

SEQUENCE LISTING

<110> Hummingbird Bioscience Holdings Pte. Ltd. (All states)
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<120> VISTA Antigen-Binding Molecules

<130> 007450851

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<151> 2018-03-29

<150> US 16/180,949

<151> 2018-11-05

<150> GB 1814562.3

<151> 2018-09-07

<160> 330

<170> PatentIn version 3.5

<210> 1

<211> 311

<212> PRT

<213> Homo sapiens VISTA

<400> 1

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	Ser
1				5					10					15	

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

Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	Glu	Gly	Gln
		35					40					45			

Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	Asp	Lys	Gly	His
	50					55					60				

Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	Ser	Arg	Gly	Glu	Val
65					70					75				80	

Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	Asn	Leu	Thr	Phe	Gln	Asp
				85					90					95	

Leu	His	Leu	His	His	Gly	Gly	His	Gln	Ala	Ala	Asn	Thr	Ser	His	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn
 115 120 125

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
 130 135 140

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
 145 150 155 160

His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser
 165 170 175

Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr
 180 185 190

Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu
 195 200 205

Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn
 210 215 220

Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
 225 230 235 240

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu
 245 250 255

Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser
 260 265 270

Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro
 275 280 285

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

Ser Pro Asn Phe Glu Val Ile
 305 310

<210> 2
<211> 279
<212> PRT
<213> Homo sapiens VISTA

<400> 2

Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
1 5 10 15

Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
20 25 30

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
35 40 45

Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
50 55 60

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
65 70 75 80

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

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
100 105 110

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
115 120 125

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

Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr
145 150 155 160

Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu
165 170 175

Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn
180 185 190

Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
195 200 205

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu
210 215 220

Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser
225 230 235 240

Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro
245 250 255

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

Ser Pro Asn Phe Glu Val Ile
275

<210> 3
<211> 162
<212> PRT
<213> Homo sapiens extracellular domain

<400> 3

Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
1 5 10 15

Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
20 25 30

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
35 40 45

Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
50 55 60

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
65 70 75 80

Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn

85

90

95

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
 100 105 110

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
 115 120 125

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

Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr
 145 150 155 160

Ala Ala

<210> 4
 <211> 21
 <212> PRT
 <213> Homo sapiens VISTA transmembrane domain

<400> 4

Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu
 1 5 10 15

Ile Leu Leu Leu Val
 20

<210> 5
 <211> 96
 <212> PRT
 <213> Homo sapiens VISTA cytoplasmic domain

<400> 5

Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg Arg Ala Gln Glu Leu Val
 1 5 10 15

Arg Met Asp Ser Asn Ile Gln Gly Ile Glu Asn Pro Gly Phe Glu Ala
 20 25 30

Ser Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val Arg His Pro Leu

35

40

45

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

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

Phe Pro Ser Leu Asp Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile
 85 90 95

<210> 6

<211> 136

<212> PRT

<213> Homo sapiens VISTA Ig-like V-type domain

<400> 6

Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
 1 5 10 15

Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
 20 25 30

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
 35 40 45

Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
 50 55 60

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
 65 70 75 80

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

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
 100 105 110

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
 115 120 125

His Gly Ala Met Glu Leu Gln Val
130 135

<210> 7

<211> 431

<212> PRT

<213> Homo sapiens VSIG 3 isoform 1

<400> 7

Met Thr Ser Gln Arg Ser Pro Leu Ala Pro Leu Leu Leu Leu Ser Leu
1 5 10 15

His Gly Val Ala Ala Ser Leu Glu Val Ser Glu Ser Pro Gly Ser Ile
20 25 30

Gln Val Ala Arg Gly Gln Pro Ala Val Leu Pro Cys Thr Phe Thr Thr
35 40 45

Ser Ala Ala Leu Ile Asn Leu Asn Val Ile Trp Met Val Thr Pro Leu
50 55 60

Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln
65 70 75 80

Met Phe Asp Gly Ala Pro Arg Phe His Gly Arg Val Gly Phe Thr Gly
85 90 95

Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln Leu
100 105 110

Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Ile
115 120 125

Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro
130 135 140

Ser Ala Pro His Cys Gln Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp
145 150 155 160

Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr
165 170 175

Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr
180 185 190

Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu
195 200 205

Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser
210 215 220

Thr Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Asn Ile
225 230 235 240

Gly Leu Ile Ala Gly Ala Ile Gly Thr Gly Ala Val Ile Ile Ile Phe
245 250 255

Cys Ile Ala Leu Ile Leu Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn
260 265 270

Lys Glu Glu Glu Glu Glu Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp
275 280 285

Leu Pro Pro Lys Cys Ser Ser Ala Lys Ala Phe His Thr Glu Ile Ser
290 295 300

Ser Ser Asp Asn Asn Thr Leu Thr Ser Ser Asn Ala Tyr Asn Ser Arg
305 310 315 320

Tyr Trp Ser Asn Asn Pro Lys Val His Arg Asn Thr Glu Ser Val Ser
325 330 335

His Phe Ser Asp Leu Gly Gln Ser Phe Ser Phe His Ser Gly Asn Ala
340 345 350

Asn Ile Pro Ser Ile Tyr Ala Asn Gly Thr His Leu Val Pro Gly Gln
355 360 365

His Lys Thr Leu Val Val Thr Ala Asn Arg Gly Ser Ser Pro Gln Val
370 375 380

Met Ser Arg Ser Asn Gly Ser Val Ser Arg Lys Pro Arg Pro Pro His

385					390					395					400	
Thr	His	Ser	Tyr	Thr	Ile	Ser	His	Ala	Thr	Leu	Glu	Arg	Ile	Gly	Ala	
				405					410					415		
Val	Pro	Val	Met	Val	Pro	Ala	Gln	Ser	Arg	Ala	Gly	Ser	Leu	Val		
				420					425					430		
<210>	8															
<211>	430															
<212>	PRT															
<213>	Homo sapiens VSIG-3 isoform 2															
<400>	8															
Met	Ser	Leu	Val	Glu	Leu	Leu	Leu	Trp	Trp	Asn	Cys	Phe	Ser	Arg	Thr	
1				5					10				15			
Gly	Val	Ala	Ala	Ser	Leu	Glu	Val	Ser	Glu	Ser	Pro	Gly	Ser	Ile	Gln	
			20					25				30				
Val	Ala	Arg	Gly	Gln	Pro	Ala	Val	Leu	Pro	Cys	Thr	Phe	Thr	Thr	Ser	
		35					40				45					
Ala	Ala	Leu	Ile	Asn	Leu	Asn	Val	Ile	Trp	Met	Val	Thr	Pro	Leu	Ser	
		50					55				60					
Asn	Ala	Asn	Gln	Pro	Glu	Gln	Val	Ile	Leu	Tyr	Gln	Gly	Gly	Gln	Met	
65					70					75				80		
Phe	Asp	Gly	Ala	Pro	Arg	Phe	His	Gly	Arg	Val	Gly	Phe	Thr	Gly	Thr	
			85					90				95				
Met	Pro	Ala	Thr	Asn	Val	Ser	Ile	Phe	Ile	Asn	Asn	Thr	Gln	Leu	Ser	
			100					105				110				
Asp	Thr	Gly	Thr	Tyr	Gln	Cys	Leu	Val	Asn	Asn	Leu	Pro	Asp	Ile	Gly	
		115					120				125					
Gly	Arg	Asn	Ile	Gly	Val	Thr	Gly	Leu	Thr	Val	Leu	Val	Pro	Pro	Ser	
		130					135				140					

Ala Pro His Cys Gln Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val
145 150 155 160

Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu
165 170 175

Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln
180 185 190

Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu Ser
195 200 205

Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser Thr
210 215 220

Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Asn Ile Gly
225 230 235 240

Leu Ile Ala Gly Ala Ile Gly Thr Gly Ala Val Ile Ile Ile Phe Cys
245 250 255

Ile Ala Leu Ile Leu Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn Lys
260 265 270

Glu Glu Glu Glu Glu Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp Leu
275 280 285

Pro Pro Lys Cys Ser Ser Ala Lys Ala Phe His Thr Glu Ile Ser Ser
290 295 300

Ser Asp Asn Asn Thr Leu Thr Ser Ser Asn Ala Tyr Asn Ser Arg Tyr
305 310 315 320

Trp Ser Asn Asn Pro Lys Val His Arg Asn Thr Glu Ser Val Ser His
325 330 335

Phe Ser Asp Leu Gly Gln Ser Phe Ser Phe His Ser Gly Asn Ala Asn
340 345 350

Ile Pro Ser Ile Tyr Ala Asn Gly Thr His Leu Val Pro Gly Gln His
355 360 365

Lys Thr Leu Val Val Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Met
370 375 380

Ser Arg Ser Asn Gly Ser Val Ser Arg Lys Pro Arg Pro Pro His Thr
385 390 395 400

His Ser Tyr Thr Ile Ser His Ala Thr Leu Glu Arg Ile Gly Ala Val
405 410 415

Pro Val Met Val Pro Ala Gln Ser Arg Ala Gly Ser Leu Val
420 425 430

<210> 9
<211> 406
<212> PRT
<213> Homo sapiens VSIG-3 isoform 3

<400> 9

Met Ser Leu Val Glu Leu Leu Leu Trp Trp Asn Cys Phe Ser Arg Thr
1 5 10 15

Gly Val Ala Ala Ser Leu Glu Val Ser Glu Ser Pro Gly Ser Ile Gln
20 25 30

Val Ala Arg Gly Gln Pro Ala Val Leu Pro Cys Thr Phe Thr Thr Ser
35 40 45

Ala Ala Leu Ile Asn Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser
50 55 60

Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met
65 70 75 80

Phe Asp Gly Ala Pro Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr
85 90 95

Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln Leu Ser
100 105 110

Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly

115

120

125

Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro Ser
 130 135 140

Ala Pro His Cys Gln Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val
 145 150 155 160

Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu
 165 170 175

Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln
 180 185 190

Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu Ser
 195 200 205

Ser Ala Gln Pro Arg Asn Ile Gly Leu Ile Ala Gly Ala Ile Gly Thr
 210 215 220

Gly Ala Val Ile Ile Ile Phe Cys Ile Ala Leu Ile Leu Gly Ala Phe
 225 230 235 240

Phe Tyr Trp Arg Ser Lys Asn Lys Glu Glu Glu Glu Glu Glu Ile Pro
 245 250 255

Asn Glu Ile Arg Glu Asp Asp Leu Pro Pro Lys Cys Ser Ser Ala Lys
 260 265 270

Ala Phe His Thr Glu Ile Ser Ser Ser Asp Asn Asn Thr Leu Thr Ser
 275 280 285

Ser Asn Ala Tyr Asn Ser Arg Tyr Trp Ser Asn Asn Pro Lys Val His
 290 295 300

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

Ser Phe His Ser Gly Asn Ala Asn Ile Pro Ser Ile Tyr Ala Asn Gly
 325 330 335

Thr His Leu Val Pro Gly Gln His Lys Thr Leu Val Val Thr Ala Asn
340 345 350

Arg Gly Ser Ser Pro Gln Val Met Ser Arg Ser Asn Gly Ser Val Ser
355 360 365

Arg Lys Pro Arg Pro Pro His Thr His Ser Tyr Thr Ile Ser His Ala
370 375 380

Thr Leu Glu Arg Ile Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
385 390 395 400

Arg Ala Gly Ser Leu Val
405

<210> 10
<211> 409
<212> PRT
<213> Homo sapiens VSIG-3 isoform 1

<400> 10

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

Pro Ala Val Leu Pro Cys Thr Phe Thr Thr Ser Ala Ala Leu Ile Asn
20 25 30

Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser Asn Ala Asn Gln Pro
35 40 45

Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met Phe Asp Gly Ala Pro
50 55 60

Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr Met Pro Ala Thr Asn
65 70 75 80

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

Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly Gly Arg Asn Ile Gly
100 105 110

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

Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val Ile Leu Leu Cys Ser
130 135 140

Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu Trp Glu Lys Leu Asp
145 150 155 160

Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln Asp Gln Val Gln Gly
165 170 175

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

Cys Val Ala Ser Asn Ala Ile Gly Thr Ser Thr Cys Leu Leu Asp Leu
195 200 205

Gln Val Ile Ser Pro Gln Pro Arg Asn Ile Gly Leu Ile Ala Gly Ala
210 215 220

Ile Gly Thr Gly Ala Val Ile Ile Ile Phe Cys Ile Ala Leu Ile Leu
225 230 235 240

Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn Lys Glu Glu Glu Glu Glu
245 250 255

Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp Leu Pro Pro Lys Cys Ser
260 265 270

Ser Ala Lys Ala Phe His Thr Glu Ile Ser Ser Ser Asp Asn Asn Thr
275 280 285

Leu Thr Ser Ser Asn Ala Tyr Asn Ser Arg Tyr Trp Ser Asn Asn Pro
290 295 300

Lys Val His Arg Asn Thr Glu Ser Val Ser His Phe Ser Asp Leu Gly
305 310 315 320

Gln Ser Phe Ser Phe His Ser Gly Asn Ala Asn Ile Pro Ser Ile Tyr
325 330 335

Ala Asn Gly Thr His Leu Val Pro Gly Gln His Lys Thr Leu Val Val
340 345 350

Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Met Ser Arg Ser Asn Gly
355 360 365

Ser Val Ser Arg Lys Pro Arg Pro Pro His Thr His Ser Tyr Thr Ile
370 375 380

Ser His Ala Thr Leu Glu Arg Ile Gly Ala Val Pro Val Met Val Pro
385 390 395 400

Ala Gln Ser Arg Ala Gly Ser Leu Val
405

<210> 11
<211> 409
<212> PRT
<213> Homo sapiens VSIG-3 isoform 2

<400> 11

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

Pro Ala Val Leu Pro Cys Thr Phe Thr Thr Ser Ala Ala Leu Ile Asn
20 25 30

Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser Asn Ala Asn Gln Pro
35 40 45

Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met Phe Asp Gly Ala Pro
50 55 60

Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr Met Pro Ala Thr Asn
65 70 75 80

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

Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly Gly Arg Asn Ile Gly
100 105 110

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

Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val Ile Leu Leu Cys Ser
130 135 140

Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu Trp Glu Lys Leu Asp
145 150 155 160

Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln Asp Gln Val Gln Gly
165 170 175

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

Cys Val Ala Ser Asn Ala Ile Gly Thr Ser Thr Cys Leu Leu Asp Leu
195 200 205

Gln Val Ile Ser Pro Gln Pro Arg Asn Ile Gly Leu Ile Ala Gly Ala
210 215 220

Ile Gly Thr Gly Ala Val Ile Ile Ile Phe Cys Ile Ala Leu Ile Leu
225 230 235 240

Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn Lys Glu Glu Glu Glu Glu
245 250 255

Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp Leu Pro Pro Lys Cys Ser
260 265 270

Ser Ala Lys Ala Phe His Thr Glu Ile Ser Ser Ser Asp Asn Asn Thr
275 280 285

Leu Thr Ser Ser Asn Ala Tyr Asn Ser Arg Tyr Trp Ser Asn Asn Pro
290 295 300

Lys Val His Arg Asn Thr Glu Ser Val Ser His Phe Ser Asp Leu Gly

305 310 315 320

Gln Ser Phe Ser Phe His Ser Gly Asn Ala Asn Ile Pro Ser Ile Tyr
325 330 335

Ala Asn Gly Thr His Leu Val Pro Gly Gln His Lys Thr Leu Val Val
340 345 350

Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Met Ser Arg Ser Asn Gly
355 360 365

Ser Val Ser Arg Lys Pro Arg Pro Pro His Thr His Ser Tyr Thr Ile
370 375 380

Ser His Ala Thr Leu Glu Arg Ile Gly Ala Val Pro Val Met Val Pro
385 390 395 400

Ala Gln Ser Arg Ala Gly Ser Leu Val
405

<210> 12
<211> 385
<212> PRT
<213> Homo sapiens VSIG-3 isoform 3

<400> 12

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

Pro Ala Val Leu Pro Cys Thr Phe Thr Thr Ser Ala Ala Leu Ile Asn
20 25 30

Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser Asn Ala Asn Gln Pro
35 40 45

Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met Phe Asp Gly Ala Pro
50 55 60

Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr Met Pro Ala Thr Asn
65 70 75 80

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

Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly Gly Arg Asn Ile Gly
100 105 110

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

Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val Ile Leu Leu Cys Ser
130 135 140

Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu Trp Glu Lys Leu Asp
145 150 155 160

Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln Asp Gln Val Gln Gly
165 170 175

Thr Val Thr Ile Arg Asn Ile Ser Ala Leu Ser Ser Ala Gln Pro Arg
180 185 190

Asn Ile Gly Leu Ile Ala Gly Ala Ile Gly Thr Gly Ala Val Ile Ile
195 200 205

Ile Phe Cys Ile Ala Leu Ile Leu Gly Ala Phe Phe Tyr Trp Arg Ser
210 215 220

Lys Asn Lys Glu Glu Glu Glu Glu Ile Pro Asn Glu Ile Arg Glu
225 230 235 240

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

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

Ser Arg Tyr Trp Ser Asn Asn Pro Lys Val His Arg Asn Thr Glu Ser
275 280 285

Val Ser His Phe Ser Asp Leu Gly Gln Ser Phe Ser Phe His Ser Gly
290 295 300

Asn Ala Asn Ile Pro Ser Ile Tyr Ala Asn Gly Thr His Leu Val Pro
305 310 315 320

Gly Gln His Lys Thr Leu Val Val Thr Ala Asn Arg Gly Ser Ser Pro
325 330 335

Gln Val Met Ser Arg Ser Asn Gly Ser Val Ser Arg Lys Pro Arg Pro
340 345 350

Pro His Thr His Ser Tyr Thr Ile Ser His Ala Thr Leu Glu Arg Ile
355 360 365

Gly Ala Val Pro Val Met Val Pro Ala Gln Ser Arg Ala Gly Ser Leu
370 375 380

Val
385

<210> 13
<211> 219
<212> PRT
<213> Homo sapiens VSIG-3 isoforms 1 and 2 extracellular domain

<400> 13

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

Pro Ala Val Leu Pro Cys Thr Phe Thr Thr Ser Ala Ala Leu Ile Asn
20 25 30

Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser Asn Ala Asn Gln Pro
35 40 45

Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met Phe Asp Gly Ala Pro
50 55 60

Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr Met Pro Ala Thr Asn
65 70 75 80

Val Ser Ile Phe Ile Asn Asn Thr Gln Leu Ser Asp Thr Gly Thr Tyr

85

90

95

Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly Gly Arg Asn Ile Gly
 100 105 110

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

Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val Ile Leu Leu Cys Ser
 130 135 140

Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu Trp Glu Lys Leu Asp
 145 150 155 160

Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln Asp Gln Val Gln Gly
 165 170 175

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

Cys Val Ala Ser Asn Ala Ile Gly Thr Ser Thr Cys Leu Leu Asp Leu
 195 200 205

Gln Val Ile Ser Pro Gln Pro Arg Asn Ile Gly
 210 215

<210> 14

<211> 195

<212> PRT

<213> Homo sapiens VSIG-3 isoform 3 extracellular domain

<400> 14

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

Pro Ala Val Leu Pro Cys Thr Phe Thr Thr Ser Ala Ala Leu Ile Asn
 20 25 30

Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser Asn Ala Asn Gln Pro
 35 40 45

Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met Phe Asp Gly Ala Pro
50 55 60

Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr Met Pro Ala Thr Asn
65 70 75 80

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

Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly Gly Arg Asn Ile Gly
100 105 110

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

Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val Ile Leu Leu Cys Ser
130 135 140

Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu Trp Glu Lys Leu Asp
145 150 155 160

Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln Asp Gln Val Gln Gly
165 170 175

Thr Val Thr Ile Arg Asn Ile Ser Ala Leu Ser Ser Ala Gln Pro Arg
180 185 190

Asn Ile Gly
195

<210> 15
<211> 21
<212> PRT
<213> Homo sapiens VSIG-3 transmembrane domain

<400> 15

Leu Ile Ala Gly Ala Ile Gly Thr Gly Ala Val Ile Ile Ile Phe Cys
1 5 10 15

Ile Ala Leu Ile Leu
20

<210> 16
 <211> 169
 <212> PRT
 <213> Homo sapiens VSIG-3 cytoplasmic domain

<400> 16

Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn Lys Glu Glu Glu Glu Glu
 1 5 10 15

Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp Leu Pro Pro Lys Cys Ser
 20 25 30

Ser Ala Lys Ala Phe His Thr Glu Ile Ser Ser Ser Asp Asn Asn Thr
 35 40 45

Leu Thr Ser Ser Asn Ala Tyr Asn Ser Arg Tyr Trp Ser Asn Asn Pro
 50 55 60

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

Gln Ser Phe Ser Phe His Ser Gly Asn Ala Asn Ile Pro Ser Ile Tyr
 85 90 95

Ala Asn Gly Thr His Leu Val Pro Gly Gln His Lys Thr Leu Val Val
 100 105 110

Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Met Ser Arg Ser Asn Gly
 115 120 125

Ser Val Ser Arg Lys Pro Arg Pro Pro His Thr His Ser Tyr Thr Ile
 130 135 140

Ser His Ala Thr Leu Glu Arg Ile Gly Ala Val Pro Val Met Val Pro
 145 150 155 160

Ala Gln Ser Arg Ala Gly Ser Leu Val
 165

<210> 17
 <211> 114

<212> PRT
<213> Homo sapiens VSIG-3 Ig-like V-type domain

<400> 17

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

Pro Ala Val Leu Pro Cys Thr Phe Thr Thr Ser Ala Ala Leu Ile Asn
20 25 30

Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser Asn Ala Asn Gln Pro
35 40 45

Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met Phe Asp Gly Ala Pro
50 55 60

Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr Met Pro Ala Thr Asn
65 70 75 80

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

Gln Cys Leu Val Asn Asn Leu Pro Asp Ile Gly Gly Arg Asn Ile Gly
100 105 110

Val Thr

<210> 18
<211> 91
<212> PRT
<213> Homo sapiens VSIG-3 Ig-like V-type domain

<400> 18

Pro Ser Ala Pro His Cys Gln Ile Gln Gly Ser Gln Asp Ile Gly Ser
1 5 10 15

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

Tyr Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala
35 40 45

Thr Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala
50 55 60

Leu Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr
65 70 75 80

Ser Thr Cys Leu Leu Asp Leu Gln Val Ile Ser
85 90

<210> 19
<211> 414
<212> PRT
<213> Homo sapiens VSIG-8

<400> 19

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

Ala Leu Leu Ser Ala Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu
20 25 30

Tyr Leu Ala Glu Gly Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu
35 40 45

Asp Pro Glu Asp Tyr Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln
50 55 60

Val Asn Ser Asp Pro Ala His His Arg Glu Asn Val Phe Leu Ser Tyr
65 70 75 80

Gln Asp Lys Arg Ile Asn His Gly Ser Leu Pro His Leu Gln Gln Arg
85 90 95

Val Arg Phe Ala Ala Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn
100 105 110

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

Lys Lys Thr Thr Met Ala Thr Arg Lys Val Ile Val Thr Val Gln Ala

130

135

140

Arg Pro Ala Val Pro Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly
 145 150 155 160

Asn Asp Val Val Leu Lys Cys Tyr Ala Ser Gly Gly Ser Gln Pro Leu
 165 170 175

Ser Tyr Lys Trp Ala Lys Ile Ser Gly His His Tyr Pro Tyr Arg Ala
 180 185 190

Gly Ser Tyr Thr Ser Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln
 195 200 205

Glu Ser Phe His Ser Ser Ile Asn Gln Gly Leu Asn Asn Gly Asp Leu
 210 215 220

Val Leu Lys Asp Ile Ser Arg Ala Asp Asp Gly Leu Tyr Gln Cys Thr
 225 230 235 240

Val Ala Asn Asn Val Gly Tyr Ser Val Cys Val Val Glu Val Lys Val
 245 250 255

Ser Asp Ser Arg Arg Ile Gly Val Ile Ile Gly Ile Val Leu Gly Ser
 260 265 270

Leu Leu Ala Leu Gly Cys Leu Ala Val Gly Ile Trp Gly Leu Val Cys
 275 280 285

Cys Cys Cys Gly Gly Ser Gly Ala Gly Gly Ala Arg Gly Ala Phe Gly
 290 295 300

Tyr Gly Asn Gly Gly Gly Val Gly Gly Gly Ala Cys Gly Asp Leu Ala
 305 310 315 320

Ser Glu Ile Arg Glu Asp Ala Val Ala Pro Gly Cys Lys Ala Ser Gly
 325 330 335

Arg Gly Ser Arg Val Thr His Leu Leu Gly Tyr Pro Thr Gln Asn Val
 340 345 350

Ser Arg Ser Leu Arg Arg Lys Tyr Ala Pro Pro Pro Cys Gly Gly Pro
355 360 365

Glu Asp Val Ala Leu Ala Pro Cys Thr Ala Ala Ala Ala Cys Glu Ala
370 375 380

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

Cys Ala Glu Gly Pro Val Gln Cys Lys Asn Gly Leu Leu Val
405 410

<210> 20

<211> 393

<212> PRT

<213> Homo sapiens VSIG-8

<400> 20

Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu Tyr Leu Ala Glu Gly
1 5 10 15

Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu Asp Pro Glu Asp Tyr
20 25 30

Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln Val Asn Ser Asp Pro
35 40 45

Ala His His Arg Glu Asn Val Phe Leu Ser Tyr Gln Asp Lys Arg Ile
50 55 60

Asn His Gly Ser Leu Pro His Leu Gln Gln Arg Val Arg Phe Ala Ala
65 70 75 80

Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn Leu Met Asn Leu Gln
85 90 95

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

Ala Thr Arg Lys Val Ile Val Thr Val Gln Ala Arg Pro Ala Val Pro
115 120 125

Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly Asn Asp Val Val Leu
130 135 140

Lys Cys Tyr Ala Ser Gly Gly Ser Gln Pro Leu Ser Tyr Lys Trp Ala
145 150 155 160

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

Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln Glu Ser Phe His Ser
180 185 190

Ser Ile Asn Gln Gly Leu Asn Asn Gly Asp Leu Val Leu Lys Asp Ile
195 200 205

Ser Arg Ala Asp Asp Gly Leu Tyr Gln Cys Thr Val Ala Asn Asn Val
210 215 220

Gly Tyr Ser Val Cys Val Val Glu Val Lys Val Ser Asp Ser Arg Arg
225 230 235 240

Ile Gly Val Ile Ile Gly Ile Val Leu Gly Ser Leu Leu Ala Leu Gly
245 250 255

Cys Leu Ala Val Gly Ile Trp Gly Leu Val Cys Cys Cys Cys Gly Gly
260 265 270

Ser Gly Ala Gly Gly Ala Arg Gly Ala Phe Gly Tyr Gly Asn Gly Gly
275 280 285

Gly Val Gly Gly Gly Ala Cys Gly Asp Leu Ala Ser Glu Ile Arg Glu
290 295 300

Asp Ala Val Ala Pro Gly Cys Lys Ala Ser Gly Arg Gly Ser Arg Val
305 310 315 320

Thr His Leu Leu Gly Tyr Pro Thr Gln Asn Val Ser Arg Ser Leu Arg
325 330 335

Arg Lys Tyr Ala Pro Pro Pro Cys Gly Gly Pro Glu Asp Val Ala Leu
340 345 350

Ala Pro Cys Thr Ala Ala Ala Ala Cys Glu Ala Gly Pro Ser Pro Val
355 360 365

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

Val Gln Cys Lys Asn Gly Leu Leu Val
385 390

<210> 21
<211> 242
<212> PRT
<213> Homo sapiens VSIG-8 extracellular domain

<400> 21

Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu Tyr Leu Ala Glu Gly
1 5 10 15

Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu Asp Pro Glu Asp Tyr
20 25 30

Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln Val Asn Ser Asp Pro
35 40 45

Ala His His Arg Glu Asn Val Phe Leu Ser Tyr Gln Asp Lys Arg Ile
50 55 60

Asn His Gly Ser Leu Pro His Leu Gln Gln Arg Val Arg Phe Ala Ala
65 70 75 80

Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn Leu Met Asn Leu Gln
85 90 95

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

Ala Thr Arg Lys Val Ile Val Thr Val Gln Ala Arg Pro Ala Val Pro
115 120 125

Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly Asn Asp Val Val Leu
130 135 140

Lys Cys Tyr Ala Ser Gly Gly Ser Gln Pro Leu Ser Tyr Lys Trp Ala
145 150 155 160

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

Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln Glu Ser Phe His Ser
180 185 190

Ser Ile Asn Gln Gly Leu Asn Asn Gly Asp Leu Val Leu Lys Asp Ile
195 200 205

Ser Arg Ala Asp Asp Gly Leu Tyr Gln Cys Thr Val Ala Asn Asn Val
210 215 220

Gly Tyr Ser Val Cys Val Val Glu Val Lys Val Ser Asp Ser Arg Arg
225 230 235 240

Ile Gly

<210> 22
<211> 21
<212> PRT
<213> Homo sapiens VSIG-8 transmembrane domain

<400> 22

Val Ile Ile Gly Ile Val Leu Gly Ser Leu Leu Ala Leu Gly Cys Leu
1 5 10 15

Ala Val Gly Ile Trp
20

<210> 23
<211> 130
<212> PRT
<213> Homo sapiens VSIG-8 cytoplasmic domain

<400> 23

Gly Leu Val Cys Cys Cys Cys Gly Gly Ser Gly Ala Gly Gly Ala Arg
1 5 10 15

Gly Ala Phe Gly Tyr Gly Asn Gly Gly Gly Val Gly Gly Gly Ala Cys
20 25 30

Gly Asp Leu Ala Ser Glu Ile Arg Glu Asp Ala Val Ala Pro Gly Cys
35 40 45

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

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

Cys Gly Gly Pro Glu Asp Val Ala Leu Ala Pro Cys Thr Ala Ala Ala
85 90 95

Ala Cys Glu Ala Gly Pro Ser Pro Val Tyr Val Lys Val Lys Ser Ala
100 105 110

Glu Pro Ala Asp Cys Ala Glu Gly Pro Val Gln Cys Lys Asn Gly Leu
115 120 125

Leu Val
130

<210> 24
<211> 120
<212> PRT
<213> Homo sapiens VSIG-8 Ig-like V-type domain

<400> 24

Val Arg Ile Asn Gly Asp Gly Gln Glu Val Leu Tyr Leu Ala Glu Gly
1 5 10 15

Asp Asn Val Arg Leu Gly Cys Pro Tyr Val Leu Asp Pro Glu Asp Tyr
20 25 30

Gly Pro Asn Gly Leu Asp Ile Glu Trp Met Gln Val Asn Ser Asp Pro
35 40 45

Ala His His Arg Glu Asn Val Phe Leu Ser Tyr Gln Asp Lys Arg Ile
50 55 60

Asn His Gly Ser Leu Pro His Leu Gln Gln Arg Val Arg Phe Ala Ala
65 70 75 80

Ser Asp Pro Ser Gln Tyr Asp Ala Ser Ile Asn Leu Met Asn Leu Gln
85 90 95

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

Ala Thr Arg Lys Val Ile Val Thr
115 120

<210> 25
<211> 112
<212> PRT
<213> Homo sapiens VSIG-8 Ig-like V-type domain

<400> 25

Pro Ala Val Pro Met Cys Trp Thr Glu Gly His Met Thr Tyr Gly Asn
1 5 10 15

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

Tyr Lys Trp Ala Lys Ile Ser Gly His His Tyr Pro Tyr Arg Ala Gly
35 40 45

Ser Tyr Thr Ser Gln His Ser Tyr His Ser Glu Leu Ser Tyr Gln Glu
50 55 60

Ser Phe His Ser Ser Ile Asn Gln Gly Leu Asn Asn Gly Asp Leu Val
65 70 75 80

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

Ala Asn Asn Val Gly Tyr Ser Val Cys Val Val Glu Val Lys Val Ser

100

105

110

<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope recognised by anti-VISTA antibody clones 4M2-C12, 4M2-B4,
4M2-C9, 4M2-D9, 4M2-D5, 4M2-A8, V4H1 and V4H2

<400> 26

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile
1 5 10

<210> 27
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope recognised by anti-VISTA antibody clones 2M1-B12 and
2M1-D2

<400> 27

Phe Gln Asp Leu His Leu His His Gly Gly His Gln Ala Ala
1 5 10

<210> 28
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope recognised by anti-VISTA antibody clones 1M2-D2, 13D5p,
13D5-1 and 13D5-13

<400> 28

Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg
1 5 10

<210> 29
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Epitope recognised by anti-VISTA antibody clone 5M1-A11

<400> 29

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr
1 5 10

<210> 30

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Epitope recognised by anti-VISTA antibody clone 9M2-C12

<400> 30

Arg His His His Ser Glu His Arg Val His Gly
1 5 10

<210> 31

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> Positions 61 to 162 of human VISTA (Q9H7M9-1, v3)

<400> 31

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser
1 5 10 15

Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu
20 25 30

Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln Ala Ala Asn
35 40 45

Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp
50 55 60

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

Ser Gly Leu Tyr Cys Cys Leu Val Val Glu Ile Arg His His His Ser
85 90 95

Glu His Arg Val His Gly
100

<210> 32
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 heavy chain variable region

<400> 32

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

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

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

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

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

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

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

Thr Thr Val Thr Val Ser Ser
115

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

<220>

<223> 4M2-C12, 4M2-B4, V4H2, 4M2-D9 heavy chain CDR1

<400> 33

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala
1 5

<210> 34

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-C12, 4M2-B4, V4H1, V4H2 heavy chain CDR2

<400> 34

Ile Thr Tyr Ser Gly Asn Ile
1 5

<210> 35

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-C12, 4M2-B4, V4H1, V4H2 heavy chain CDR3

<400> 35

Ala Arg Ser Leu Tyr Tyr Pro Trp Tyr Phe Asp Val
1 5 10

<210> 36

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-C12 heavy chain FR1

<400> 36

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

Ser Leu Ser Leu Thr Cys Thr Val Thr
20 25

<210> 37
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12, 4M2-B4 heavy chain FR2

<400> 37

Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met Gly
1 5 10 15

Tyr

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

<220>
<223> 4M2-C12, 4M2-B4 heavy chain FR3

<400> 38

Ser Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Phe Leu Gln Leu Asn Ser Val Thr Pro Glu Asp
20 25 30

Thr Ala Thr Tyr Ser Cys
35

<210> 39
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12, 4M2-B4, V4H1, V4H2, 13D5p, 13D5-1, 13D5-13 heavy chain
FR4

<400> 39

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 40
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 light chain variable region

<400> 40

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

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

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

Gly Ser Gly Thr Ser Asn Ser Leu Thr Ile Thr Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

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

<210> 41
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12, 4M2-B4, V4H1, V4H2 light chain CDR1

<400> 41

Ser Ser Val Gly Tyr
1 5

<210> 42

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

<220>
<223> 4M2-C12, 4M2-B4 light chain CDR2

<400> 42

Ala Thr Ser
1

<210> 43
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12, 4M2-B4, V4H1, V4H2 light chain CDR3

<400> 43

Gln Gln Trp Ser Ser Tyr Pro Pro Ile Thr
1 5 10

<210> 44
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 light chain FR1

<400> 44

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser
20 25

<210> 45
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12, 4M2-B4 light chain FR2

<400> 45

Ile His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile
1 5 10 15

Tyr

<210> 46
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12, 4M2-B4 light chain FR3

<400> 46

Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

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

Thr Tyr Tyr Cys
35

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12, 4M2-B4, V4H1, V4H2 light chain FR4

<400> 47

Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
1 5 10

<210> 48
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-B4 heavy chain variable region

<400> 48

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

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

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

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

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

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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 49
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-B4 heavy chain FR1

<400> 49

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

Ser Leu Ser Leu Thr Cys Thr Val Thr
20 25

<210> 50
<211> 107
<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-B4 light chain variable region

<400> 50

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

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

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

Gly Ser Gly Thr Ser Asn Ser Leu Thr Ile Thr Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

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

<210> 51

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-B4 light chain FR1

<400> 51

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

Glu Lys Val Thr Met Thr Cys Arg Ala
20 25

<210> 52

<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 heavy chain variable region

<400> 52

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

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

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

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

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

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

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

Thr Thr Val Thr Val Ser Ser
115

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

<220>
<223> V4H1 heavy chain CDR1

<400> 53

Gly Tyr Thr Ile Thr Ser Asp Tyr Ala
1 5

<210> 54
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 heavy chain FR1

<400> 54

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 55
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 heavy chain FR2

<400> 55

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

Val

<210> 56
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 heavy chain FR3

<400> 56

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

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys
35

<210> 57
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 light chain variable region

<400> 57

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Leu
20 25 30

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

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

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

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

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

<210> 58
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 light chain CDR2

<400> 58

Asp Thr Ser

1

<210> 59
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 light chain FR1

<400> 59

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala
20 25

<210> 60
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 light chain FR2

<400> 60

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile
1 5 10 15

Tyr

<210> 61
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 light chain FR3

<400> 61

Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala

20

25

30

Val Tyr Tyr Cys
35

<210> 62

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> V4H2 heavy chain variable region

<400> 62

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

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

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

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Asp Cys
85 90 95

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

Thr Thr Val Thr Val Ser Ser
115

<210> 63

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> V4H2 heavy chain FR1

<400> 63

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

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 64

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> V4H2 heavy chain FR2

<400> 64

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

Tyr

<210> 65

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> V4H2 heavy chain FR3

<400> 65

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

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
20 25 30

Thr Ala Val Tyr Asp Cys
35

<210> 66

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

<220>
<223> V4H2 light chain variable region

<400> 66

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 Ser Ser Val Gly Tyr Leu
20 25 30

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

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

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

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

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

<210> 67
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H2, 4M2-D9 light chain CDR2

<400> 67

Ala Ala Ser
1

<210> 68
<211> 25
<212> PRT

<213> Artificial Sequence

<220>

<223> V4H2 light chain FR1

<400> 68

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
			20					25

<210> 69

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> V4H2 light chain FR2

<400> 69

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Leu	Ile
1				5				10						15	

Tyr

<210> 70

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> V4H2 light chain FR3

<400> 70

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

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

Thr	Tyr	Tyr	Cys
			35

<210> 71
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12 heavy chain variable region

<400> 71

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

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

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

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

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

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

Ala Gln Ile Pro Leu Tyr Tyr Gly His Tyr Arg Ser Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 72
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12, 2M1-D2, 13D5p, 13D5-1, 13D5-13 heavy chain CDR1

<400> 72

Gly Tyr Thr Phe Thr Asn Tyr Trp

1 5

<210> 73
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12, 2M1-D2 heavy chain CDR2

<400> 73

Ile Phe Pro Gly Gly Gly His Thr
1 5

<210> 74
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12, 2M1-D2 heavy chain CDR3

<400> 74

Ala Gln Ile Pro Leu Tyr Tyr Gly His Tyr Arg Ser Ala Tyr
1 5 10

<210> 75
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12 heavy chain FR1

<400> 75

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

Ser Val Lys Thr Ser Cys Lys Ala Ser
20 25

<210> 76
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> 2M1-B12, 2M1-D2 heavy chain FR2

<400> 76

Leu Gly Trp Val Lys Glu Arg Ala Gly His Gly Leu Glu Trp Ile Gly
1 5 10 15

Glu

<210> 77

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12, 2M1-D2 heavy chain FR3

<400> 77

Asn Tyr Lys Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr
1 5 10 15

Ser Ser Ser Thr Ala Tyr Met Lys Leu Ser Ser Leu Thr Ser Glu Asp
20 25 30

Ser Ala Val Tyr Phe Cys
35

<210> 78

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12, 2M1-D2, 1M2-D2 heavy chain FR4

<400> 78

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
1 5 10

<210> 79

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12 light chain variable region

<400> 79

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

Glu Thr Val Ala Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
20 25 30

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

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
65 70 75 80

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

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

<210> 80

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12, 2M1-D2 light chain CDR1

<400> 80

Glu Asn Ile Tyr Gly Ala
1 5

<210> 81

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12, 2M1-D2 light chain CDR2

<400> 81

Gly Ala Thr
1

<210> 82

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12, 2M1-D2 light chain CDR3

<400> 82

Gln Asn Val Leu Ser Thr Pro Tyr Thr
1 5

<210> 83

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12 light chain FR1

<400> 83

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

Glu Thr Val Ala Ile Thr Cys Gly Ala Ser
20 25

<210> 84

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 2M1-B12, 2M1-D2 light chain FR2

<400> 84

Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
1 5 10 15

Tyr

<210> 85
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12, 2M1-D2 light chain FR3

<400> 85

Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro Asp Asp Val Ala
20 25 30

Thr Tyr Tyr Cys
35

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

<220>
<223> 2M1-B12, 4M2-C9, 2M1-D2, 4M2-D9, 1M2-D2, 5M1-A11, 4M2-D5, 4M2-A8,
9M2-C12, 13D5p, 13D5-1, 13d5-13 light chain FR4

<400> 86

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 87
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 heavy chain variable region

<400> 87

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Leu Asp Gly Tyr Asn Asp Pro Tyr Tyr Phe Asp Tyr
100 105 110

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

<210> 88
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9, 5M1-A11 heavy chain CDR1

<400> 88

Gly Phe Ser Leu Ser Thr Ser Gly Met Gly
1 5 10

<210> 89
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9, 5M1-A11 heavy chain CDR2

<400> 89

Ile Tyr Trp Asp Asp Asp Lys
1 5

<210> 90
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9, 5M1-A11 heavy chain CDR3

<400> 90

Ala	Arg	Arg	Leu	Asp	Gly	Tyr	Asn	Asp	Pro	Tyr	Tyr	Phe	Asp	Tyr
1			5						10				15	

<210> 91
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 heavy chain FR1

<400> 91

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

Thr	Leu	Ser	Leu	Thr	Cys	Ser	Phe	Ser
			20					25

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

<220>
<223> 4M2-C9, 5M1-A11 heavy chain FR2

<400> 92

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

His

<210> 93
<211> 38

<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9, 5M1-A11 heavy chain FR3

<400> 93

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

Ser Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp
20 25 30

Thr Ala Thr Tyr Tyr Cys
35

<210> 94
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 heavy chain FR4

<400> 94

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 95
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 light chain variable region

<400> 95

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

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

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

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

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

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

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

<210> 96
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 light chain CDR1

<400> 96

Gln Asn Val Asn Val Trp
1 5

<210> 97
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 light chain CDR2

<400> 97

Lys Ala Ser
1

<210> 98
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 light chain CDR3

<400> 98

Gln Gln Gly Gln Ser Tyr Pro Leu Thr
1 5

<210> 99

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-C9 light chain FR1

<400> 99

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

Asp Thr Val Thr Ile Thr Cys His Ala Ser
20 25

<210> 100

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-C9 light chain FR2

<400> 100

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 101

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-C9 light chain FR3

<400> 101

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

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

Thr Tyr Tyr Cys
35

<210> 102
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-D2 heavy chain variable region

<400> 102

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

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

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

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

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

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

Ala Gln Ile Pro Leu Tyr Tyr Gly His Tyr Arg Ser Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 103
<211> 25

<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-D2, 13D5p, 13D5-1, 13D5-13 heavy chain FR1

<400> 103

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

Ser Val Lys Ile Ser Cys Lys Ala Ser
20 25

<210> 104
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-D2 light chain variable region

<400> 104

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

Glu Thr Val Ala Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
20 25 30

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

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
65 70 75 80

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

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

<210> 105
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-D2 light chain FR1

<400> 105

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

Glu Thr Val Ala Ile Thr Cys Gly Ala Ser
20 25

<210> 106
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 heavy chain variable region

<400> 106

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

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

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

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

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

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

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

Ala Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 107
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 heavy chain CDR2

<400> 107

Ile Ser Tyr Ser Gly Phe Thr
1 5

<210> 108
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 heavy chain CDR3

<400> 108

Ala Arg Asn His Tyr Gly Gly Ser Tyr Trp Tyr Phe Asp Val
1 5 10

<210> 109
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 heavy chain FR1

<400> 109

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

Ser Leu Ser Leu Thr Cys Thr Val Thr
20 25

<210> 110
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 heavy chain FR2

<400> 110

Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Arg Leu Glu Trp Met Gly
1 5 10 15

Phe

<210> 111
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 heavy chain FR3

<400> 111

Thr Tyr Ser Pro Ser Leu Glu Ser Arg Ile Ser Ile Thr Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Phe Leu Gln Leu Ile Ser Val Thr Thr Glu Asp
20 25 30

Thr Ala Thr Tyr Tyr Cys
35

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

<220>
<223> 4M2-D9 heavy chain FR4

<400> 112

Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
1 5 10

<210> 113
<211> 111

<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 light chain variable region

<400> 113

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

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

Gly Thr Ser Leu Met Gln Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

Pro Val Glu Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

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

<210> 114
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 light chain CDR1

<400> 114

Glu Ser Val Glu Tyr Tyr Gly Thr Ser Leu
1 5 10

<210> 115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> 4M2-D9 light chain CDR3

<400> 115

Gln Gln Ser Arg Lys Val Pro Trp Thr
1 5

<210> 116

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-D9 light chain FR1

<400> 116

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

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

<210> 117

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-D9 light chain FR2

<400> 117

Met Gln Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 118

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-D9 light chain FR3

<400> 118

Asn Val Glu Ser Gly Val Pro Asp Arg Phe Arg Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala
20 25 30

Met Tyr Phe Cys
35

<210> 119

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> 1M2-D2 heavy chain variable region

<400> 119

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

Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ala
20 25 30

Trp Met Asp Trp Val His Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala Glu Ile Arg Ser Lys Ala Asn Asn His Ala Thr Tyr Tyr Val Glu
50 55 60

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

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

Tyr Cys Thr Arg Arg Asp Gly Tyr Tyr Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 120
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 heavy chain CDR1

<400> 120

Gly Phe Thr Phe Ser Asp Ala Trp
1 5

<210> 121
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 heavy chain CDR2

<400> 121

Ile Arg Ser Lys Ala Asn Asn His Ala Thr
1 5 10

<210> 122
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 heavy chain CDR3

<400> 122

Thr Arg Arg Asp Gly Tyr Tyr Phe Ala Tyr
1 5 10

<210> 123
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 heavy chain FR1

<400> 123

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

Ser Met Lys Leu Ser Cys Ala Ala Ser
20 25

<210> 124
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 heavy chain FR2

<400> 124

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

Glu

<210> 125
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 heavy chain FR3

<400> 125

Tyr Tyr Val Glu Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asp
1 5 10 15

Ser Lys Ser Ser Val Phe Leu Gln Val Asn Ser Leu Arg Pro Glu Asp
20 25 30

Thr Gly Ile Tyr Tyr Cys
35

<210> 126
<211> 105
<212> PRT
<213> Artificial Sequence

<220>

<223> 1M2-D2 light chain variable region

<400> 126

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

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

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

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

Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Gly
65 70 75 80

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

Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 127

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 1M2-D2 light chain CDR1

<400> 127

Ser Ser Ser Val Arg Asp
1 5

<210> 128

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 1M2-D2 light chain CDR2

<400> 128

Asn Thr Phe
1

<210> 129

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 1M2-D2 light chain CDR3

<400> 129

His Gln Trp Ser Ser Tyr Pro Thr
1 5

<210> 130

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 1M2-D2 light chain FR1

<400> 130

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

Glu Glu Ile Thr Leu Thr Cys Ser Ala
20 25

<210> 131

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 1M2-D2 light chain FR2

<400> 131

Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Val Leu Ile
1 5 10 15

Tyr

<210> 132
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 light chain FR3

<400> 132

Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

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

Ala Tyr Tyr Cys
35

<210> 133
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 heavy chain variable region

<400> 133

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Leu Asp Gly Tyr Asn Asp Pro Tyr Tyr Phe Asp Tyr
100 105 110

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

<210> 134
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 heavy chain FR1

<400> 134

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser
20 25

<210> 135
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11, 4M2-D5, 4M2-A8 heavy chain FR4

<400> 135

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> 136
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 light chain variable region

<400> 136

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

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

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

<210> 137
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 light chain CDR1

<400> 137

Ser Ser Val Ser Tyr
1 5

<210> 138
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 light chain CDR2

<400> 138

Leu Thr Ser
1

<210> 139
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 light chain CDR3

<400> 139

Gln Gln Trp Asn Ser Asn Pro Tyr Thr
1 5

<210> 140
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 light chain FR1

<400> 140

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser
20 25

<210> 141
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 light chain FR2

<400> 141

Met Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile
1 5 10 15

Tyr

<210> 142
<211> 36

<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 light chain FR3

<400> 142

Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 143
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 heavy chain variable region

<400> 143

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

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

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

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

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

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

Thr Arg His Ser Tyr Gly Asn Tyr Gly Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 144
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 heavy chain CDR1

<400> 144

Gly Tyr Thr Phe Thr Ser Tyr Thr
1 5

<210> 145
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 heavy chain CDR2

<400> 145

Ile Asn Pro Asp Ser Asp Tyr Thr
1 5

<210> 146
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 heavy chain CDR3

<400> 146

Thr Arg His Ser Tyr Gly Asn Tyr Gly Asp Tyr
1 5 10

<210> 147
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> 4M2-D5 heavy chain FR1

<400> 147

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

Ser Val Arg Met Ser Cys Lys Ala Ser
20 25

<210> 148

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-D5 heavy chain FR2

<400> 148

Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
1 5 10 15

Phe

<210> 149

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-D5 heavy chain FR3

<400> 149

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

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Tyr Asp Asp
20 25 30

Ser Ala Val Tyr Tyr Cys
35

<210> 150
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 light chain variable region

<400> 150

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

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

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

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

Ser Gly Phe Gly Thr Asp Phe Thr Phe Thr Ile Asn Thr Val Gln Ala
65 70 75 80

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

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

<210> 151
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 light chain CDR1

<400> 151

Gln Ser Val Thr Asn Asp
1 5

<210> 152
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5, 4M2-A8 light chain CDR2

<400> 152

Tyr Ala Ser
1

<210> 153
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5, 4M2-A8 light chain CDR3

<400> 153

Gln Gln Asp Tyr Ser Ser Pro Tyr Thr
1 5

<210> 154
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 light chain FR1

<400> 154

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5, 4M2-A8 light chain FR2

<400> 155

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

Tyr

<210> 156
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 light chain FR3

<400> 156

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

Thr Asp Phe Thr Phe Thr Ile Asn Thr Val Gln Ala Glu Asp Leu Ala
20 25 30

Val Tyr Phe Cys
35

<210> 157
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-A8 heavy chain variable region

<400> 157

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

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

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

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

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

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

Ala Arg His Ser Tyr Gly Asn Tyr Gly Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 158
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-A8 heavy chain CDR1

<400> 158

Gly Tyr Thr Phe Ile Asp Tyr Thr
1 5

<210> 159
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-A8 heavy chain CDR2

<400> 159

Ile Asn Pro Ser Asn Asp Tyr Thr
1 5

<210> 160
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-A8 heavy chain CDR3

<400> 160

Ala Arg His Ser Tyr Gly Asn Tyr Gly Asp Tyr
1 5 10

<210> 161

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-A8 heavy chain FR1

<400> 161

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

Ser Val Lys Met Ser Cys Lys Ala Ser
20 25

<210> 162

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-A8 heavy chain FR2

<400> 162

Val His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
1 5 10 15

Phe

<210> 163

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-A8 heavy chain FR3

<400> 163

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

Ser Ser Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp
20 25 30

Ser Ala Val Tyr Tyr Cys
35

<210> 164
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-A8 light chain variable region

<400> 164

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

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

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

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

Ser Gly Phe Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

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

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

<210> 165
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> 4M2-A8 light chain CDR1

<400> 165

Gln Ser Val Thr Asn Gly
1 5

<210> 166

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-A8 light chain FR1

<400> 166

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

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
20 25

<210> 167

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-A8 light chain FR3

<400> 167

Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Phe Gly
1 5 10 15

Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala Glu Asp Leu Ala
20 25 30

Val Tyr Phe Cys
35

<210> 168

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> 9M2-C12 heavy chain variable region

<400> 168

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

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

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

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Cys Asn Gln Arg Phe
50 55 60

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

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

Ala Arg Trp Ala Tyr Gly Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
115

<210> 169

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 9M2-C12 heavy chain CDR1

<400> 169

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 170

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 9M2-C12 heavy chain CDR2

<400> 170

Ile Asp Pro Ser Asp Ser Tyr Thr
1 5

<210> 171

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 9M2-C12 heavy chain CDR3

<400> 171

Ala Arg Trp Ala Tyr Gly Pro Tyr Ala Met Asp Tyr
1 5 10

<210> 172

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> 9M2-C12 heavy chain FR1

<400> 172

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

Ser Val Arg Leu Ser Cys Lys Ala Ser
20 25

<210> 173

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 9M2-C12 heavy chain FR2

<400> 173

Met His Trp Val Arg Gln Arg Pro Gly Leu Gly Leu Glu Trp Ile Gly
1 5 10 15

Glu

<210> 174
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 heavy chain FR3

<400> 174

Asn Cys Asn Gln Arg Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys
1 5 10 15

Ser Ser Ser Thr Ala Tyr Thr Gln Leu Ser Ser Leu Thr Ser Glu Asp
20 25 30

Ser Ala Val Tyr Tyr Cys
35

<210> 175
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 heavy chain FR4

<400> 175

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
1 5 10

<210> 176
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 light chain variable region

<400> 176

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

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

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

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

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

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

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

<210> 177
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 light chain CDR1

<400> 177

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 178
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12, 13D5p, 13D5-1, 13D5-13 light chain CDR2

<400> 178

Lys Val Ser
1

<210> 179
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 light chain CDR3

<400> 179

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 180
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 light chain FR1

<400> 180

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
20 25

<210> 181
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 light chain FR2

<400> 181

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 182
<211> 36
<212> PRT
<213> Artificial Sequence

<220>

<223> 9M2-C12 light chain FR3

<400> 182

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
20 25 30

Val Tyr Phe Cys
35

<210> 183

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 13D5p heavy chain variable region

<400> 183

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

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

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

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

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

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

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

Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 184
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p, 13D5-1, 13D5-13 heavy chain CDR2

<400> 184

Ile Tyr Pro Gly Gly Gly Tyr Thr
1 5

<210> 185
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p heavy chain CDR3

<400> 185

Ala Arg Gly Gly Tyr Tyr Tyr Gly Ser Ser Trp Tyr Phe Asp Val
1 5 10 15

<210> 186
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p, 13D5-1, 13D5-13 heavy chain FR2

<400> 186

Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly
1 5 10 15

Asp

<210> 187
<211> 38

<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p, 13D5-1 heavy chain FR3

<400> 187

Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr
1 5 10 15

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
20 25 30

Ser Ala Val Tyr Phe Cys
35

<210> 188
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p light chain variable region

<400> 188

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

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

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

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

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

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

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

<210> 189
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p light chain CDR1

<400> 189

Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 190
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p, 13D5-1, 13D5-13 light chain CDR3

<400> 190

Phe Gln Gly Ser His Val Pro Pro Thr
1 5

<210> 191
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p, 13D5-1, 13D5-13 light chain FR1

<400> 191

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
20 25

<210> 192
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> 13D5p, 13D5-13 light chain FR2

<400> 192

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

Tyr

<210> 193

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> 13D5p, 13D5-1 light chain FR3

<400> 193

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
20 25 30

Val Tyr Tyr Cys
35

<210> 194

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> 13D5-1 heavy chain variable region

<400> 194

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

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

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

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

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

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

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

Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 195
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-1 heavy chain CDR3

<400> 195

Val Arg Ser Gly Tyr Tyr Tyr Gly Ser Ser Trp Tyr Phe Asp Val
1 5 10 15

<210> 196
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-1 light chain variable region

<400> 196

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

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

Ser Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Asp Gln Ser
35 40 45

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

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

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

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

<210> 197
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-1 light chain CDR1

<400> 197

Gln Ser Ile Val His Ser Ser Gly Asn Thr Tyr
1 5 10

<210> 198
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-1 light chain FR2

<400> 198

Leu Glu Trp Tyr Leu Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 199
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-13 heavy chain variable region

<400> 199

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

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

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

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

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

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

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

Gly Ala Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 200
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-13 heavy chain CDR3

<400> 200

Val Arg Gly Gly Tyr Tyr Tyr Gly Ser Ser Trp Tyr Phe Asp Val
1 5 10 15

<210> 201
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-13 heavy chain FR3

<400> 201

Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Ile
1 5 10 15

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
20 25 30

Ser Ala Asp Tyr Phe Cys
35

<210> 202
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-13 light chain variable region

<400> 202

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

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

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

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

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

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

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

<210> 203
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-13 light chain CDR1

<400> 203

Gln Ser Thr Val His Ser Ile Gly Asn Thr Tyr
1 5 10

<210> 204
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-13 light chain FR3

<400> 204

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Glu Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
20 25 30

Val Tyr Tyr Cys
35

<210> 205
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 constant region (IGHG1; UniProt:P01857-1, v1)

<400> 205

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

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

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

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 206
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1 IgG1 (positions 1-98 of P01857-1, v1)

<400> 206

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

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

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

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

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

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

Lys Val

<210> 207
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge IgG1 (positions 99-110 of P01857-1, v1)
<400> 207

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

<210> 208
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> CH2 IgG1 (positions 111-223 of P01857-1, v1)
<400> 208

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

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
35 40 45

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

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

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

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys

<210> 209
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3 IgG1 (positions 224-330 of P01857-1, v1)

<400> 209

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

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

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

<220>

<223> CH3 (D356E, L358M; positions numbered according to EU numbering)

<400> 210

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

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

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

<220>

<223> Ckappa CL (IGCK; UniProt: P01834-1, v2)

<400> 211

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

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

<220>
<223> 4M2-C12 VH-CH1-CH2-CH3

<400> 212

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

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

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

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

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

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

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

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

<220>
<223> 4M2-C12 VL-Ckappa

<400> 213

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

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

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

Gly Ser Gly Thr Ser Asn Ser Leu Thr Ile Thr Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 214

<211> 449

<212> PRT
<213> Artificial Sequence

<220>

<223> 4M2-B4 VH-CH1-CH2-CH3

<400> 214

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

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

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

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

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

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

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 215
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-B4 VL-Ckappa

<400> 215

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

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

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

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

Gly Ser Gly Thr Ser Asn Ser Leu Thr Ile Thr Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 216
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 VH-CH1-CH2-CH3

<400> 216

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

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

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

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

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

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

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 217
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H1 VL-Ckappa

<400> 217

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Leu
20 25 30

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

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

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

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 218
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H2 VH-CH1-CH2-CH3

<400> 218

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

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

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

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

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

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Asp Cys
85 90 95

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

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 219
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4H2 VL-Ckappa

<400> 219

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 Ser Ser Val Gly Tyr Leu
20 25 30

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

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

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

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 220
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12 VH-CH1-CH2-CH3

<400> 220

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

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

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

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

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

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

Ala Gln Ile Pro Leu Tyr Tyr Gly His Tyr Arg Ser Ala Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 221

<211> 214

<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-B12 VL-Ckappa

<400> 221

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

Glu Thr Val Ala Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
20 25 30

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

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu 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> 222
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 VH-CH1-CH2-CH3

<400> 222

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Leu Asp Gly Tyr Asn Asp Pro Tyr Tyr Phe Asp Tyr
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Pro Gly Lys
450

<210> 223
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C9 VL-Ckappa

<400> 223

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu 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> 224
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-D2 VH-CH1-CH2-CH3

<400> 224

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

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

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

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

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

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

Ala Gln Ile Pro Leu Tyr Tyr Gly His Tyr Arg Ser Ala Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 225
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 2M1-D2 VL-Ckappa

<400> 225

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

Glu Thr Val Ala Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala
20 25 30

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

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu 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> 226
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 VH-CH1-CH2-CH3

<400> 226

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 227
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D9 VL-Ckappa

<400> 227

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

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

Gly Thr Ser Leu Met Gln Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

Pro Val Glu Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

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

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

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

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

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

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

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

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

<210> 228
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 VH-CH1-CH2-CH3

<400> 228

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

Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ala
20 25 30

Trp Met Asp Trp Val His Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala Glu Ile Arg Ser Lys Ala Asn Asn His Ala Thr Tyr Tyr Val Glu
50 55 60

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

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

Tyr Cys Thr Arg Arg Asp Gly Tyr Tyr Phe Ala Tyr Trp Gly Gln Gly
100 105 110

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

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 229
<211> 212
<212> PRT
<213> Artificial Sequence

<220>
<223> 1M2-D2 VL-Ckappa

<400> 229

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

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

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

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

Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Gly
65 70 75 80

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

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

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

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

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

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

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

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
195 200 205

Arg Gly Glu Cys
210

<210> 230
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 VH-CH1-CH2-CH3

<400> 230

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

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

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

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Leu Asp Gly Tyr Asn Asp Pro Tyr Tyr Phe Asp Tyr
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Pro Gly Lys
450

<210> 231
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> 5M1-A11 VL-Ckappa

<400> 231

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Arg Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

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

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

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

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

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

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

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

Asn Arg Gly Glu Cys
210

<210> 232

<211> 448

<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 VH-CH1-CH2-CH3

<400> 232

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

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

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

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

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

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

Thr Arg His Ser Tyr Gly Asn Tyr Gly Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 233
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-D5 VL-Ckappa

<400> 233

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

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

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

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

Ser Gly Phe Gly Thr Asp Phe Thr Phe Thr Ile Asn Thr Val Gln Ala
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu 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> 234
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-A8 VH-CH1-CH2-CH3

<400> 234

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

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

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

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

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

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

Ala Arg His Ser Tyr Gly Asn Tyr Gly Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 235
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-A8 VL-Ckappa

<400> 235

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

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

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

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

Ser Gly Phe Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Leu 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> 236
<211> 449
<212> PRT
<213> Artificial Sequence

<220>

<223> 9M2-C12 VH-CH1-CH2-CH3

<400> 236

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

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

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

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Cys Asn Gln Arg Phe
50 55 60

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

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

Ala Arg Trp Ala Tyr Gly Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

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

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

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys

<210> 237
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 9M2-C12 VL-Ckappa

<400> 237

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 238
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p VH-CH1-CH2-CH3

<400> 238

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

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

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

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

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

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

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

Gly Ala Gly Thr Thr 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 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 239
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p VL-Ckappa

<400> 239

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 240
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-1 VH-CH1-CH2-CH3

<400> 240

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

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

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

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

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

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

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

Gly Ala Gly Thr Thr 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 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 241
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-1 VL-Ckappa

<400> 241

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

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

Ser Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Asp Gln Ser
35 40 45

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

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

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

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

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

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

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

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

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

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

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

<210> 242
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5-13 VH-CH1-CH2-CH3

<400> 242

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

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

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

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

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

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

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

Gly Ala Gly Thr Thr 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 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

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

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

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 243
<211> 219
<212> PRT
<213> Artificial Sequence

<220>

<223> 13D5-13 VL-Ckappa

<400> 243

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Thr Val His Ser
20 25 30

Ile Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Glu Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 244
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 derived heavy chain CDR1 consensus

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = S or T

<400> 244

Gly Tyr Xaa Ile Thr Ser Asp Tyr Ala
1 5

<210> 245
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 derived light chain CDR2 consensus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = A or D

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = T or A

<400> 245

Xaa Xaa Ser
1

<210> 246

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p derived heavy chain CDR3 consensus

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = V or A

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = G or S

<400> 246

Xaa	Arg	Xaa	Gly	Tyr	Tyr	Tyr	Gly	Ser	Ser	Trp	Tyr	Phe	Asp	Val
1				5				10						15

<210> 247
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 13D5p derived light chain CDR1 consensus

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa = I or T

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = N, S or I

<400> 247

Gln	Ser	Xaa	Val	His	Ser	Xaa	Gly	Asn	Thr	Tyr
1				5				10		

<210> 248
<211> 449
<212> PRT
<213> Artificial Sequence

<220>

<223> 4M2-C12 mIgG2a HC

<400> 248

Glu Val Lys Leu Val Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Thr Tyr Ser Gly Asn Ile Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Ser Cys
85 90 95

Ala Arg Ser Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser
180 185 190

Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser

195

200

205

Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys
 210 215 220

Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
 245 250 255

Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
 260 265 270

Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
 275 280 285

Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
 290 295 300

Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
 305 310 315 320

Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
 325 330 335

Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val
 340 345 350

Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
 355 360 365

Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
 370 375 380

Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
 405 410 415

Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
420 425 430

Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
435 440 445

Lys

<210> 249
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 mIgG2a LALA PG HC

<400> 249

Glu Val Lys Leu Val Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Thr Tyr Ser Gly Asn Ile Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Ser Cys
85 90 95

Ala Arg Ser Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser
180 185 190

Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys
210 215 220

Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Ala Ala Gly Gly Pro
225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
245 250 255

Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
260 265 270

Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
275 280 285

Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
290 295 300

Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
305 310 315 320

Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Gly Ala Pro Ile Glu Arg
325 330 335

Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val

340

345

350

Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
 355 360 365

Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
 370 375 380

Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
 405 410 415

Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
 420 425 430

Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
 435 440 445

Lys

<210> 250
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4M2-C12 LC

<400> 250

Asp Ile Val Ile Thr Gln Thr Pro Ala Ile Leu Ser Thr Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser

50

55

60

Gly Ser Gly Thr Ser Asn Ser Leu Thr Ile Thr Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys Arg Ala Asp Ala Ala
100 105 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
115 120 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130 135 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145 150 155 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 251

<211> 97

<212> PRT

<213> Artificial Sequence

<220>

<223> mIgG2a CH1

<400> 251

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly

1	5	10	15
Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr	20	25	30
Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser	35	40	45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu	50	55	60
Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile	65	70	75
Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys	85	90	95

Ile

<210> 252
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mIgG2a Hinge

<400> 252

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro	1	5	10	15
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<210> 253
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mIgG2a CH2

<400> 253

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys	1	5	10	15
---	---	---	----	----

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
65 70 75 80

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
85 90 95

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
100 105 110

<210> 254
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG2a CH2 LALA PG

<400> 254

Ala Pro Asn Ala Ala Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
65 70 75 80

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
85 90 95

Asp Leu Gly Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
100 105 110

<210> 255
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG2a CH3

<400> 255

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
1 5 10 15

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
20 25 30

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
35 40 45

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
50 55 60

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
65 70 75 80

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
85 90 95

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
100 105

<210> 256
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse Ig gamma-2A chain C region, A allele

<400> 256

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly
1 5 10 15

Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
20 25 30

Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
50 55 60

Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
85 90 95

Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
100 105 110

Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
115 120 125

Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
130 135 140

Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
145 150 155 160

Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
165 170 175

Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
180 185 190

His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
195 200 205

Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
210 215 220

Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
225 230 235 240

Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
245 250 255

Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
260 265 270

Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
275 280 285

Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
290 295 300

Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
305 310 315 320

Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
325 330

<210> 257
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG2a CH2, CH3 LALA PG

<400> 257

Ala Pro Asn Ala Ala Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
65 70 75 80

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
85 90 95

Asp Leu Gly Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
100 105 110

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
115 120 125

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
130 135 140

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
145 150 155 160

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
165 170 175

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
180 185 190

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
195 200 205

Lys Ser Phe Ser Arg Thr Pro Gly Lys
210 215

<210> 258
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 mIgG2a NQ HC

<400> 258

Glu Val Lys Leu Val Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Thr Tyr Ser Gly Asn Ile Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Ser Cys
85 90 95

Ala Arg Ser Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser
180 185 190

Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys

210

215

220

Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
 245 250 255

Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
 260 265 270

Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
 275 280 285

Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Gln Ser Thr Leu Arg Val
 290 295 300

Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
 305 310 315 320

Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
 325 330 335

Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val
 340 345 350

Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
 355 360 365

Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
 370 375 380

Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
 405 410 415

Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
 420 425 430

Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
435 440 445

Lys

<210> 259
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG2a CH2 NQ

<400> 259

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60

Asp Tyr Gln Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
65 70 75 80

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
85 90 95

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
100 105 110

<210> 260
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG2a CH2, CH3 NQ

<400> 260

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60

Asp Tyr Gln Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
65 70 75 80

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
85 90 95

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
100 105 110

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
115 120 125

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
130 135 140

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
145 150 155 160

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
165 170 175

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
180 185 190

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
195 200 205

Lys Ser Phe Ser Arg Thr Pro Gly Lys
210 215

<210> 261
<211> 324
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse IGHG1

<400> 261

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
1 5 10 15

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
50 55 60

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
85 90 95

Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
100 105 110

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
115 120 125

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
130 135 140

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
145 150 155 160

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
165 170 175

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
180 185 190

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
195 200 205

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
210 215 220

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
225 230 235 240

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
245 250 255

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
260 265 270

Pro Ile Met Asn Thr Asn Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
275 280 285

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
290 295 300

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
305 310 315 320

Ser Pro Gly Lys

<210> 262
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG1 CH1

<400> 262

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
1 5 10 15

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
50 55 60

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
85 90 95

Ile

<210> 263
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG1 Hinge

<400> 263

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr
1 5 10

<210> 264
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> mIgG1 CH2

<400> 264

Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp

1	5	10	15												
Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	Val	Thr	Cys	Val	Val	Val	Asp
			20					25					30		
Ile	Ser	Lys	Asp	Asp	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp
		35					40					45			
Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn
	50					55					60				
Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp
65					70					75					80
Leu	Asn	Gly	Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro
				85					90					95	
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys					
			100					105							

<210> 265
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mIgG1 CH3

<400> 265

Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu
1				5					10					15	
Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe
			20					25					30		
Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala
		35					40					45			
Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	Ile	Met	Asn	Thr	Asn	Gly	Ser	Tyr
	50					55					60				
Phe	Val	Tyr	Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly

65		70		75		80
Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His						
		85		90		95
Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys						
		100		105		
<210> 266						
<211> 443						
<212> PRT						
<213> Artificial Sequence						
<220>						
<223> 4M2-C12 mIgG1 HC						
<400> 266						
Glu Val Lys Leu Val Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln						
1		5		10		15
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp						
		20		25		30
Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp						
		35		40		45
Met Gly Tyr Ile Thr Tyr Ser Gly Asn Ile Ser Tyr Asn Pro Ser Leu						
		50		55		60
Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe						
65				70		75
						80
Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Ser Cys						
		85		90		95
Ala Arg Ser Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Ala Gly						
		100		105		110
Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr						
		115		120		125
Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu						

130

135

140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
 145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Val Thr Val Pro Ser Ser
 180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
 210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
 225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
 245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
 260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
 290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
 305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
 325 330 335

Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu
 340 345 350

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn Gly Ser Tyr
385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> 267
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> IGN175A HC

<400> 267

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Thr His
20 25 30

Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Ser Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Leu Leu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val

290

295

300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 268

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> IGN175A LC

<400> 268

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1	5	10	15
Asp	Gln	Ala	Ser
	20		
Ile	Ser	Cys	Arg
		25	
Ser	Ser	Gln	Ser
Ile	Val	His	Ser
	30		
Asn	Gly	Asn	Thr
	35		
Tyr	Leu	Glu	Trp
		40	
Tyr	Leu	Gln	Lys
Pro	Gly	Gln	Ser
	45		
Pro	Lys	Leu	Leu
	50		
Ile	Tyr	Lys	Leu
		55	
Ser	Asn	Arg	Phe
			60
Ser	Gly	Val	Pro
Asp	Arg	Phe	Ser
	65		
Gly	Ser	Gly	Ser
	70		
Gly	Thr	Asp	Phe
		75	
Thr	Leu	Lys	Ile
			80
Ser	Arg	Val	Glu
Ala	Glu	Asp	Leu
	85		
Gly	Val	Tyr	Tyr
Cys	Phe	Gln	Gly
		95	
Ser	His	Phe	Pro
Tyr	Thr	Phe	Gly
Gly	Gly	Thr	Lys
	105		
Leu	Glu	Ile	Lys
	110		
Arg	Thr	Val	Ala
Ala	Pro	Ser	Val
Phe	Ile	Phe	Pro
Pro	Pro	Ser	Asp
	125		
Gln	Leu	Lys	Ser
	130		
Gly	Thr	Ala	Ser
Val	Val	Cys	Leu
Leu	Leu	Asn	Asn
	140		
Tyr	Pro	Arg	Glu
Ala	Lys	Val	Gln
Trp	Lys	Val	Asp
Asn	Ala	Leu	Gln
	155		
Ser	Gly	Asn	Ser
Gln	Glu	Ser	Val
Thr	Glu	Gln	Asp
Ser	Lys	Asp	Ser
	175		
Thr	Tyr	Ser	Leu
Ser	Ser	Thr	Leu
Thr	Leu	Ser	Lys
Ala	Asp	Tyr	Glu
	190		
Lys	His	Lys	Val
Tyr	Ala	Cys	Glu
Val	Thr	His	Gln
Gly	Leu	Ser	Ser
	205		
Pro	Val	Thr	Lys
Ser	Phe	Asn	Arg
Gly	Glu	Cys	
	215		

<210> 269
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> VSTB112 HC

<400> 269

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Leu Leu Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Ser Tyr Gly Trp Ser Tyr Glu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

 <210> 270
 <211> 214
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> VSTB112 LC

 <400> 270

 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Thr Arg
 20 25 30

 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

 Tyr Ser Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ala Tyr Asn Pro Ile
 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> 271
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VSTB112 major epitope 1

<400> 271

Pro Val Asp Lys Gly His Asp Val Thr Phe
 1 5 10

<210> 272
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VSTB112 major epitope 2

<400> 272

Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp Leu
1 5 10

<210> 273
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> VSTB112 minor epitope 1

<400> 273

Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val Gln Thr Cys Ser
1 5 10

<210> 274
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VSTB112 minor epitope 2

<400> 274

Glu Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu
1 5 10 15

Leu

<210> 275
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> IGN175A epitope

<400> 275

Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
1 5 10 15

Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
20 25 30

<210> 276
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1 heavy chain variable region

<400> 276

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Thr Tyr Ser Gly Tyr Ile Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Ser Cys
85 90 95

Ala Arg Ala Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 277
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1 heavy chain CDR2

<400> 277

Ile Thr Tyr Ser Gly Tyr Ile

1

5

<210> 278
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1, V4-C9, V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31
heavy chain CDR3

<400> 278

Ala Arg Ala Leu Tyr Tyr Pro Trp Tyr Phe Asp Val
1 5 10

<210> 279
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1, V4-C9 heavy chain FR2

<400> 279

Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10 15

Tyr

<210> 280
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1, V4-C9 heavy chain FR3

<400> 280

Ser Tyr Asn Pro Ser Leu Arg Ser Arg Val Thr Ile Ser Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
20 25 30

Thr Ala Val Tyr Ser Cys
35

<210> 281
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1, V4-C9, V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31
heavy chain FR4

<400> 281

Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 282
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1 light chain variable region

<400> 282

Glu Ile Val Ile Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys

100

105

<210> 283
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> V4-C1, V4-C9, V4-C24, V4-C27, V4-C28, V4-C30, V4-C31 light chain
 FR2

<400> 283

Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile
 1 5 10 15

Tyr

<210> 284
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> V4-C1, V4-C9, V4-C26, V4-C27 light chain FR3

<400> 284

Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
 1 5 10 15

Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Ser Ala
 20 25 30

Val Tyr Tyr Cys
 35

<210> 285
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> V4-C9 heavy chain variable region

<400> 285

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Thr Tyr Ser Gly Tyr Val Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Ser Cys
85 90 95

Ala Arg Ala Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 286
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C9 heavy chain CDR2

<400> 286

Ile Thr Tyr Ser Gly Tyr Val
1 5

<210> 287
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C9 light chain variable region

<400> 287

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 288

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> V4-C9, V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31 light chain
FR1

<400> 288

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
20 25

<210> 289

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31 heavy chain variable region

<400> 289

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Thr Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly His Ile Thr Tyr Ser Gly Ser Val Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Ser Cys
85 90 95

Ala Arg Ala Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 290

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31 heavy chain CDR1

<400> 290

Gly Tyr Ser Ile Thr Ser Asp Tyr Thr
1 5

<210> 291

<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31 heavy chain CDR2

<400> 291

Ile Thr Tyr Ser Gly Ser Val
1 5

<210> 292
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31 heavy chain FR2

<400> 292

Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10 15

His

<210> 293
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C24, V4-C26, V4-C27, V4-C28, V4-C30, V4-C31 heavy chain FR3

<400> 293

Ser Tyr Asn Pro Ser Leu Arg Ser Arg Val Thr Ile Ser Arg Asp Thr
1 5 10 15

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
20 25 30

Thr Ala Thr Tyr Ser Cys
35

<210> 294
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C24 light chain variable region

<400> 294

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Thr Thr Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 295
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C24, V4-C26 light chain CDR2

<400> 295

Thr Thr Ser
1

<210> 296
<211> 36
<212> PRT
<213> Artificial Sequence

<220>

<223> V4-C24, V4-C28, V4-C30 light chain FR3

<400> 296

Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Ser Ala
20 25 30

Val Tyr Tyr Cys
35

<210> 297

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> V4-C26 light chain variable region

<400> 297

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Ile Ile Tyr
35 40 45

Thr Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 298
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C26 light chain FR2

<400> 298

Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Ile Ile
1 5 10 15

Tyr

<210> 299
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C27 light chain variable region

<400> 299

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Tyr Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 300
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C27, V4-C30, V4-C31 light chain CDR2

<400> 300

Ala Thr Tyr
1

<210> 301
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C28 light chain variable region

<400> 301

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 302
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C30 light chain variable region

<400> 302

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Tyr Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 303
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C31 light chain variable region

<400> 303

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Tyr Tyr Arg Thr Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 304
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C31 light chain FR3

<400> 304

Tyr Arg Thr Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Ser Ala
20 25 30

Val Tyr Tyr Cys
35

<210> 305
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 derived heavy chain CDR1 consensus

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X = S or T

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X = T or A

<400> 305

Gly Tyr Xaa Ile Thr Ser Asp Tyr Xaa
1 5

<210> 306
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 derived heavy chain CDR2 consensus

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X = S, N or Y

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X = V or I

<400> 306

Ile Thr Tyr Ser Gly Xaa Xaa
1 5

<210> 307
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 4M2-C12 derived heavy chain CDR3 consensus

<220>
<221> MISC_FEATURE
<222> (3)..(3)

<223> X = A or S

<400> 307

Ala	Arg	Xaa	Leu	Tyr	Tyr	Pro	Trp	Tyr	Phe	Asp	Val
1				5					10		

<210> 308

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 4M2-C12 derived light chain CDR2 consensus

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> X = A, T or D

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X = T or A

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> X = S or Y

<400> 308

Xaa	Xaa	Xaa
1		

<210> 309

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> C24/C26/C27 light chain CDR2 consensus

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> X = T or A

<220>

<221> MISC_FEATURE

<222> (3)..(3)
<223> X = S or Y

<400> 309

Xaa Thr Xaa
1

<210> 310
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> C24/C26/C27 light chain variable region consensus

<220>
<221> MISC_FEATURE
<222> (46)..(46)
<223> X = L or I

<220>
<221> MISC_FEATURE
<222> (49)..(49)
<223> X = T or A

<220>
<221> MISC_FEATURE
<222> (51)..(51)
<223> X = S or Y

<220>
<221> MISC_FEATURE
<222> (52)..(52)
<223> X = N or Y

<400> 310

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Xaa Ile Tyr
35 40 45

Xaa Thr Xaa Xaa Tyr Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro
85 90 95

Pro Ile Thr Phe Gly Gly Gly Thr Lys Leu Glu Val Lys
100 105

<210> 311
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1 VH-CH1-CH2-CH3

<400> 311

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Thr Tyr Ser Gly Tyr Ile Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Ser Cys
85 90 95

Ala Arg Ala Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 312
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C1 VL-Ckappa

<400> 312

Glu Ile Val Ile Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 313
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C9 VH-CH1-CH2-CH3

<400> 313

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Thr Tyr Ser Gly Tyr Val Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Ser Cys
85 90 95

Ala Arg Ala Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 314
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C9 VL-Ckappa

<400> 314

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 315
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C24/C26/C27/C28/C30/C31 VH-CH1-CH2-CH3

<400> 315

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Thr Trp Asn Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly His Ile Thr Tyr Ser Gly Ser Val Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Ser Cys
85 90 95

Ala Arg Ala Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Thr Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 316
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C24 VL-Ckappa

<400> 316

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Thr Thr Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 317
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> V4-C26 VL-Ckappa

<400> 317

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Ile Ile Tyr
35 40 45

Thr Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 318
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C27 VL-Ckappa

<400> 318

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Tyr Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 319
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C28 VL-Ckappa

<400> 319

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 320
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C30 VL-Ckappa

<400> 320

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Tyr Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 321
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> V4-C31 VL-Ckappa

<400> 321

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Gly Tyr Ile
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Pro Leu Ile Tyr
35 40 45

Ala Thr Tyr Tyr Arg Thr Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Asn Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
65 70 75 80

Asp Ser Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Val 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> 322
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> VISTA sequence to which 4M2-C12 and derivatives bind

<400> 322

Ser Arg Gly Glu Val Gln
1 5

<210> 323
<211> 412
<212> PRT
<213> Homo sapiens PSGL-1 isoform 1 (UniProt: Q14242-1, v1)

<400> 323

Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
1 5 10 15

Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
20 25 30

Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
35 40 45

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
50 55 60

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
65 70 75 80

Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
85 90 95

Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
100 105 110

Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
115 120 125

Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
130 135 140

Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu
145 150 155 160

Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
165 170 175

Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
180 185 190

Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
195 200 205

Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
210 215 220

Gln Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu
225 230 235 240

Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu
245 250 255

Ala Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu
260 265 270

Ser Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val
275 280 285

Ser Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser
290 295 300

Val Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys
305 310 315 320

Leu Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val
325 330 335

Cys Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr

340

345

350

Pro Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu
 355 360 365

Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu
 370 375 380

Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg
 385 390 395 400

Glu Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
 405 410

<210> 324

<211> 428

<212> PRT

<213> Homo sapiens PSGL-1 isoform 2 (UniProt: Q14242-2)

<400> 324

Met Ala Val Gly Ala Ser Gly Leu Glu Gly Asp Lys Met Ala Gly Ala
 1 5 10 15

Met Pro Leu Gln Leu Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
 20 25 30

Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
 35 40 45

Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
 50 55 60

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
 65 70 75 80

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
 85 90 95

Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
 100 105 110

Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
115 120 125

Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
130 135 140

Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
145 150 155 160

Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu
165 170 175

Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
180 185 190

Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
195 200 205

Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
210 215 220

Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
225 230 235 240

Gln Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu
245 250 255

Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu
260 265 270

Ala Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu
275 280 285

Ser Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val
290 295 300

Ser Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser
305 310 315 320

Val Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys
325 330 335

Leu Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val
340 345 350

Cys Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr
355 360 365

Pro Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu
370 375 380

Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu
385 390 395 400

Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg
405 410 415

Glu Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
420 425

<210> 325

<211> 395

<212> PRT

<213> Homo sapiens Mature human PSGL-1 isoform 1 (Q14242-1, v1 positions 18 to 412)

<400> 325

Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly
1 5 10 15

Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu
20 25 30

Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg Asn
35 40 45

Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser Thr
50 55 60

Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly Gly
65 70 75 80

Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser
85 90 95

Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala Thr
100 105 110

Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr Pro
115 120 125

Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu Ala
130 135 140

Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
145 150 155 160

Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln Thr
165 170 175

Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala Met
180 185 190

Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr Gln
195 200 205

Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu Ala
210 215 220

Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala
225 230 235 240

Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu Ser
245 250 255

Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val Ser
260 265 270

Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser Val
275 280 285

Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys Leu
290 295 300

Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val Cys
305 310 315 320

Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr Pro
325 330 335

Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu Leu
340 345 350

Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu Ser
355 360 365

Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg Glu
370 375 380

Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
385 390 395

<210> 326
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> PSGL-1 extracellular domain (Q14242-1, v1 positions 18 to 320)

<400> 326

Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly
1 5 10 15

Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu
20 25 30

Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg Asn
35 40 45

Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser Thr
50 55 60

Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly Gly
65 70 75 80

Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser
85 90 95

Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala Thr
100 105 110

Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr Pro
115 120 125

Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu Ala
130 135 140

Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
145 150 155 160

Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln Thr
165 170 175

Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala Met
180 185 190

Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr Gln
195 200 205

Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu Ala
210 215 220

Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala
225 230 235 240

Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu Ser
245 250 255

Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val Ser
260 265 270

Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser Val
275 280 285

Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys
290 295 300

<210> 327
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> PSGL-1 transmembrane domain (Q14242-1, v1 positions 321 to 341)

<400> 327

Leu Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val
1 5 10 15

Cys Thr Val Val Leu
20

<210> 328
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> PSGL-1 cytoplasmic domain (Q14242-1, v1 positions 342 to 412)

<400> 328

Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr
1 5 10 15

Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly
20 25 30

Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser
35 40 45

Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg Glu Gly Asp Asp Leu
50 55 60

Thr Leu His Ser Phe Leu Pro
65 70

<210> 329
<211> 140

<212> PRT
<213> Artificial Sequence

<220>

<223> PSGL-1 extracellular domain repeat region (Q14242-1, v1 positions 122 to 261)

<400> 329

Gln Thr Thr Gln Pro Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Val
1 5 10 15

Pro Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr
20 25 30

Thr Arg Leu Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr
35 40 45

Glu Ala Gln Thr Thr Pro Pro Ala Ala Thr Glu Ala Gln Thr Thr Gln
50 55 60

Pro Thr Gly Leu Glu Ala Gln Thr Thr Ala Pro Ala Ala Met Glu Ala
65 70 75 80

Gln Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Pro Pro Ala
85 90 95

Ala Met Glu Ala Gln Thr Thr Gln Thr Thr Ala Met Glu Ala Gln Thr
100 105 110

Thr Ala Pro Glu Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Ala Thr
115 120 125

Glu Ala Gln Thr Thr Pro Leu Ala Ala Met Glu Ala
130 135 140

<210> 330
<211> 446
<212> PRT
<213> Artificial Sequence

<220>

<223> 4M2-C12 VH-CH1-CH2-CH3 IgG4

<400> 330

Glu Val Lys Leu Val Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Thr Tyr Ser Gly Asn Ile Ser Tyr Asn Pro Ser Leu
50 55 60

Arg Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Ser Cys
85 90 95

Ala Arg Ser Leu Tyr Tyr Pro Trp Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro

210

215

220

Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
 260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
	435						440					445	