

Ser Lys Asp Trp Ser Phe Tyr Ile Leu Ala His Thr Glu Phe Thr Pro
85 90 95

Thr Glu Thr Asp Thr Tyr Ala Cys Arg Val Lys His Asp Ser Met Ala
100 105 110

Glu Pro Lys Thr Val Tyr Trp Asp Arg Asp Met Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Pro His Ser Leu Arg Tyr Phe Val Thr Ala Val Ser Arg Pro Gly Leu
145 150 155 160

Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln Phe
165 170 175

Val Arg Phe Asp Ser Asp Ala Asp Asn Pro Arg Phe Glu Pro Arg Ala
180 185 190

Pro Trp Met Glu Gln Glu Gly Pro Glu Tyr Trp Glu Glu Gln Thr Gln
195 200 205

Arg Ala Lys Ser Asp Glu Gln Trp Phe Arg Val Ser Leu Arg Thr Ala
210 215 220

Gln Arg Cys Tyr Asn Gln Ser Lys Gly Gly Ser His Thr Phe Gln Arg
225 230 235 240

Met Phe Gly Cys Asp Val Gly Ser Asp Trp Arg Leu Leu Arg Gly Tyr
245 250 255

Gln Gln Phe Ala Tyr Asp Gly Arg Asp Tyr Ile Ala Leu Asn Glu Asp
260 265 270

Leu Lys Thr Trp Thr Ala Ala Asp Thr Ala Ala Leu Ile Thr Arg Arg
275 280 285

Lys Trp Glu Gln Ala Gly Asp Ala Glu Tyr Tyr Arg Ala Tyr Leu Glu
290 295 300

Gly Glu Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Leu Gly Asn Glu
305 310 315 320

Thr Leu Leu Arg Thr Asp Ser Pro Lys Ala His Val Thr Tyr His Pro
325 330 335

Arg Ser Gln Val Asp Val Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr
340 345 350

Pro Ala Asp Ile Thr Leu Thr Trp Gln Leu Asn Gly Glu Asp Leu Thr
355 360 365

Gln Asp Met Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe
370 375 380

Gln Lys Trp Ala Ala Val Val Val Pro Leu Gly Lys Glu Gln Asn Tyr
385 390 395 400

Thr Cys His Val His His Lys Gly Leu Pro Glu Pro Leu Thr Leu Arg
405 410 415

Trp Lys Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
420 425 430

Trp His Glu His His His His His His
435 440

<210> 42

<211> 441

<212> PRT

<213> Artificial

<220>

<223> exemplary human HLA-G/ mouse H2Kd β 2M MHC class I complex wherein
the positions specific for human HLA-G are grafted onto the mouse
H2Kd framework

<400> 42

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

Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Lys Thr Pro Gln Ile Gln
20 25 30

Val Tyr Ser Arg His Pro Pro Glu Asn Gly Lys Pro Asn Ile Leu Asn
35 40 45

Cys Tyr Val Thr Gln Phe His Pro Pro His Ile Glu Ile Gln Met Leu
50 55 60

Lys Asn Gly Lys Lys Ile Pro Lys Val Glu Met Ser Asp Met Ser Phe
65 70 75 80

Ser Lys Asp Trp Ser Phe Tyr Ile Leu Ala His Thr Glu Phe Thr Pro
85 90 95

Thr Glu Thr Asp Thr Tyr Ala Cys Arg Val Lys His Asp Ser Met Ala
100 105 110

Glu Pro Lys Thr Val Tyr Trp Asp Arg Asp Met Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Pro His Ser Leu Arg Tyr Phe Val Thr Ala Val Ser Arg Pro Gly Leu
145 150 155 160

Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln Phe
165 170 175

Val Arg Phe Asp Ser Asp Ser Ala Ser Pro Arg Phe Glu Pro Arg Ala
180 185 190

Pro Trp Val Glu Gln Glu Gly Pro Glu Tyr Trp Glu Glu Gln Thr Gln
195 200 205

Arg Ala Lys Ser Asp Glu Gln Trp Phe Arg Met Ser Leu Gln Thr Ala
210 215 220

Arg Gly Cys Tyr Asn Gln Ser Glu Ala Ser Ser His Thr Phe Gln Arg
225 230 235 240

Met Phe Gly Cys Asp Leu Gly Ser Asp Gly Arg Leu Leu Arg Gly Tyr
245 250 255

Gln Gln Phe Ala Tyr Asp Gly Arg Asp Tyr Ile Ala Leu Asn Glu Asp
260 265 270

Leu Arg Ser Trp Thr Ala Ala Asp Thr Ala Ala Leu Ile Thr Lys Arg
275 280 285

Lys Trp Glu Ala Ala Asn Asp Ala Glu Tyr Tyr Arg Ala Tyr Leu Glu
290 295 300

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

Met Leu Gln Arg Thr Asp Ser Pro Lys Ala His Val Thr His His Pro
325 330 335

Val Phe Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr
340 345 350

Pro Ala Glu Ile Ile Leu Thr Trp Gln Leu Asn Gly Glu Asp Leu Thr
355 360 365

Gln Asp Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe
370 375 380

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

Thr Cys His Val Gln His Glu Gly Leu Pro Glu Pro Leu Met Leu Arg
405 410 415

Trp Lys Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
420 425 430

Trp His Glu His His His His His His
435 440

<210> 43
<211> 440
<212> PRT
<213> rat

<400> 43

Ala Gln Phe Ser Ala Ser Ala Ser Arg Gly Cys Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Lys Thr Pro Gln Ile Gln
20 25 30

Val Tyr Ser Arg His Pro Pro Glu Asn Gly Lys Pro Asn Phe Leu Asn
35 40 45

Cys Tyr Val Ser Gln Phe His Pro Pro Gln Ile Glu Ile Glu Leu Leu
50 55 60

Lys Asn Gly Lys Lys Ile Pro Asn Ile Glu Met Ser Asp Leu Ser Phe
65 70 75 80

Ser Lys Asp Trp Ser Phe Tyr Ile Leu Ala His Thr Glu Phe Thr Pro
85 90 95

Thr Glu Thr Asp Val Tyr Ala Cys Arg Val Lys His Val Thr Leu Lys
100 105 110

Glu Pro Lys Thr Val Thr Trp Asp Arg Asp Met Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Ser His Ser Leu Arg Tyr Phe Tyr Thr Ala Val Ser Arg Pro Gly Leu
145 150 155 160

Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Glu Phe
165 170 175

Val Arg Phe Asp Ser Asp Ala Glu Asn Pro Arg Met Glu Pro Arg Ala
180 185 190

Arg Trp Met Glu Arg Glu Gly Pro Glu Tyr Trp Glu Gln Gln Thr Arg
195 200 205

Ile Ala Lys Glu Trp Glu Gln Ile Tyr Arg Val Asp Leu Arg Thr Leu
210 215 220

Arg Gly Cys Tyr Asn Gln Ser Glu Gly Gly Ser His Thr Ile Gln Glu

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

<210> 44
<211> 440
<212> PRT
<213> Artificial

<220>

<223> exemplary human HLA-G/ rat RT1A β 2M MHC class I complex wherein the positions specific for human HLA-G are grafted onto the rat RT1A framework

<400> 44

Ala Gln Phe Ser Ala Ser Ala Ser Arg Gly Cys Gly Gly Ser Gly Gly
1 5 10 15

Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Lys Thr Pro Gln Ile Gln
20 25 30

Val Tyr Ser Arg His Pro Pro Glu Asn Gly Lys Pro Asn Phe Leu Asn
35 40 45

Cys Tyr Val Ser Gln Phe His Pro Pro Gln Ile Glu Ile Glu Leu Leu
50 55 60

Lys Asn Gly Lys Lys Ile Pro Asn Ile Glu Met Ser Asp Leu Ser Phe
65 70 75 80

Ser Lys Asp Trp Ser Phe Tyr Ile Leu Ala His Thr Glu Phe Thr Pro
85 90 95

Thr Glu Thr Asp Val Tyr Ala Cys Arg Val Lys His Val Thr Leu Lys
100 105 110

Glu Pro Lys Thr Val Thr Trp Asp Arg Asp Met Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Ser His Ser Leu Arg Tyr Phe Tyr Thr Ala Val Ser Arg Pro Gly Leu
145 150 155 160

Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Glu Phe

165

170

175

Val Arg Phe Asp Ser Asp Ser Ala Ser Pro Arg Met Glu Pro Arg Ala
 180 185 190

Pro Trp Val Glu Gln Glu Gly Pro Glu Tyr Trp Glu Gln Gln Thr Arg
 195 200 205

Ile Ala Lys Glu Trp Glu Gln Ile Tyr Arg Met Asp Leu Gln Thr Leu
 210 215 220

Arg Gly Cys Tyr Asn Gln Ser Glu Ala Ser Ser His Thr Ile Gln Glu
 225 230 235 240

Met Tyr Gly Cys Asp Leu Gly Ser Asp Gly Arg Leu Leu Arg Gly Tyr
 245 250 255

Arg Gln Asp Ala Tyr Asp Gly Arg Asp Tyr Ile Ala Leu Asn Glu Asp
 260 265 270

Leu Arg Ser Trp Thr Ala Ala Asp Phe Ala Ala Gln Ile Thr Lys Arg
 275 280 285

Lys Trp Glu Ala Ala Asn Tyr Ala Glu Arg Leu Arg Ala Tyr Leu Glu
 290 295 300

Gly Thr Cys Val Glu Trp Leu His Arg Tyr Leu Glu Asn Gly Lys Glu
 305 310 315 320

Met Leu Gln Arg Ala Asp Pro Pro Glu Ala His Val Thr His His Pro
 325 330 335

Val Phe Asp Tyr Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr
 340 345 350

Pro Ala Glu Ile Ile Leu Thr Trp Gln Leu Asn Gly Glu Asp Leu Thr
 355 360 365

Gln Asp Val Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe
 370 375 380

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

Thr Cys Arg Val Gln His Glu Gly Leu Pro Lys Pro Leu Met Leu Arg
405 410 415

Trp Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
420 425 430

His Glu His His His His His His
435 440

<210> 45
<211> 33
<212> PRT
<213> Artificial

<220>
<223> linker and his-Tag

<400> 45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser Gly Leu Asn Asp
1 5 10 15

Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu His His His His His
20 25 30

His

<210> 46
<211> 9
<212> PRT
<213> Artificial

<220>
<223> peptide

<400> 46

Val Leu Asp Phe Ala Pro Pro Gly Ala
1 5

<210> 47

<211> 107
<212> PRT
<213> Homo Sapiens

<400> 47

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> 48
<211> 105
<212> PRT
<213> Homo Sapiens

<400> 48

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> 49

<211> 328

<212> PRT

<213> Homo Sapiens

<400> 49

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
325

<210> 50

<211> 328

<212> PRT
<213> homo sapiens

<400> 50

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
 325

<210> 51
 <211> 325
 <212> PRT
 <213> Homo Sapiens

<400> 51

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
325

<210> 52
<211> 6
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-H1, P035-093 (abbreviated as P035)

<400> 52

Ser Tyr Ala Met Asn Trp
1 5

<210> 53
<211> 18
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-H2, P035-093

<400> 53

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys

<210> 54
<211> 14
<212> PRT
<213> Artificial

<220>

<223> heavy chain CDR-H3, P035-093

<400> 54

Ala	Ser	Asn	Phe	Pro	Ala	Ser	Tyr	Val	Ser	Tyr	Phe	Ala	Tyr
1				5					10				

<210> 55

<211> 14

<212> PRT

<213> Artificial

<220>

<223> light chain CDR-L1, P035-093

<400> 55

Gly	Ser	Ser	Thr	Gly	Ala	Val	Thr	Thr	Ser	Asn	Tyr	Ala	Asn
1				5					10				

<210> 56

<211> 7

<212> PRT

<213> Artificial

<220>

<223> light chain CDR-L2, P035-093

<400> 56

Gly	Thr	Asn	Lys	Arg	Ala	Pro
1				5		

<210> 57

<211> 9

<212> PRT

<213> Artificial

<220>

<223> light chain CDR-L3, P035-093

<400> 57

Ala	Leu	Trp	Tyr	Ser	Asn	Leu	Trp	Val
1				5				

<210> 58

<211> 125

<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain VH, P035-093

<400> 58

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 Ser 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 Ala Ser Asn Phe Pro Ala Ser Tyr Val Ser Tyr Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 59
<211> 109
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, P035-093

<400> 59

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
100 105

<210> 60
<211> 5
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-H1, Clone 22 (abbreviated as C122)

<400> 60

Ser Tyr Ala Met Asn
1 5

<210> 61
<211> 18
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-H2, Clone 22

<400> 61

Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys

<210> 62
<211> 14
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-H3, Clone 22

<400> 62

His	Thr	Thr	Phe	Pro	Ser	Ser	Tyr	Val	Ser	Tyr	Tyr	Gly	Tyr
1				5					10				

<210> 63
<211> 14
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L1, Clone 22

<400> 63

Gly	Ser	Ser	Thr	Gly	Ala	Val	Thr	Thr	Ser	Asn	Tyr	Ala	Asn
1				5					10				

<210> 64
<211> 7
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L2, Clone 22

<400> 64

Gly	Thr	Asn	Lys	Arg	Ala	Pro
1				5		

<210> 65
<211> 9
<212> PRT
<213> Artificial

<220>
<223> light chain CDR-L3, Clone 22

<400> 65

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 66
<211> 125
<212> PRT
<213> Artificial

<220>
<223> heavy chain variable domain VH, Clone 22

<400> 66

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 Gln Phe Ser Ser 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 Thr Thr Phe Pro Ser Ser Tyr Val Ser Tyr Tyr
100 105 110

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

<210> 67
<211> 109
<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, Clone 22

<400> 67

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
100 105

<210> 68

<211> 5

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR-H1, V9

<400> 68

Gly Tyr Thr Met Asn
1 5

<210> 69

<211> 17

<212> PRT

<213> Artificial

<220>

<223> heavy chain CDR-H2, V9

<400> 69

Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 70
<211> 13
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-H3, V9

<400> 70

Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val
1 5 10

<210> 71
<211> 11
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-L1, V9

<400> 71

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

<210> 72
<211> 7
<212> PRT
<213> Artificial

<220>
<223> heavy chain CDR-L2, V9

<400> 72

Tyr Thr Ser Arg Leu Glu Ser
1 5

<210> 73
<211> 9
<212> PRT
<213> Artificial

<220>

<223> heavy chain CDR-L3, V9

<400> 73

Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 74

<211> 122

<212> PRT

<213> Artificial

<220>

<223> heavy chain variable domain VH, V9

<400> 74

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

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

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

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

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

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

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

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

<210> 75

<211> 107

<212> PRT
<213> Artificial

<220>
<223> light chain variable domain VL, V9

<400> 75

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

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

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

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

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

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

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

<210> 76
<211> 232
<212> PRT
<213> Artificial

<220>
<223> light chain 1 P1AF7977

<400> 76

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 Ser 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 Ala Ser Asn Phe Pro Ala Ser Tyr Val Ser Tyr 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> 77

<211> 220

<212> PRT
<213> Artificial

<220>
<223> light chain 2 P1AF7977

<400> 77

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 Ser Ser Gln Ser Val Leu Asn Pro
20 25 30

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

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

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

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

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Arg Lys Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

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

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 78
<211> 449
<212> PRT
<213> Artificial

<220>
<223> heavy chain 1 P1AF7977

<400> 78

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Phe Ser Leu Arg Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Gln Gly Val 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

<210> 79
<211> 674
<212> PRT
<213> Artificial

<220>
<223> heavy chain 2 P1AF7977

<400> 79

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Phe Ser Leu Arg Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Gln Gly Val 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 Gly 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
305 310 315 320

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
385 390 395 400

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
465 470 475 480

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> 80

<211> 232

<212> PRT

<213> Artificial

<220>

<223> light chain 1 P1AF7978

<400> 80

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 Gln Phe Ser Ser 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 Thr Thr Phe Pro Ser Ser Tyr Val Ser Tyr Tyr
100 105 110

Gly 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> 81
<211> 220
<212> PRT
<213> Artificial

<220>
<223> light chain 2 P1AF7978

<400> 81

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 Ser Ser Gln Ser Val Leu Asn Pro
20 25 30

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

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

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

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

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Arg Lys Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

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

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 82
<211> 449
<212> PRT
<213> Artificial

<220>
<223> heavy chain 1 P1AF7978

<400> 82

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Phe Ser Leu Arg Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Gln Gly Val 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

<210> 83
<211> 674
<212> PRT
<213> Artificial

<220>
<223> heavy chain 2 P1AF7978

<400> 83

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Phe Ser Leu Arg Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Gln Gly Val 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 Gly 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
305 310 315 320

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
385 390 395 400

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
465 470 475 480

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> 84
<211> 229
<212> PRT
<213> Artificial

<220>
<223> light chain 1 P1AF7979

<400> 84

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys
225

<210> 85
<211> 220
<212> PRT
<213> Artificial

<220>
<223> light chain 2 P1AF7979

<400> 85

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 Ser Ser Gln Ser Val Leu Asn Pro
20 25 30

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

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

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

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

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

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Arg Lys Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

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

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

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

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 86
<211> 449
<212> PRT
<213> Artificial

<220>
<223> heavy chain 1 P1AF7979

<400> 86

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Phe Ser Leu Arg Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Gln Gly Val 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

<210> 87
<211> 672

<212> PRT
<213> Artificial

<220>
<223> heavy chain 2 P1AF7979

<400> 87

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

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

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Phe Ser Leu Arg Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

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

Gln Gly Val 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 Gly Asp Ile Gln Met Thr
225 230 235 240

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
245 250 255

Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
260 265 270

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
275 280 285

Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
290 295 300

Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
305 310 315 320

Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gln Gly
325 330 335

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

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

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
385 390 395 400

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
405 410 415

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
420 425 430

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
435 440 445

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
450 455 460

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
465 470 475 480

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
485 490 495

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
500 505 510

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
515 520 525

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
530 535 540

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
545 550 555 560

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
565 570 575

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
580 585 590

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
595 600 605

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
610 615 620

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
625 630 635 640

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
645 650 655

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
660 665 670

<210> 88
<211> 207
<212> PRT
<213> homo sapiens

<400> 88

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
20 25 30

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

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65 70 75 80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85 90 95

Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
100 105 110

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
115 120 125

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

130

135

140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
 145 150 155 160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
 165 170 175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
 180 185 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
 195 200 205

<210> 89

<211> 198

<212> PRT

<213> Cynomolgus

<400> 89

Met Gln Ser Gly Thr Arg Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
 1 5 10 15

Ile Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Ser Ile Thr
 20 25 30

Gln Thr Pro Tyr Gln Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
 35 40 45

Cys Ser Gln His Leu Gly Ser Glu Ala Gln Trp Gln His Asn Gly Lys
 50 55 60

Asn Lys Glu Asp Ser Gly Asp Arg Leu Phe Leu Pro Glu Phe Ser Glu
 65 70 75 80

Met Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly Ser Asn Pro
 85 90 95

Glu Asp Ala Ser His His Leu Tyr Leu Lys Ala Arg Val Cys Glu Asn
 100 105 110

Cys Met Glu Met Asp Val Met Ala Val Ala Thr Ile Val Ile Val Asp
115 120 125

Ile Cys Ile Thr Leu Gly Leu Leu Leu Leu Val Tyr Tyr Trp Ser Lys
130 135 140

Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly
145 150 155 160

Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro Asn
165 170 175

Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Gln Asp Leu Tyr Ser Gly
180 185 190

Leu Asn Gln Arg Arg Ile
195

<210> 90
<211> 360
<212> PRT
<213> Artificial

<220>
<223> Human CD3 epsilon stalk - Fc(knob) - Avi

<400> 90

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

Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro
20 25 30

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

Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys
50 55 60

Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg
65 70 75 80

Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg
85 90 95

Val Ser Glu Asn Cys Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser
100 105 110

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
115 120 125

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
130 135 140

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
145 150 155 160

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
165 170 175

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
180 185 190

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
195 200 205

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
210 215 220

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
225 230 235 240

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
245 250 255

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
260 265 270

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
275 280 285

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
290 295 300

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
325 330 335

Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu
340 345 350

Ala Gln Lys Ile Glu Trp His Glu
355 360

<210> 91
<211> 325
<212> PRT
<213> Artificial

<220>
<223> Human CD3 delta stalk - Fc (hole) - Avi

<400> 91

Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys
1 5 10 15

Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val Gly Thr Leu Leu Ser
20 25 30

Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly
35 40 45

Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr
50 55 60

Val Gln Val His Tyr Arg Met Cys Arg Ser Glu Gln Leu Tyr Phe Gln
65 70 75 80

Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
85 90 95

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
100 105 110

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
115 120 125

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
130 135 140

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
145 150 155 160

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
165 170 175

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
180 185 190

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
195 200 205

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

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
225 230 235 240

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
245 250 255

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
260 265 270

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
275 280 285

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
290 295 300

Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys
305 310 315 320

Ile Glu Trp His Glu
325

<210> 92
<211> 125
<212> PRT
<213> Artificial

<220>
<223> CD3orig VH

<400> 92

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
115 120 125

<210> 93
<211> 109
<212> PRT
<213> Artificial

<220>
<223> CD3orig VL

<400> 93

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
100 105

<210> 94

<211> 453

<212> PRT

<213> Artificial

<220>

<223> CD3orig IgG HC

<400> 94

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 Thr
115 120 125

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

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

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

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

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

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

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

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

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

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

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

Leu Ser Leu Ser Pro
450

<210> 95

<211> 453

<212> PRT

<213> Artificial

<220>

<223> P035 IgG HC

<400> 95

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 Gln Phe Ser Ser 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 Thr Thr Phe Pro Ser Ser Tyr Val Ser Tyr Tyr
100 105 110

Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

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

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

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

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

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

Leu Ser Leu Ser Pro
450

<210> 96
<211> 216
<212> PRT
<213> Artificial

<220>
<223> CD3orig / P035 IgG LC

<400> 96

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 Arg Thr Val
100 105 110

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
210 215