

SEQUENCE LISTING

<110> Immatics Biotechnologies GmbH

<120> Antigen binding proteins specifically binding MAGE-A

<130> 1017-18 PCT

<150> US 62/882,131

<151> 2019-08-02

<150> US 62/905,782

<151> 2019-09-25

<150> DE 10 2019 121 007.0

<151> 2019-08-02

<160> 182

<170> PatentIn version 3.5

<210> 1

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> MAG-003 peptide

<400> 1

Lys Val Leu Glu His Val Val Arg Val
1 5

<210> 2

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5 TCR alpha chain full length

<400> 2

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
1 5 10 15

Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
20 25 30

Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser
35 40 45

Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
 50 55 60

Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
 65 70 75 80

Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg
 85 90 95

Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
 100 105 110

Tyr Ser Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser
 115 120 125

Ile Arg Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
 130 135 140

Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
 145 150 155 160

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
 165 170 175

Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
 180 185 190

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
 195 200 205

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
 210 215 220

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
 225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
 245 250 255

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

<210> 3
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 alpha leader

<400> 3

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
1 5 10 15

Asp Cys Met Ser Arg
20

<210> 4
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 alpha variable

<400> 4

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

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

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

Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu
50 55 60

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

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

Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
100 105 110

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 CDRa1

<400> 5

Asp Ser Ser Ser Thr Tyr
1 5

<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 CDRa2

<400> 6

Ile Phe Ser Asn Met Asp Met
1 5

<210> 7
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 CDRa3

<400> 7

Cys Ala Glu Tyr Ser Ser Ala Ser Lys Ile Ile Phe
1 5 10

<210> 8
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 alpha constant

<400> 8

Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15

Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30

Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
35 40 45

Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60

Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80

Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95

Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110

Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 9
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 TCR beta chain full length

<400> 9

Met Gly Ser Trp Thr Leu Cys Cys Val Ser Leu Cys Ile Leu Val Ala
1 5 10 15

Lys His Thr Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr
20 25 30

Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Ser Gly His
35 40 45

Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu

50

55

60

Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro
 65 70 75 80

Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu
 85 90 95

Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala
 100 105 110

Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
 115 120 125

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
 130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
 145 150 155 160

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
 165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
 180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
 195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
 210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
 225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
 245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly
 260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr

275

280

285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
 290 295 300

Arg Lys Asp Ser Arg Gly
 305 310

<210> 10
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> R7P1D5 beta leader

<400> 10

Met Gly Ser Trp Thr Leu Cys Cys Val Ser Leu Cys Ile Leu Val Ala
 1 5 10 15

Lys His Thr

<210> 11
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> R7P1D5 beta variabl

<400> 11

Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu Met Gly
 1 5 10 15

Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Ser Gly His Asp Tyr Leu
 20 25 30

Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu Ile Tyr
 35 40 45

Phe Asn Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro Glu Asp Arg
 50 55 60

Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln

65707580

Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser Arg Ala

859095

Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu

100105110

<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5 CDRb1

<400> 12

Ser Gly His Asp Tyr

15

<210> 13

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5 CDRb2

<400> 13

Phe Asn Asn Asn Val Pro

15

<210> 14

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5 CDRb3

<400> 14

Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe

1510

<210> 15

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5 beta constant

<400> 15

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

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

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

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65 70 75 80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
85 90 95

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

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115 120 125

Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser
130 135 140

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145 150 155 160

Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
165 170 175

Ser Arg Gly

<210> 16

<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> Aga2p-R7P1D5

<400> 16

Met Gln Leu Leu Arg Cys Phe Ser Ile Phe Ser Val Ile Ala Ser Val
1 5 10 15

Leu Ala Gln Glu Leu Thr Thr Ile Cys Glu Gln Ile Pro Ser Pro Thr
20 25 30

Leu Glu Ser Thr Pro Tyr Ser Leu Ser Thr Thr Thr Ile Leu Ala Asn
35 40 45

Gly Lys Ala Met Gln Gly Val Phe Glu Tyr Tyr Lys Ser Val Thr Phe
50 55 60

Val Ser Asn Cys Gly Ser His Pro Ser Thr Thr Ser Lys Gly Ser Pro
65 70 75 80

Ile Asn Thr Gln Tyr Val Phe Gly Gly Gly Gly Ser Asp Tyr Lys Asp
85 90 95

Asp Asp Asp Lys Gly Gly Gly Ala Ser Gly Glu Asp Val Glu Gln Ser
100 105 110

Leu Phe Leu Ser Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr
115 120 125

Tyr Thr Asp Ser Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro
130 135 140

Gly Ala Gly Leu Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met
145 150 155 160

Lys Gln Asp Gln Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His
165 170 175

Leu Ser Leu Arg Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr
180 185 190

Phe Cys Ala Glu Tyr Ser Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly
 195 200 205

 Thr Arg Leu Ser Ile Arg Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly
 210 215 220

 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 225 230 235 240

 Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu Met Gly
 245 250 255

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

 Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu Ile Tyr
 275 280 285

 Phe Asn Asn Asn Val Pro Ile Asp Asp Ser Gly Met Pro Glu Asp Arg
 290 295 300

 Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln
 305 310 315 320

 Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser Arg Ala
 325 330 335

 Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu
 340 345 350

 Ala Ala Ala Gly Gly Ser Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu
 355 360 365

 Asp Leu
 370

<210> 17

<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Leader sequence and Aga2p

<400> 17

Met Gln Leu Leu Arg Cys Phe Ser Ile Phe Ser Val Ile Ala Ser Val
1 5 10 15

Leu Ala Gln Glu Leu Thr Thr Ile Cys Glu Gln Ile Pro Ser Pro Thr
20 25 30

Leu Glu Ser Thr Pro Tyr Ser Leu Ser Thr Thr Thr Ile Leu Ala Asn
35 40 45

Gly Lys Ala Met Gln Gly Val Phe Glu Tyr Tyr Lys Ser Val Thr Phe
50 55 60

Val Ser Asn Cys Gly Ser His Pro Ser Thr Thr Ser Lys Gly Ser Pro
65 70 75 80

Ile Asn Thr Gln Tyr Val Phe
85

<210> 18

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG tag plus linkers

<400> 18

Gly Gly Gly Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
1 5 10 15

Ala Ser

<210> 19

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Single chain variable domains of R7P1D5 with linker

<400> 19

Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly Asp

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

Gly Ser Arg Leu Thr Val Leu
245

<210> 20
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker and Myc tag

<400> 20

Ala Ala Ala Gly Gly Ser Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu
1 5 10 15

Asp Leu

<210> 21
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD Ra2 mutant 1 (aF57Y)

<400> 21

Ile Tyr Ser Asn Met Asp Met
1 5

<210> 22
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> scTv R7P1D5S (Stabilized version of scTv R7P1D5)

<400> 22

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

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

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

Ile Tyr Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu
 50 55 60

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

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

Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly
 100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro Arg
 130 135 140

His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro
 145 150 155 160

Ile Ser Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg
 165 170 175

Gly Leu Glu Leu Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp Asp
 180 185 190

Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser
 195 200 205

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

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

Gly Ser Arg Leu Thr Val Leu
 245

<210> 23
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> RABGAP1L-001

<400> 23

Phe Leu Leu Glu Thr Val Val Arg Val
1 5

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> AXIN1-001

<400> 24

Ile Leu Asp Glu His Val Gln Arg Val
1 5

<210> 25
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> ANO5-001

<400> 25

Ile Val Met Glu His Val Val Phe Leu
1 5

<210> 26
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TPX2-001

<400> 26

Lys Ile Leu Glu Asp Val Val Gly Val
1 5

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

<220>
<223> SYNE3-001

<400> 27

Lys Leu Leu Asp Leu Gln Val Arg Val
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MIA3-001

<400> 28

Lys Val Leu Asp Lys Val Phe Arg Ala
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HERC4-001

<400> 29

Lys Val Leu Glu Ile Leu His Arg Val
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PSME2-001

<400> 30

Lys Val Leu Glu Arg Val Asn Ala Val
1 5

<210> 31
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HEATR5A-001

<400> 31

Lys Val Leu Glu Thr Leu Val Thr Val
1 5

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CNOT1-003

<400> 32

Lys Val Leu Gly Ile Val Val Gly Val
1 5

<210> 33
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> TEP1-003

<400> 33

Ala Val Glu Glu His Val Val Ser Val
1 5

<210> 34
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PITPNM3-001

<400> 34

Ser Val Leu Glu Lys Val Thr Arg Ala
1 5

<210> 35
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDra3 mutant 1

<400> 35

Cys	Ala	Glu	Met	Thr	Ser	Glu	Ser	Lys	Ile	Ile	Phe
1				5					10		

<210> 36
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDra3 mutant 2

<400> 36

Cys	Ala	Glu	Phe	Thr	Ser	Glu	Ser	Lys	Ile	Ile	Phe
1				5					10		

<210> 37
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDra3 mutant 3

<400> 37

Cys	Ala	Glu	Phe	Asn	Ser	Glu	Ser	Lys	Ile	Ile	Phe
1				5					10		

<210> 38
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDra3 mutant 4

<400> 38

Cys	Ala	Glu	Phe	Ser	Ser	Ala	Ser	Lys	Ile	Ile	Phe
1				5					10		

<210> 39
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD Ra3 mutant 5

<400> 39

Cys Ala Glu Ala Thr Ser Glu Ser Lys Ile Ile Phe
1 5 10

<210> 40
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 - alpha chain variant 1

<400> 40

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
1 5 10 15

Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
20 25 30

Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser
35 40 45

Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
50 55 60

Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
65 70 75 80

Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg
85 90 95

Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
100 105 110

Met Thr Ser Glu Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser
115 120 125

Ile Arg Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
130 135 140

Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
145 150 155 160

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
165 170 175

Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
180 185 190

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
195 200 205

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
210 215 220

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
245 250 255

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

<210> 41
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 - alpha chain variant 2

<400> 41

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
1 5 10 15

Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
20 25 30

Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser

35

40

45

Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
 50 55 60

Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
 65 70 75 80

Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg
 85 90 95

Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
 100 105 110

Phe Thr Ser Glu Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser
 115 120 125

Ile Arg Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
 130 135 140

Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
 145 150 155 160

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
 165 170 175

Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
 180 185 190

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
 195 200 205

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
 210 215 220

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
 225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
 245 250 255

Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser

260

265

270

<210> 42
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> R7P1D5 - alpha chain variant 3

<400> 42

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
 1 5 10 15

Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
 20 25 30

Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser
 35 40 45

Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
 50 55 60

Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
 65 70 75 80

Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg
 85 90 95

Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
 100 105 110

Phe Asn Ser Glu Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser
 115 120 125

Ile Arg Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
 130 135 140

Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
 145 150 155 160

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
 165 170 175

Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
180 185 190

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
195 200 205

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
210 215 220

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
245 250 255

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

<210> 43
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5 - alpha chain variant 4

<400> 43

Met Lys Thr Phe Ala Gly Phe Ser Phe Leu Phe Leu Trp Leu Gln Leu
1 5 10 15

Asp Cys Met Ser Arg Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser
20 25 30

Val Arg Glu Gly Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser
35 40 45

Ser Ser Thr Tyr Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu
50 55 60

Gln Leu Leu Thr Tyr Ile Phe Ser Asn Met Asp Met Lys Gln Asp Gln
65 70 75 80

Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg

85

90

95

Ile Ala Asp Thr Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu
 100 105 110

Phe Ser Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser
 115 120 125

Ile Arg Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
 130 135 140

Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
 145 150 155 160

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
 165 170 175

Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
 180 185 190

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
 195 200 205

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
 210 215 220

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
 225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
 245 250 255

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

<210> 44

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5 - alpha chain variant 5

<400> 44

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

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
245 250 255

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

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> NYES01-001

<400> 45

Ser Leu Leu Met Trp Ile Thr Gln Val
1 5

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

<220>
<223> MAG-003_A1

<400> 46

Ala Val Leu Glu His Val Val Arg Val
1 5

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MAG-003_A2

<400> 47

Lys Ala Leu Glu His Val Val Arg Val
1 5

<210> 48

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

<220>
<223> MAG-003_A3

<400> 48

Lys Val Ala Glu His Val Val Arg Val
1 5

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MAG-003_A4

<400> 49

Lys Val Leu Ala His Val Val Arg Val
1 5

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MAG-003_A5

<400> 50

Lys Val Leu Glu Ala Val Val Arg Val
1 5

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

<220>
<223> MAG-003_A6

<400> 51

Lys Val Leu Glu His Ala Val Arg Val
1 5

<210> 52

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

<220>
<223> MAG-003_A7

<400> 52

Lys Val Leu Glu His Val Ala Arg Val
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MAG-003_A8

<400> 53

Lys Val Leu Glu His Val Val Ala Val
1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MAG-003_A9

<400> 54

Lys Val Leu Glu His Val Val Arg Ala
1 5

<210> 55
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRa1 mutant 1 (equals mutation aD27E)

<400> 55

Glu Ser Ser Ser Thr Tyr
1 5

<210> 56

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

 <220>
 <223> CDra2 mutant 2 (equals CDra2 mutant 5 + mutation aS65Q)

 <400> 56

Ile Tyr Ser Ser Gln Asp Gln
 1 5

<210> 57
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDra2 mutant 3

 <400> 57

Ile Tyr Ser Ser Gln Asp Val
 1 5

<210> 58
 <211> 488
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 75-NU(17)-R7P1D5#1

 <400> 58

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

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

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

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

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
 210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
 245 250 255

Asp Ser Ala Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
 260 265 270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr
 275 280 285

Tyr Ile Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val
 290 295 300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met
405 410 415

Arg Gly Leu Glu Leu Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp
420 425 430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly
465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu
485

<210> 59

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CD Ra2 mutant 4

<400> 59

Ile Tyr Ser Ser Gln Asp Ser
1 5

<210> 60

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> 75-NU(17)-R7P1D5#20

<400> 60

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

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

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

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

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
245 250 255

Asp Ser Ala Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
260 265 270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr
275 280 285

Tyr Ile Tyr Ser Ser Gln Asp Ser Lys Gln Asp Gln Arg Leu Thr Val
290 295 300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met
405 410 415

Arg Gly Leu Glu Leu Leu Ile Tyr Phe Cys Tyr Gly Thr Pro Cys Asp
420 425 430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asp Thr Gly Glu Leu Phe Phe Gly
465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu
485

<210> 61
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> 75-NU(17)-R7P1D5#21

<400> 61

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

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

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

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

Gln Asp Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr

65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	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	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	Lys	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	Lys	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Ala	Pro	Pro	Val	Ala
225					230					235					240
Gly	Gly	Glu	Asp	Val	Glu	Gln	Ser	Leu	Phe	Leu	Ser	Val	Arg	Glu	Gly
			245						250					255	
Asp	Ser	Ala	Val	Ile	Asn	Cys	Thr	Tyr	Thr	Asp	Ser	Ser	Ser	Thr	Tyr
		260						265					270		
Leu	Tyr	Trp	Tyr	Lys	Gln	Glu	Pro	Gly	Ala	Gly	Leu	Gln	Leu	Leu	Thr
	275						280					285			
Tyr	Ile	Tyr	Ser	Ser	Gln	Asp	Ser	Lys	Gln	Asp	Gln	Arg	Leu	Thr	Val

290

295

300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
 305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
 325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
 340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
 370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
 385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met
 405 410 415

Arg Gly Leu Glu Leu Leu Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp
 420 425 430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
 435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
 450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asp Thr Gly Glu Leu Phe Phe Gly
 465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu
 485

<210> 62

<211> 5

<212> PRT

<213> Artificial Sequence

<220>
<223> CDRb1 mutant 1

<400> 62

Pro Gly His Asp Tyr
1 5

<210> 63
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRb2 mutant 1

<400> 63

Phe Cys Tyr Gly His Pro
1 5

<210> 64
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRb2 mutant 2

<400> 64

Phe Cys Tyr Gly Val Pro
1 5

<210> 65
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRb2 mutant 3

<400> 65

Phe Cys Tyr Gly Thr Pro
1 5

<210> 66
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRb2 mutant 4

<400> 66

Phe Cys Tyr Gly Ala Pro
1 5

<210> 67
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> 75-NU(17)-R7P1D5#29

<400> 67

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

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

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

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

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
245 250 255

Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
260 265 270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Pro Gln Leu Leu Thr
275 280 285

Tyr Ile Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val
290 295 300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
355 360 365

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

370	375	380															
Arg	His	Glu	Val	Thr	Glu	Met	Gly	Gln	Glu	Val	Thr	Leu	Arg	Cys	Lys		
385					390					395					400		
Pro	Ile	Pro	Gly	His	Asp	Tyr	Leu	Phe	Trp	Tyr	Arg	Gln	Thr	Pro	Gly		
				405					410					415			
Arg	Gly	Leu	Glu	Leu	Leu	Ile	Tyr	Phe	Asn	Asn	Asn	Val	Pro	Ile	Asp		
			420					425					430				
Asp	Ser	Gly	Met	Pro	Glu	Asp	Arg	Phe	Ser	Ala	Lys	Met	Pro	Asn	Ala		
		435					440					445					
Ser	Phe	Ser	Thr	Leu	Lys	Ile	Gln	Pro	Ser	Glu	Pro	Arg	Asp	Ser	Ala		
	450					455					460						
Val	Tyr	Phe	Cys	Ala	Ser	Arg	Ala	Asn	Thr	Gly	Glu	Leu	Phe	Phe	Gly		
465					470					475					480		
Glu	Gly	Ser	Arg	Leu	Thr	Val	Leu										
				485													

<210> 68
 <211> 488
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 75-NU(17)-R7P1D5#30

<400> 68

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala		
1				5					10					15			
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr		
			20					25					30				
Thr	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met		
		35					40					45					
Gly	Leu	Ile	Asn	Pro	Tyr	Lys	Gly	Val	Ser	Thr	Tyr	Ala	Gln	Lys	Phe		
	50					55					60						

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
 210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
 245 250 255

Asp Ser Ala Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
 260 265 270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Pro Gln Leu Leu Thr
 275 280 285

Tyr Ile Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val
 290 295 300

 Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
 305 310 315 320

 Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
 325 330 335

 Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
 340 345 350

 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 355 360 365

 Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
 370 375 380

 Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
 385 390 395 400

 Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Pro Gly
 405 410 415

 Arg Gly Leu Glu Leu Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp
 420 425 430

 Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
 435 440 445

 Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
 450 455 460

 Val Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly
 465 470 475 480

 Glu Gly Ser Arg Leu Thr Val Leu
 485

<210> 69
 <211> 488
 <212> PRT

<213> Artificial Sequence

<220>

<223> 75-NU(17)-R7P1D5#31

<400> 69

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

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

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

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

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
 210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
 245 250 255

Asp Ser Ser Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
 260 265 270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Lys Gly Pro Gln Leu Leu Thr
 275 280 285

Tyr Ile Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val
 290 295 300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
 305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
 325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
 340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
 370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
 385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Pro Gly
 405 410 415

Arg Gly Leu Glu Leu Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp

420

425

430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
 435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
 450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly
 465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu
 485

<210> 70
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRb2 mutant 5

<400> 70

Phe Cys Tyr Gly Met Pro
 1 5

<210> 71
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRb3 mutant 1 (bN109D)

<400> 71

Cys Ala Ser Arg Ala Asp Thr Gly Glu Leu Phe Phe
 1 5 10

<210> 72
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRa1 consensus - ACT + TCER

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> wherein Xaa is any amino acid, preferably D or E, more preferably E

<400> 72

Xaa Ser Ser Ser Thr Tyr
1 5

<210> 73
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRa2 consensus - ACT + TCER

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> wherein Xaa is any amino acid, preferably F or Y, more preferably Y

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> wherein Xaa is any amino acid, preferably N or S, more preferably S

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> wherein Xaa is any amino acid, preferably Q or M, more preferably Q

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> wherein Xaa is any amino acid, preferably M, V, S or Q, preferably S or Q, more preferably Q

<400> 73

Ile Xaa Ser Xaa Xaa Asp Xaa
1 5

<210> 74
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRa2 consensus p1 - TCER

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa is any amino acid, preferably Q, V or S, preferably Q

<400> 74

Ile Tyr Ser Ser Gln Asp Xaa
1 5

<210> 75
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> 75-NU(17)-R7P1D5#32 heavy chain

<400> 75

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

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

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

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

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
 210 215 220

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

 Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
 245 250 255

 Asp Ser Val Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
 260 265 270

 Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Pro Gln Leu Leu Thr
 275 280 285

 Tyr Ile Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val
 290 295 300

 Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
 305 310 315 320

 Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
 325 330 335

 Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
 340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Pro Gly
405 410 415

Arg Gly Leu Glu Leu Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp
420 425 430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly
465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu
485

<210> 76

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> 75-NU(17)-R7P1D5#2-heavy chain

<400> 76

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

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

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

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

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
 210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
 245 250 255

Asp Ser Ala Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr

260

265

270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr
 275 280 285

Tyr Ile Tyr Ser Ser Gln Asp Ser Lys Gln Asp Gln Arg Leu Thr Val
 290 295 300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
 305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
 325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
 340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
 370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
 385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met
 405 410 415

Arg Gly Leu Glu Leu Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp
 420 425 430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
 435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
 450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly
 465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu

<210> 77
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRa3 consensus ACT + TCER

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> wherein Xaa is any amino acid, preferably Xaa is A, F or M, more preferably M

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> wherein Xaa is any amino acid, preferably Xaa is S, T, or N, more preferably T

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> wherein Xaa is any amino acid, preferably Xaa is E or A, preferably E

<400> 77

Cys	Ala	Glu	Xaa	Xaa	Ser	Xaa	Ser	Lys	Ile	Ile	Phe
1				5					10		

<210> 78
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRb1 consensus - ACT + TCER

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa is any amino acid, preferably P,S, more preferably P

<400> 78

Xaa	Gly	His	Asp	Tyr
1			5	

<210> 79
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRb2 consensus - ACT + TCER

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> wherein Xaa is any amino acid, preferably Xaa is C or N, more preferably C

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> wherein Xaa is any amino acid, preferably Xaa is Y or N, more preferably Y

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> wherein Xaa is any amino acid, preferably Xaa is G or N, more preferably G

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> wherein Xaa is any amino acid, preferably Xaa is H, V, T, A or M, preferably H or T, most preferably T

<400> 79

Phe Xaa Xaa Xaa Xaa Pro
1 5

<210> 80
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 75-NU(17)-R7P1D5x- common light chain

<400> 80

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 His 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 Ile Ala Thr Tyr Phe Cys Gln Gln Gly Gln Thr Leu Pro Trp
 85 90 95
 Thr Phe Gly Gln 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 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> 81

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRb2 consensus p3 - TCER

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is any amino acid, preferably H,T, more preferably T

<400> 81

Phe Cys Tyr Gly Xaa Pro
1 5

<210> 82
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRb3 consensus ACT + TCER

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is any amino acid, preferably N,D, preferably D

<400> 82

Cys Ala Ser Arg Ala Xaa Thr Gly Glu Leu Phe Phe
1 5 10

<210> 83
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> FR1-a

<400> 83

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

Ser Val Ile Asn Cys Thr Tyr Thr
20

<210> 84
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> FR2-a

<400> 84

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr
1 5 10 15

Tyr

<210> 85
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> FR3-a

<400> 85

Lys Gln Asp Gln Arg Leu Thr Val Leu Leu Asn Lys Lys Asp Lys His
1 5 10 15

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

Phe

<210> 86
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> FR4-a

<400> 86

Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
1 5 10

<210> 87
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> FR1-b

<400> 87

Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu Met Gly
1 5 10 15

Gln Glu Val Thr Leu Arg Cys Lys Pro Ile
20 25

<210> 88

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> FR2-b

<400> 88

Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu Ile
1 5 10 15

Tyr

<210> 89

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> FR3-b

<400> 89

Ile Asp Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro
1 5 10 15

Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp
20 25 30

Ser Ala Val Tyr Phe
35

<210> 90

<211> 9

<212> PRT

<213> Artificial Sequence

<220>
<223> FR4-b

<400> 90

Gly Glu Gly Ser Arg Leu Thr Val Leu
1 5

<210> 91
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> FR1-a(19V)

<400> 91

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

Val Val Ile Asn Cys Thr Tyr Thr
20

<210> 92
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> FR2-a (48K)

<400> 92

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Lys Gly Leu Gln Leu Leu Thr
1 5 10 15

Tyr

<210> 93
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> FR2-b (54F)

<400> 93

Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu Phe

1 5 10 15

Tyr

<210> 94
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> FR3-b (66C)

<400> 94

Cys Asp Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro
1 5 10 15

Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp
20 25 30

Ser Ala Val Tyr Phe
35

<210> 95
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MUM-001

<400> 95

Lys Leu Val Glu Tyr Ile Val Lys Ala
1 5

<210> 96
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 96

Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 97
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGA4 (P43358)

<400> 97

Met Ser Ser Glu Gln Lys Ser Gln His Cys Lys Pro Glu Glu Gly Val
1 5 10 15

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

Thr Glu Glu Gln Glu Ala Ala Val Ser Ser Ser Ser Pro Leu Val Pro
35 40 45

Gly Thr Leu Glu Glu Val Pro Ala Ala Glu Ser Ala Gly Pro Pro Gln
50 55 60

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

Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Gly Pro
85 90 95

Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn
100 105 110

Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys
115 120 125

Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr
130 135 140

Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys
145 150 155 160

Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Ser Asn Thr
165 170 175

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

180

185

190

Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly
 195 200 205

Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu
 210 215 220

Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr
 225 230 235 240

Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr
 245 250 255

Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe
 260 265 270

Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu
 275 280 285

Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser
 290 295 300

Leu Arg Glu Ala Ala Leu Leu Glu Glu Glu Glu Gly Val
 305 310 315

<210> 98

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGA8 (P43361)

<400> 98

Met Leu Leu Gly Gln Lys Ser Gln Arg Tyr Lys Ala Glu Glu Gly Leu
 1 5 10 15

Gln Ala Gln Gly Glu Ala Pro Gly Leu Met Asp Val Gln Ile Pro Thr
 20 25 30

Ala Glu Glu Gln Lys Ala Ala Ser Ser Ser Ser Thr Leu Ile Met Gly
 35 40 45

Thr Leu Glu Glu Val Thr Asp Ser Gly Ser Pro Ser Pro Pro Gln Ser
 50 55 60

Pro Glu Gly Ala Ser Ser Ser Leu Thr Val Thr Asp Ser Thr Leu Trp
 65 70 75 80

Ser Gln Ser Asp Glu Gly Ser Ser Ser Asn Glu Glu Glu Gly Pro Ser
 85 90 95

Thr Ser Pro Asp Pro Ala His Leu Glu Ser Leu Phe Arg Glu Ala Leu
 100 105 110

Asp Glu Lys Val Ala Glu Leu Val Arg Phe Leu Leu Arg Lys Tyr Gln
 115 120 125

Ile Lys Glu Pro Val Thr Lys Ala Glu Met Leu Glu Ser Val Ile Lys
 130 135 140

Asn Tyr Lys Asn His Phe Pro Asp Ile Phe Ser Lys Ala Ser Glu Cys
 145 150 155 160

Met Gln Val Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Gly
 165 170 175

His Ser Tyr Ile Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu
 180 185 190

Leu Gly Asp Asp Gln Ser Thr Pro Lys Thr Gly Leu Leu Ile Ile Val
 195 200 205

Leu Gly Met Ile Leu Met Glu Gly Ser Arg Ala Pro Glu Glu Ala Ile
 210 215 220

Trp Glu Ala Leu Ser Val Met Gly Leu Tyr Asp Gly Arg Glu His Ser
 225 230 235 240

Val Tyr Trp Lys Leu Arg Lys Leu Leu Thr Gln Glu Trp Val Gln Glu
 245 250 255

Asn Tyr Leu Glu Tyr Arg Gln Ala Pro Gly Ser Asp Pro Val Arg Tyr
 260 265 270

Glu Phe Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys
275 280 285

Val Leu Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ser Tyr
290 295 300

Pro Ser Leu His Glu Glu Ala Leu Gly Glu Glu Lys Gly Val
305 310 315

<210> 99
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 99

Thr Val Ala Ala Pro
1 5

<210> 100
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 100

Gly Gly Gly Ser
1

<210> 101
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> GGGGS

<400> 101

Gly Gly Gly Gly Ser
1 5

<210> 102

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

<220>
<223> Linker

<400> 102

Thr Val Leu Arg Thr
1 5

<210> 103
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 103

Thr Val Ser Ser Ala Ser
1 5

<210> 104
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 104

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

<210> 105
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 105

Gly Gly Gly Gly Ser Ala Ala Ala
1 5

<210> 106

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

<220>
<223> Linker

<400> 106

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 107
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 107

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser
20 25

<210> 108
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 108

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 109

Thr Val Leu Ser Ser Ala Ser
1 5

<210> 110

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 111

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> native Fc amino acid sequence of IGHG1*01

<400> 111

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

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

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

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

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

85

90

95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 112

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc with knob mutation [S354C and T366W] +

<400> 112

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

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 20 25 30

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

<210> 113
 <211> 229
 <212> PRT

<213> Artificial Sequence

<220>

<223> Fc hole [(Y349C, T366S, L368A and Y407V) +

<400> 113

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

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
20 25 30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
35 40 45

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65 70 75 80

Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
85 90 95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
100 105 110

Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
115 120 125

Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
130 135 140

Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
145 150 155 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
165 170 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
180 185 190

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

195

200

205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 210 215 220

Leu Ser Leu Ser Pro
 225

<210> 114
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1-hinge

<400> 114

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

Pro Glu Leu Leu Gly
 20

<210> 115
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IG2-hinge

<400> 115

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
 1 5 10 15

Ala Gly Pro

<210> 116
 <211> 53
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IG3-hinge

<400> 116

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

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
20 25 30

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala
35 40 45

Pro Glu Leu Leu Gly
50

<210> 117
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> IG4-hinge

<400> 117

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly

<210> 118
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5_aMTSE

<400> 118

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

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

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

Phe Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
100 105

<210> 119

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5_aFTSE

<400> 119

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

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

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

Phe Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
100 105

<210> 120

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

<220>
<223> R7P1D5_aFNSE

<400> 120

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

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

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

Phe Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
100 105

<210> 121
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5_aFSSA

<400> 121

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

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

Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr Tyr Ile

35

40

45

Phe Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
 50 55 60

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

Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Phe Ser Ser Ala Ser Lys
 85 90 95

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
 100 105

<210> 122

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5_aATSE

<400> 122

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

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

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

Phe Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
 50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
 100 105

<210> 123
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 75-NU (V9) light chain for CR7P1D5S

<400> 123

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 Arg 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

Asn 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> 124

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> 75-NU(V9)-CR7P1D5S (HC)

<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 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
210 215 220

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

Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly Asp
245 250 255

Ser Ala Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr Leu
260 265 270

Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr Tyr
275 280 285

Ile Tyr Ser Asn Met Asp Met Lys Gln Asp Gln Arg Leu Thr Val Leu
290 295 300

Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr Gln
305 310 315 320

Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Tyr Ser Ser Ala Ser
325 330 335

Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly
340 345 350

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro Arg
370 375 380

His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro
385 390 395 400

Ile Ser Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg
405 410 415

Gly Leu Glu Leu Leu Ile Tyr Phe Asn Asn Asn Val Pro Ile Asp Asp
420 425 430

Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser
435 440 445

Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val
450 455 460

Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly Glu
465 470 475 480

Gly Ser Arg Leu Thr Val Leu
485

<210> 125

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> 75-NU(Var17)-CR7P1D5#19 (HC)

<400> 125

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

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

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

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

50

55

60

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
245 250 255

Asp Ser Ala Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
260 265 270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr

275

280

285

Tyr Ile Tyr Ser Ser Gln Asp Ser Lys Gln Asp Gln Arg Leu Thr Val
 290 295 300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
 305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
 325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
 340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
 370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
 385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met
 405 410 415

Arg Gly Leu Glu Leu Leu Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp
 420 425 430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
 435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
 450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly
 465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu
 485

<210> 126

<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> 75-NU(Var17)-CR7P1D5I (HC)

<400> 126

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

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

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

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

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

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

Ala Arg 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 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 Lys 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 Lys Lys Val Glu Pro Lys Ser
210 215 220

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

Gly Gly Glu Asp Val Glu Gln Ser Leu Phe Leu Ser Val Arg Glu Gly
245 250 255

Asp Ser Ala Val Ile Asn Cys Thr Tyr Thr Asp Ser Ser Ser Thr Tyr
260 265 270

Leu Tyr Trp Tyr Lys Gln Glu Pro Gly Ala Gly Leu Gln Leu Leu Thr
275 280 285

Tyr Ile Tyr Ser Ser Gln Asp Ser Lys Gln Asp Gln Arg Leu Thr Val
290 295 300

Leu Leu Asn Lys Lys Asp Lys His Leu Ser Leu Arg Ile Ala Asp Thr
305 310 315 320

Gln Thr Gly Asp Ser Ala Ile Tyr Phe Cys Ala Glu Met Thr Ser Glu
325 330 335

Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly
340 345 350

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala Gly Val Ile Gln Ser Pro
370 375 380

Arg His Glu Val Thr Glu Met Gly Gln Glu Val Thr Leu Arg Cys Lys
385 390 395 400

Pro Ile Pro Gly His Asp Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met
405 410 415

Arg Gly Leu Glu Leu Leu Ile Tyr Phe Cys Tyr Gly Thr Pro Cys Asp
420 425 430

Asp Ser Gly Met Pro Glu Asp Arg Phe Ser Ala Lys Met Pro Asn Ala
435 440 445

Ser Phe Ser Thr Leu Lys Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala
450 455 460

Val Tyr Phe Cys Ala Ser Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly
465 470 475 480

Glu Gly Ser Arg Leu Thr Val Leu
485

<210> 127

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> 100(A)-NU(V17)-R7P1D5#114-iso0-dSFcK0-GK (first polypeptide
(alpha-VL))

<400> 127

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

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

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

Tyr Ser Ser Gln Asp Ser Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
115 120 125

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
130 135 140

Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
145 150 155 160

Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro
165 170 175

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
180 185 190

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
195 200 205

Gln Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
210 215 220

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

Pro Pro Val Ala 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

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

Asn Gln Val Ser Leu Trp 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> 128

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> 100(A)-NU(V17)-R7P1D5#112-dsFcK0-GK (VH-beta)

<400> 128

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

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

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

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

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

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

Ala Arg 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 Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu
 130 135 140

Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp
 145 150 155 160

Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu
 165 170 175

Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu
 180 185 190

Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys
 195 200 205

Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser
 210 215 220

Arg Ala Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr
 225 230 235 240

Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 260 265 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
275 280 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
290 295 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305 310 315 320

Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
325 330 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
340 345 350

Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
355 360 365

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
370 375 380

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro
465 470

<210> 129

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> ZFC-001

<400> 129

Lys Leu Gln Glu Gln Ile His Arg Val
1 5

<210> 130
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> 100(A)-NU(V17)-R7P1D5#114-dsFckO-GK (VH-beta)

<400> 130

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

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

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

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

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

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

Ala Arg 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 Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu
130 135 140

Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp
 145 150 155 160

Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu
 165 170 175

Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu
 180 185 190

Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys
 195 200 205

Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser
 210 215 220

Arg Ala Asp Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr
 225 230 235 240

Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 260 265 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 275 280 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 290 295 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 305 310 315 320

Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 325 330 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 340 345 350

Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 355 360 365

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
370 375 380

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro
465 470

<210> 131
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> 100(A)-NU(V17)-R7P1D5#114-iso1-dsFck0-GK (alpha-VL)

<400> 131

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

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

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

Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
115 120 125

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
130 135 140

Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
145 150 155 160

Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro
165 170 175

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
180 185 190

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
195 200 205

Gln Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
210 215 220

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

Pro Pro Val Ala 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

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

Asn Gln Val Ser Leu Trp 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> 132
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G4 alpha chain

<400> 132

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
1 5 10 15

Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val
 20 25 30

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

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

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
 65 70 75 80

Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile
 85 90 95

Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg
 100 105 110

Pro Thr Ser Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser
 115 120 125

Leu Ile Val His Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
 130 135 140

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
 145 150 155 160

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
 165 170 175

Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
 180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
 195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro
 210 215 220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
 225 230 235 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
245 250 255

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
260 265 270

Ser Ser

<210> 133
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> 100(A)-NU(V17)-R7P1D5#114-iso2-dsFcK0-GK (alpha-VL)

<400> 133

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

Val Val Ile Asn Cys Thr Tyr Thr Glu Ser Ser Ser Thr Tyr Leu Tyr
20 25 30

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

Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
115 120 125

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
 130 135 140

Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 145 150 155 160

Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro
 165 170 175

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
 180 185 190

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
 195 200 205

Gln Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 210 215 220

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

Pro Pro Val Ala 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

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

Asn Gln Val Ser Leu Trp 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> 134
<211> 311
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G4 beta chain

<400> 134

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

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

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
 85 90 95

Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 100 105 110

Ser Tyr Val Gly Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg
 115 120 125

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
 130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
 145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
 165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
 180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
 195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
 210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
 225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
 245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
 260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
 275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
 290 295 300

Lys Arg Lys Asp Ser Arg Gly
305 310

<210> 135

<211> 466

<212> PRT

<213> Artificial Sequence

<220>

<223> 100(D)-NB(V36)-R7P1D5#114-iso0-dsFcK0-GK (alpha-VH)

<400> 135

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

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

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

Tyr Ser Ser Gln Asp Ser Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val
115 120 125

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
130 135 140

Lys Phe Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Gln
145 150 155 160

Gly Leu Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys
165 170 175

Tyr Ala Glu Lys Phe Gln Gly Arg Val Thr Leu Thr Ser Asp Thr Ser
180 185 190

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
195 200 205

Ala Val His Tyr Cys Ala Arg Gly Ser Tyr Tyr Asp Tyr Glu Gly Phe
210 215 220

Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Glu Pro Lys
225 230 235 240

Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val
245 250 255

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr
305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365

Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
370 375 380

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

Ser Pro
465

<210> 136
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> 100(D)-NB(V36)-R7P1D5#114-dsFcK0-GK (VL-beta)

<400> 136

Gln 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 Ser Ala Thr Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

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

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

Gly Gly Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu
 115 120 125

Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp
 130 135 140

Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu
 145 150 155 160

Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu
 165 170 175

Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys
 180 185 190

Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser
 195 200 205

Arg Ala Asp Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr
 210 215 220

Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Ser Leu Ser Leu Ser Pro
450 455

<210> 137

<211> 466

<212> PRT

<213> Artificial Sequence

<220>

<223> 100(D)-NB(V36)-R7P1D5#114_iso1-dsFckO-GK (alpha-VH)

<400> 137

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

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

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

Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val
115 120 125

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
130 135 140

Lys Phe Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Gln
145 150 155 160

Gly Leu Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys
165 170 175

Tyr Ala Glu Lys Phe Gln Gly Arg Val Thr Leu Thr Ser Asp Thr Ser
180 185 190

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
195 200 205

Ala Val His Tyr Cys Ala Arg Gly Ser Tyr Tyr Asp Tyr Glu Gly Phe
210 215 220

Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Glu Pro Lys
225 230 235 240

Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val
245 250 255

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr
305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365

Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
370 375 380

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

Ser Pro
465

<210> 138
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5# 114-iso0-Valpha

<400> 138

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

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

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

Tyr Ser Ser Gln Asp Ser Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
100 105

<210> 139
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> 100(D)-NB(V36)-R7P1D5#114_iso2-dsFcKO-GK (alpha-VH)

<400> 139

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

Val Val Ile Asn Cys Thr Tyr Thr Glu Ser Ser Ser Thr Tyr Leu Tyr
20 25 30

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

Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val
115 120 125

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
130 135 140

Lys Phe Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Gln
145 150 155 160

Gly Leu Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys
165 170 175

Tyr Ala Glu Lys Phe Gln Gly Arg Val Thr Leu Thr Ser Asp Thr Ser
180 185 190

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
195 200 205

Ala Val His Tyr Cys Ala Arg Gly Ser Tyr Tyr Asp Tyr Glu Gly Phe
210 215 220

Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Glu Pro Lys
225 230 235 240

Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val
245 250 255

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr
305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser
340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365

Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
370 375 380

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

Ser Pro
465

<210> 140
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 140

Gly Gly Ser Gly Gly
1 5

<210> 141
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 141

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

<210> 142
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> 100(A)-NU(V23)-R7P1D5#114_dsFcK0-GK (VH-beta)

<400> 142

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

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

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

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

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

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

Ala Arg 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 Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu
 130 135 140

Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp
 145 150 155 160

Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu
 165 170 175

Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu
 180 185 190

Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys
 195 200 205

Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser
 210 215 220

Arg Ala Asp Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr
 225 230 235 240

Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 260 265 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 275 280 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 290 295 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305 310 315 320

Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
325 330 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
340 345 350

Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
355 360 365

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
370 375 380

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro
465 470

<210> 143
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 143

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15

<210> 144
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 144

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10 15

Gly Ser Gly Gly
20

<210> 145
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 145

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
1 5 10 15

Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25

<210> 146
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 146

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Gly Lys
1 5 10 15

Ser

<210> 147
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 147

Gly Gly Gln Gly Ser Gly Gly Thr Gly Ser Gly Gly Gln Gly Ser Gly
1 5 10 15

Gly Thr Gly Ser Gly Gly Gln Gly Ser
20 25

<210> 148
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 148

Gly Gly Gly Gly Ser Gly Thr
1 5

<210> 149
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5#112-Vbeta

<400> 149

Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu Met Gly
1 5 10 15

Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp Tyr Leu
20 25 30

Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu Phe Tyr
35 40 45

Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu Asp Arg
50 55 60

Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln
65 70 75 80

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

Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu
100 105 110

<210> 150

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> R7P1D5#114 VBETA

<400> 150

Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu Met Gly
1 5 10 15

Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp Tyr Leu
20 25 30

Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu Phe Tyr
35 40 45

Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu Asp Arg
50 55 60

Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys Ile Gln
65 70 75 80

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

Asp Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu
100 105 110

<210> 151

<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5#114-iso1-Valpha

<400> 151

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

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

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

Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
100 105

<210> 152
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> R7P1D5#114-iso2-Valpha100

<400> 152

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

Val Val Ile Asn Cys Thr Tyr Thr Glu Ser Ser Ser Thr Tyr Leu Tyr
20 25 30

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

Tyr Ser Ser Gln Asp Gln Lys Gln Asp Gln Arg Leu Thr Val Leu Leu
50 55 60

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

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

Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
100 105

<210> 153
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> UCHT1(V17) VL

<400> 153

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 His 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 Ile Ala Thr Tyr Phe Cys Gln Gln Gly Gln Thr Leu Pro Trp
85 90 95

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

<210> 154
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> UCHT1(V17) VH

<400> 154

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

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

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

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

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

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

Ala Arg 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> 155
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 155

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

<210> 156
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> UCHT1(23) VH

<400> 156

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

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

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

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

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

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

Ala Arg 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> 157
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> BMA(10) VL

<400> 157

Gln 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 Ser Ala Thr Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

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

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

<210> 158
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> BMA(10) VH

<400> 158

Glu 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 Lys Phe Thr Ser Tyr
20 25 30

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 159
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> BMA(36) VL

<400> 159

Gln 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 Ser Ala Thr Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

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

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

<210> 160
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> BMA(36)- VH

<400> 160

Glu 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 Lys Phe Thr Ser Tyr
20 25 30

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 161
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 161

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Thr

<210> 162
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> UCHT1(17opt) VH

<400> 162

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

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

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

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

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

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

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

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

<210> 163
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 163

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Thr
20

<210> 164
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> UCHT1(21) VH

<400> 164

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

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

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

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

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

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

Ala Arg 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> 165
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 165

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Thr
20 25

<210> 166

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> 100(A)-NU(V21)-R7P1D5#114-dsFcKO-GK (VH-beta)

<400> 166

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

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

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

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

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

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

Ala Arg 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 Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu
130 135 140

Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp
145 150 155 160

Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu
165 170 175

Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu
 180 185 190

Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys
 195 200 205

Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser
 210 215 220

Arg Ala Asp Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr
 225 230 235 240

Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 245 250 255

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 260 265 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 275 280 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 290 295 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 305 310 315 320

Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 325 330 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 340 345 350

Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 355 360 365

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
 370 375 380

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
 385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 420 425 430

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 450 455 460

Lys Ser Leu Ser Leu Ser Pro
 465 470

<210> 167
 <211> 471
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 100(A)-NU(V17opt)-R7P1D5#114-dsFcK0-GK (VH-beta)

<400> 167

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

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

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

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

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

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

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

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

Gly Gly Asp Ala Gly Val Ile Gln Ser Pro Arg His Glu Val Thr Glu
130 135 140

Met Gly Gln Glu Val Thr Leu Arg Cys Lys Pro Ile Pro Gly His Asp
145 150 155 160

Tyr Leu Phe Trp Tyr Arg Gln Thr Met Met Arg Gly Leu Glu Leu Leu
165 170 175

Phe Tyr Phe Cys Tyr Gly Thr Pro Cys Asp Asp Ser Gly Met Pro Glu
180 185 190

Asp Arg Phe Ser Ala Lys Met Pro Asn Ala Ser Phe Ser Thr Leu Lys
195 200 205

Ile Gln Pro Ser Glu Pro Arg Asp Ser Ala Val Tyr Phe Cys Ala Ser
210 215 220

Arg Ala Asp Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr
225 230 235 240

Val Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
260 265 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
275 280 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
290 295 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305 310 315 320

Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
325 330 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
340 345 350

Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
355 360 365

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
370 375 380

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro
465 470

<210> 168
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> PRAME-004

<400> 168

Ser Leu Leu Gln His Leu Ile Gly Leu
1 5

<210> 169
<211> 461

<212> PRT
<213> Artificial Sequence

<220>
<223> 100(A)-NU(17)-PRAME-dsFcKO-GK (alpha-VL)

<400> 169

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

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

Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile Met
35 40 45

Ser Ile Tyr Gln Glu Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

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

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

Gln Gly Gly Ile Leu Thr Phe Gly Thr Gly Thr Arg Leu Thr Ile Ile
100 105 110

Pro Asn Ile Gln Asn Gly Gly Gly Ser Gly Gly Gly Gly Asp Ile Gln
115 120 125

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
130 135 140

Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp
145 150 155 160

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr
165 170 175

Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
180 185 190

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile
195 200 205

Ala Thr Tyr Phe Cys Gln Gln Gly Gln Thr Leu Pro Trp Thr Phe Gly
210 215 220

Gln Gly Thr Lys Val Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys Thr
225 230 235 240

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
275 280 285

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
340 345 350

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

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
370 375 380

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

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

<210> 170

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> 100(A)-NU(17)-PRAME-dsFcK0-GK (VH-beta)

<400> 170

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

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

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

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

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

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

Ala Arg 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 Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Lys Ala Gly Val Thr Gln Thr Pro Arg Tyr Leu Ile Lys Thr
130 135 140

Arg Gly Gln Gln Val Thr Leu Ser Cys Ser Pro Ile Pro Gly His Arg
 145 150 155 160

Ala Val Ser Trp Tyr Gln Gln Thr Pro Gly Gln Gly Leu Gln Phe Leu
 165 170 175

Phe Glu Tyr Val His Gly Glu Glu Arg Asn Lys Gly Asn Phe Pro Gly
 180 185 190

Arg Phe Ser Gly Arg Gln Phe Ser Asn Ser Ser Ser Glu Met Asn Ile
 195 200 205

Ser Asn Leu Glu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser
 210 215 220

Pro Trp Asp Ser Pro Asn Val Gln Tyr Phe Gly Pro Gly Thr Arg Leu
 225 230 235 240

Thr Val Thr Glu Asp Leu Lys Asn Glu Pro Lys Ser Ser Asp Lys Thr
 245 250 255

His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
 260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser
 325 330 335

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 340 345 350

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile
 355 360 365

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
370 375 380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
420 425 430

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465 470 475

<210> 171
<211> 9
<212> PRT
<213> Homo sapiens

<400> 171

Lys Leu Leu Asp Leu Met Pro Arg Leu
1 5

<210> 172
<211> 9
<212> PRT
<213> Homo sapiens

<400> 172

Lys Leu Leu Ser Tyr Ile Gln Arg Leu
1 5

<210> 173
<211> 9
<212> PRT
<213> Homo sapiens

<400> 173

Ser Ile Ile Gly Arg Leu Leu Glu Val
1 5

<210> 174

<211> 9

<212> PRT

<213> Homo sapiens

<400> 174

Lys Ile Tyr Glu Gly Gln Val Glu Val
1 5

<210> 175

<211> 9

<212> PRT

<213> Homo sapiens

<400> 175

Ile Leu Leu Glu His Asn Tyr Ala Leu
1 5

<210> 176

<211> 9

<212> PRT

<213> Homo sapiens

<400> 176

Ala Leu Ser Asn Leu Glu Val Lys Leu
1 5

<210> 177

<211> 9

<212> PRT

<213> Homo sapiens

<400> 177

Leu Leu Asp Val Pro Thr Ala Ala Val
1 5

<210> 178

<211> 9

<212> PRT

<213> Homo sapiens

<400> 178

Ile Leu Asp Gln Lys Ile Asn Glu Val
1 5

<210> 179

<211> 9

<212> PRT

<213> Homo sapiens

<400> 179

Lys Leu Leu Pro Tyr Ile Val Gly Val
1 5

<210> 180

<211> 9

<212> PRT

<213> Homo sapiens

<400> 180

Lys Leu Gly Ser Val Pro Val Thr Val
1 5

<210> 181

<211> 9

<212> PRT

<213> Homo sapiens

<400> 181

Lys Leu Phe Gly His Leu Thr Ser Ala
1 5

<210> 182

<211> 9

<212> PRT

<213> Homo sapiens

<400> 182

Lys Thr Leu Ser Ala Ile Leu Arg Ile
1 5