

eolf-seql
SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG
<120> Antigen Binding Molecules comprising a TNF family ligand trimer
<130> P32429-W0
<150> EP14193260.8
<151> 2014-11-14
<150> EP15183736.6
<151> 2015-09-03
<150> EP15188142.2
<151> 2015-10-02
<160> 375
<170> PatentIn version 3.5
<210> 1
<211> 184
<212> PRT
<213> Homo sapiens
<400> 1

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

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Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu
180

<210> 2
<211> 170
<212> PRT
<213> Homo sapiens

<400> 2

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

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
20 25 30

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
35 40 45

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu

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50

55

60

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
65 70 75 80

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
85 90 95

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

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
115 120 125

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
130 135 140

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
145 150 155 160

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
165 170

<210> 3
<211> 175
<212> PRT
<213> Homo sapiens

<400> 3

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
1 5 10 15

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
20 25 30

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
35 40 45

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Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
50 55 60

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
65 70 75 80

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
85 90 95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
145 150 155 160

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

<210> 4
<211> 203
<212> PRT
<213> Homo sapiens

<400> 4

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
1 5 10 15

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
20 25 30

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Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
 35 40 45

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
 50 55 60

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

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
 85 90 95

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
 100 105 110

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
 115 120 125

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
 130 135 140

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
 145 150 155 160

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
 165 170 175

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
 180 185 190

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 195 200

<210> 5
 <211> 378
 <212> PRT

eolf-seql

<213> Artificial sequence

<220>

<223> hu 4-1BBL (71-254) connected by (G4S)₂ to hu 4-1BBL (71-254)

<400> 5

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala

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165

170

175

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile

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355

360

365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
370 375

<210> 6

<211> 194

<212> PRT

<213> Artificial sequence

<220>

<223> hu 4-1BBL (71-254) plus (G4S)2

<400> 6

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

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Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
 180 185 190

Gly Ser

<210> 7
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(28H1) CDR-H1

<400> 7

Ser His Ala Met Ser
 1 5

<210> 8
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(28H1) CDR-H2

<400> 8

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

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<210> 9
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> FAP(28H1) CDR-H3

<400> 9

Gly Trp Leu Gly Asn Phe Asp Tyr
1 5

<210> 10
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> FAP(28H1) CDR-L1

<400> 10

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

<210> 11
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> FAP(28H1) CDR-L2

<400> 11

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 12
<211> 9
<212> PRT
<213> Artificial sequence

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<220>

<223> FAP(28H1) CDR-L3

<400> 12

Gln Gln Gly Gln Val Ile Pro Pro Thr
1 5

<210> 13

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> (G4S)2 peptide linker

<400> 13

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

<210> 14

<211> 718

<212> PRT

<213> Artificial sequence

<220>

<223> dimeric hu 4-1BBL (71-254) plus CH1 plus Fc knob chain

<400> 14

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

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Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

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Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
385 390 395 400

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
405 410 415

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
420 425 430

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
435 440 445

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Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
450 455 460

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
465 470 475 480

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
500 505 510

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
515 520 525

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
530 535 540

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
545 550 555 560

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
565 570 575

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
580 585 590

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
595 600 605

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
610 615 620

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
625 630 635 640

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Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
645 650 655

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
660 665 670

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
675 680 685

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
690 695 700

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
705 710 715

<210> 15
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> hu 4-1BBL (71-254) -CL

<400> 15

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg

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65		70		75		80
Arg	Val	Val	Ala	Gly	Glu	Gly
			85			
				Ser	Gly	Ser
				90		
				Val	Ser	Leu
						Ala
						Leu
						His
						95
Leu	Gln	Pro	Leu	Arg	Ser	Ala
			100			
				Ala	Ala	Gly
				105		
				Ala	Ala	Ala
						Leu
						Ala
						Leu
						Thr
						110
Val	Asp	Leu	Pro	Pro	Ala	Ser
			115			
				Ser	Ser	Glu
				120		
				Ala	Arg	Asn
						Ser
						Ala
						Phe
						Gly
						125
Phe	Gln	Gly	Arg	Leu	Leu	His
						135
						Leu
						Ser
						Ala
						Gly
						Gln
						Arg
						Leu
						Gly
						Val
						140
His	Leu	His	Thr	Glu	Ala	Arg
						150
						Ala
						Arg
						His
						Ala
						Trp
						Gln
						Leu
						Thr
						Gln
						160
Gly	Ala	Thr	Val	Leu	Gly	Leu
				165		
						Phe
						Arg
						Val
						Thr
						Pro
						Glu
						Ile
						Pro
						Ala
						175
Gly	Leu	Pro	Ser	Pro	Arg	Ser
			180			
						Glu
						185
						Gly
						Gly
						Gly
						Ser
						Gly
						Gly
						Gly
						190
Gly	Ser	Arg	Thr	Val	Ala	Ala
						200
						Pro
						Ser
						Val
						Phe
						Ile
						Phe
						Pro
						Pro
						Ser
						195
Asp	Glu	Gln	Leu	Lys	Ser	Gly
						215
						Thr
						Ala
						Ser
						Val
						Val
						Cys
						Leu
						Leu
						Asn
						210
Asn	Phe	Tyr	Pro	Arg	Glu	Ala
						230
						Lys
						Val
						Gln
						Trp
						Lys
						Val
						Asp
						Asn
						Ala
						225
Leu	Gln	Ser	Gly	Asn	Ser	Gln
						245
						Glu
						Ser
						Val
						Thr
						Glu
						Gln
						Asp
						Ser
						Lys
						255
Asp	Ser	Thr	Tyr	Ser	Leu	Ser
						Ser
						Thr
						Leu
						Thr
						Leu
						Ser
						Lys
						Ala
						Asp

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260

265

270

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
275 280 285

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
290 295 300

<210> 16

<211> 116

<212> PRT

<213> Artificial sequence

<220>

<223> FAP(28H1) VH

<400> 16

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

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

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

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Thr Val Ser Ser
115

<210> 17
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> FAP(28H1) VL

<400> 17

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

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

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

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

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

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

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

<210> 18
<211> 446
<212> PRT
<213> Artificial sequence

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<220>

<223> FAP(28H1) heavy chain Fc hole

<400> 18

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

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

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 His Glu Asp Pro Glu Val
260 265 270

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

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

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

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

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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 Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln 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 Pro Gly Lys
435 440 445

<210> 19
<211> 215
<212> PRT
<213> Artificial sequence

<220>
<223> FAP(28H1) light chain

<400> 19

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

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

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

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

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

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

<210> 20
 <211> 760
 <212> PRT
 <213> Homo sapiens

<400> 20

Met	Lys	Thr	Trp	Val	Lys	Ile	Val	Phe	Gly	Val	Ala	Thr	Ser	Ala	Val
1				5					10					15	

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Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
20 25 30

Asn Ser Glu Glu Asn Thr Met Arg Ala Leu Thr Leu Lys Asp Ile Leu
35 40 45

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

Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
65 70 75 80

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

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

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
115 120 125

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

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145 150 155 160

Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
165 170 175

Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile
180 185 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
195 200 205

eolf-seql

Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly Lys Phe Leu Ala Tyr Ala
210 215 220

Glu Phe Asn Asp Thr Asp Ile Pro Val Ile Ala Tyr Ser Tyr Tyr Gly
225 230 235 240

Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
245 250 255

Ala Lys Asn Pro Val Val Arg Ile Phe Ile Ile Asp Thr Thr Tyr Pro
260 265 270

Ala Tyr Val Gly Pro Gln Glu Val Pro Val Pro Ala Met Ile Ala Ser
275 280 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Thr Asp Glu Arg Val
290 295 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
305 310 315 320

Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln
325 330 335

Glu His Ile Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
340 345 350

Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe
355 360 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
370 375 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile
385 390 395 400

eolf-seql

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
405 410 415

Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
420 425 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
435 440 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
450 455 460

Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
465 470 475 480

Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
485 490 495

Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
500 505 510

Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
515 520 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
530 535 540

Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
545 550 555 560

Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly
565 570 575

Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
580 585 590

eolf-seql

Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
595 600 605

Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
610 615 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625 630 635 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
645 650 655

Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
660 665 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
675 680 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
690 695 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705 710 715 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
725 730 735

Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
740 745 750

Lys Gln Cys Phe Ser Leu Ser Asp
755 760

<210> 21
<211> 748

eolf-seql

<212> PRT

<213> Artificial sequence

<220>

<223> hu FAP ectodomain+poly-lys-tag+his6-tag

<400> 21

Arg Pro Ser Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
1 5 10 15

Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe
20 25 30

Pro Asn Trp Ile Ser Gly Gln Glu Tyr Leu His Gln Ser Ala Asp Asn
35 40 45

Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
50 55 60

Ser Asn Arg Thr Met Lys Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser
65 70 75 80

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
85 90 95

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

Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
115 120 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
130 135 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
145 150 155 160

eolf-seql

Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
165 170 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
180 185 190

Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
195 200 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
210 215 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val Arg Ile Phe Ile
225 230 235 240

Ile Asp Thr Thr Tyr Pro Ala Tyr Val Gly Pro Gln Glu Val Pro Val
245 250 255

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
260 265 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
275 280 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
290 295 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
305 310 315 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
325 330 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
340 345 350

eolf-seql

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
355 360 365

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
370 375 380

Ser Ser Asn Glu Phe Glu Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385 390 395 400

Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
405 410 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
420 425 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
435 440 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
450 455 460

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

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
485 490 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
500 505 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
515 520 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
530 535 540

eolf-seq1

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
545 550 555 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
565 570 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
580 585 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
595 600 605

Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
610 615 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu Arg Phe Met Gly
625 630 635 640

Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
645 650 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
660 665 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
675 680 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
690 695 700

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
705 710 715 720

His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly Lys
725 730 735

eolf-seql

Lys Lys Lys Lys Lys Gly His His His His His His
740 745

<210> 22
<211> 2244
<212> DNA
<213> Artificial sequence

<220>
<223> hu FAP ectodomain+poly-lys-tag+his6-tag

<400> 22
cgcccttcaa gagttcataa ctctgaagaa aatacaatga gagcactcac actgaaggat 60
attttaaagt gaacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa 120
tatcttcac aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180
tataccattt tgagtaatag aaccatgaaa agtgtgaatg cttcaaatta cggcttatca 240
cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac 300
acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360
cctcgtccaa ttcagtattt atgctggctg cctgttggga gtaaattagc atatgtctat 420
caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaa ataacattta 480
ggaagagaaa ataaaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540
gctacaaaat atgctctctg gtgggtctcct aatggaaaat ttttggcata tgcggaattt 600
aatgatacgg atataccagt tattgcctat tcctattatg gcgatgaaca atacctaaga 660
acaataaata ttccataccc aaaggctgga gctaagaatc ccgttggtcg gatattttatt 720
atcgatacca cttaccctgc gtatgtaggt cccaggaag tgcctgttcc agcaatgata 780
gcctcaagtg attattattt cagttggctc acgtgggtta ctgatgaacg agtatgtttg 840
cagttggctaa aaagagtcca gaatgtttcg gtcctgtcta tatgtgactt cagggaagac 900
tggcagacat gggattgtcc aaagaccag gagcatatag aagaaagcag aactggatgg 960
gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc gtactacaaa 1020
atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgttgaaaat 1080

eolf-seql

gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat	1140
tcactgtttt attctagcaa tgaatttgaa gaataccctg gaagaagaaa catctacaga	1200
attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa	1260
aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc	1320
tacggcccag gcatcccat ttccaccctt catgatggac gcactgatca agaaattaaa	1380
atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag	1440
gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct	1500
caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt	1560
cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg	1620
atggtcattg ccttggtgga tggtcgagga acagctttcc aaggtgacaa actcctctat	1680
gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa	1740
ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga	1800
ggatacgttt catcactggc ccttgcatct ggaactggtc ttttcaaagtg tggatatagca	1860
gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt	1920
ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca	1980
gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac	2040
tttcaaaact cagcacagat tgctaaagct ctggttaatg cacaagtgga tttccaggca	2100
atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc	2160
cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa	2220
aagggccacc accatcacca tcac	2244

<210> 23
 <211> 761
 <212> PRT
 <213> Mus musculus
 <400> 23

eolf-seql

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

Leu Ala Leu Val Val Ile Cys Ile Val Leu Arg Pro Ser Arg Val Tyr
20 25 30

Lys Pro Glu Gly Asn Thr Lys Arg Ala Leu Thr Leu Lys Asp Ile Leu
35 40 45

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

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

Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu Ser Asn Ser Thr Met Lys
85 90 95

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

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
115 120 125

Thr Tyr Tyr Ile Tyr Asp Leu Gln Asn Gly Glu Phe Val Arg Gly Tyr
130 135 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145 150 155 160

Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
165 170 175

Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr Gly Arg Glu Asn Arg Ile
180 185 190

eolf-seql

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
 195 200 205

Lys Tyr Ala Leu Trp Trp Ser Pro Asp Gly Lys Phe Leu Ala Tyr Val
 210 215 220

Glu Phe Asn Asp Ser Asp Ile Pro Ile Ile Ala Tyr Ser Tyr Tyr Gly
 225 230 235 240

Asp Gly Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
 245 250 255

Ala Lys Asn Pro Val Val Arg Val Phe Ile Val Asp Thr Thr Tyr Pro
 260 265 270

His His Val Gly Pro Met Glu Val Pro Val Pro Glu Met Ile Ala Ser
 275 280 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Ser Ser Glu Arg Val
 290 295 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
 305 310 315 320

Cys Asp Phe Arg Glu Asp Trp His Ala Trp Glu Cys Pro Lys Asn Gln
 325 330 335

Glu His Val Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
 340 345 350

Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr Ser Tyr Tyr Lys Ile Phe
 355 360 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
 370 375 380

eolf-seql

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

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
405 410 415

Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Asn Ser
420 425 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
435 440 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys Ala Lys Tyr Tyr Ala Leu
450 455 460

Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser Thr Leu His Asp Gly Arg
465 470 475 480

Thr Asp Gln Glu Ile Gln Val Leu Glu Glu Asn Lys Glu Leu Glu Asn
485 490 495

Ser Leu Arg Asn Ile Gln Leu Pro Lys Val Glu Ile Lys Lys Leu Lys
500 505 510

Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
515 520 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
530 535 540

Cys Ser Gln Ser Val Lys Ser Val Phe Ala Val Asn Trp Ile Thr Tyr
545 550 555 560

Leu Ala Ser Lys Glu Gly Ile Val Ile Ala Leu Val Asp Gly Arg Gly
565 570 575

eolf-seql

Thr Ala Phe Gln Gly Asp Lys Phe Leu His Ala Val Tyr Arg Lys Leu
580 585 590

Gly Val Tyr Glu Val Glu Asp Gln Leu Thr Ala Val Arg Lys Phe Ile
595 600 605

Glu Met Gly Phe Ile Asp Glu Glu Arg Ile Ala Ile Trp Gly Trp Ser
610 615 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625 630 635 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
645 650 655

Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
660 665 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
675 680 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
690 695 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705 710 715 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Ile
725 730 735

Ser Ser Gly Arg Ser Gln Asn His Leu Tyr Thr His Met Thr His Phe
740 745 750

Leu Lys Gln Cys Phe Ser Leu Ser Asp
755 760

eolf-seql

<210> 24
<211> 749
<212> PRT
<213> Artificial sequence

<220>
<223> Murine FAP ectodomain+poly-lys-tag+his6-tag

<400> 24

Arg Pro Ser Arg Val Tyr Lys Pro Glu Gly Asn Thr Lys Arg Ala Leu
1 5 10 15

Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr Lys Thr Tyr Phe
20 25 30

Pro Asn Trp Ile Ser Glu Gln Glu Tyr Leu His Gln Ser Glu Asp Asp
35 40 45

Asn Ile Val Phe Tyr Asn Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu
50 55 60

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

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
85 90 95

Arg Tyr Ser Tyr Thr Ala Thr Tyr Tyr Ile Tyr Asp Leu Gln Asn Gly
100 105 110

Glu Phe Val Arg Gly Tyr Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
115 120 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
130 135 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr

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

eolf-seql

340

345

350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
355 360 365

Trp Glu Ala Ile Tyr Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
370 375 380

Ser Ser Asn Glu Phe Glu Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385 390 395 400

Ile Ser Ile Gly Asn Ser Pro Pro Ser Lys Lys Cys Val Thr Cys His
405 410 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys
420 425 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser
435 440 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Gln Val Leu Glu Glu
450 455 460

Asn Lys Glu Leu Glu Asn Ser Leu Arg Asn Ile Gln Leu Pro Lys Val
465 470 475 480

Glu Ile Lys Lys Leu Lys Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met
485 490 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
500 505 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Lys Ser Val Phe Ala
515 520 525

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

eolf-seql

530

535

540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Phe Leu His
545 550 555 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Leu Thr
565 570 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Glu Arg Ile
580 585 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
595 600 605

Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala Val Ala Pro Val
610 615 620

Ser Ser Trp Glu Tyr Tyr Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly
625 630 635 640

Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
645 650 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
660 665 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
675 680 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
690 695 700

Asp Gln Asn His Gly Ile Leu Ser Gly Arg Ser Gln Asn His Leu Tyr
705 710 715 720

Thr His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly

725 eolf-seql 730 735

Lys Lys Lys Lys Lys Lys Gly His His His His His His
740 745

<210> 25
<211> 2247
<212> DNA
<213> Artificial sequence

<220>
<223> Murine FAP ectodomain+poly-lys-tag+his6-tag

<400> 25
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tatcttcatc aatctgagga tgataacata gtattttata atattgaaac aagagaatca 180
tatatcattt tgagtaatag caccatgaaa agtgtgaatg ctacagatta tggtttgtca 240
cctgatcggc aatttgtgta tctagaaagt gattattcaa agctctggcg atattcatac 300
acagcgacat actacatcta cgaccttcag aatggggaat ttgtaagagg atacgagctc 360
cctcgtccaa ttcagtatct atgctggtcg cctgttggga gtaaattagc atatgtatat 420
caaaacaata tttatttgaa acaaagacca ggagatccac cttttcaaat aacttatact 480
ggaagagaaa atagaatatt taatggaata ccagactggg tttatgaaga ggaaatgctt 540
gccacaaaat atgctctttg gtggtctcca gatggaaaat ttttggcata tgtagaattt 600
aatgattcag atataccaat tattgcctat tcttattatg gtgatggaca gtatcctaga 660
actataaata ttccatatcc aaaggctggg gctaagaatc cggttggttcg tgtttttatt 720
gttgacacca cctaccctca ccacgtgggc ccaatggaag tgccagttcc agaaatgata 780
gcctcaagtg actattatct cagctggctc acatgggtgt ccagtgaacg agtatgcttg 840
cagtggctaa aaagagtgca gaatgtctca gtcctgtcta tatgtgattt cagggaagac 900
tggcatgcat gggaatgtcc aaagaaccag gagcatgtag aagaaagcag aacaggatgg 960

eolf-seq1

gctggtggat tctttgtttc gacaccagct tttagccagg atgccacttc ttactacaaa	1020
atatttagcg acaaggatgg ttacaaacat attcactaca tcaaagacac tgtggaaaat	1080
gctattcaaa ttacaagtgg caagtgggag gccatatata tattccgcgt aacacaggat	1140
tcactgtttt attctagcaa tgaatttgaa ggttaccctg gaagaagaaa catctacaga	1200
attagcattg gaaactctcc tccgagcaag aagtgtgtta cttgccatct aaggaaagaa	1260
aggtgccaat attacacagc aagtttcagc tacaaagcca agtactatgc actcgtctgc	1320
tatggccctg gcctcccat ttccaccctc catgatggcc gcacagacca agaaatacaa	1380
gtattagaag aaaacaaaga actggaaaat tctctgagaa atatccagct gcctaaagtg	1440
gagattaaga agctcaaaga cgggggactg actttctgggt acaagatgat tctgcctcct	1500
cagtttgaca gatcaaagaa gtaccctttg ctaattcaag tgtatgggtg tcctttagc	1560
cagagtgtta agtctgtgtt tgctgttaat tggataactt atctcgcaag taaggagggg	1620
atagtcattg ccctggtaga tggtcggggc actgctttcc aaggtagcaa attcctgcat	1680
gccgtgtatc gaaaactggg tgtatatgaa gttgaggacc agctcacagc tgtcagaaaa	1740
ttcatagaaa tgggtttcat tgatgaagaa agaatagcca tatggggctg gtcctacgga	1800
ggttatgttt catccctggc ctttgcattc ggaactggtc ttttcaaagtg tggcatagca	1860
gtggctccag tctccagctg ggaatattac gcatctatct actcagagag attcatgggc	1920
ctcccaacaa aggacgacaa tctcgaacac tataaaaatt caactgtgat ggcaagagca	1980
gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac	2040
tttcagaact cagcacagat tgctaaagct ttggttaatg cacaagtgga tttccaggcg	2100
atgtggtact ctgaccagaa ccatgggtata ttatctgggc gctcccagaa tcatttatat	2160
accacatga cgcacttcct caagcaatgc ttttctttat cagacggcaa aaagaaaaag	2220
aaaaagggcc accaccatca ccatcac	2247

<210> 26
 <211> 748
 <212> PRT

eolf-seql

<213> Artificial sequence

<220>

<223> Cynomolgus FAP ectodomain+poly-lys-tag+his6-tag

<400> 26

Arg Pro Pro Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
1 5 10 15

Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe
20 25 30

Pro Asn Trp Ile Ser Gly Gln Glu Tyr Leu His Gln Ser Ala Asp Asn
35 40 45

Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
50 55 60

Ser Asn Arg Thr Met Lys Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser
65 70 75 80

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
85 90 95

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

Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
115 120 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
130 135 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
145 150 155 160

Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu

eolf-seql

165

170

175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
180 185 190

Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
195 200 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
210 215 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Phe Val Arg Ile Phe Ile
225 230 235 240

Ile Asp Thr Thr Tyr Pro Ala Tyr Val Gly Pro Gln Glu Val Pro Val
245 250 255

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
260 265 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
275 280 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
290 295 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
305 310 315 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
325 330 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
340 345 350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys

eolf-seql

355

360

365

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
 370 375 380

Ser Ser Asn Glu Phe Glu Asp Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
 385 390 395 400

Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
 405 410 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
 420 425 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
 435 440 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
 450 455 460

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

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
 485 490 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
 500 505 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
 515 520 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
 530 535 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr

eolf-seql

545		550		555		560									
Ala	Val	Tyr	Arg	Lys	Leu	Gly	Val	Tyr	Glu	Val	Glu	Asp	Gln	Ile	Thr
				565					570					575	
Ala	Val	Arg	Lys	Phe	Ile	Glu	Met	Gly	Phe	Ile	Asp	Glu	Lys	Arg	Ile
			580					585					590		
Ala	Ile	Trp	Gly	Trp	Ser	Tyr	Gly	Gly	Tyr	Val	Ser	Ser	Leu	Ala	Leu
		595					600					605			
Ala	Ser	Gly	Thr	Gly	Leu	Phe	Lys	Cys	Gly	Ile	Ala	Val	Ala	Pro	Val
	610					615					620				
Ser	Ser	Trp	Glu	Tyr	Tyr	Ala	Ser	Val	Tyr	Thr	Glu	Arg	Phe	Met	Gly
625					630					635					640
Leu	Pro	Thr	Lys	Asp	Asp	Asn	Leu	Glu	His	Tyr	Lys	Asn	Ser	Thr	Val
			645						650					655	
Met	Ala	Arg	Ala	Glu	Tyr	Phe	Arg	Asn	Val	Asp	Tyr	Leu	Leu	Ile	His
		660						665					670		
Gly	Thr	Ala	Asp	Asp	Asn	Val	His	Phe	Gln	Asn	Ser	Ala	Gln	Ile	Ala
		675					680					685			
Lys	Ala	Leu	Val	Asn	Ala	Gln	Val	Asp	Phe	Gln	Ala	Met	Trp	Tyr	Ser
	690					695					700				
Asp	Gln	Asn	His	Gly	Leu	Ser	Gly	Leu	Ser	Thr	Asn	His	Leu	Tyr	Thr
705					710					715					720
His	Met	Thr	His	Phe	Leu	Lys	Gln	Cys	Phe	Ser	Leu	Ser	Asp	Gly	Lys
			725						730					735	
Lys	Lys	Lys	Lys	Lys	Gly	His	His	His	His	His	His				

<210> 27
 <211> 2244
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Cynomolgus FAP ectodomain+poly-lys-tag+his6-tag

<400> 27
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 attttaaatg ggacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa 120
 tatcttcac aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180
 tataaccattt tgagtaacag aaccatgaaa agtgtgaatg cttcaaatta tggcttatca 240
 cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac 300
 acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360
 cctcgtccaa ttcagtatct atgctggctg cctgttggga gtaaattagc atatgtctat 420
 caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaa ataacattta 480
 ggaagagaaa ataaaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540
 gctacaaaat atgctctctg gtgggtctct aatggaaaat ttttggcata tgcggaattt 600
 aatgatacag atataccagt tattgcctat tcctattatg gcgatgaaca atatcccaga 660
 acaataaata ttccataccc aaaggccgga gctaagaatc cttttgttcg gatattttatt 720
 atcgatacca cttaccctgc gtatgtaggt cccaggaag tgcctgttcc agcaatgata 780
 gcctcaagtg attattatct cagttggctc acgtgggtta ctgatgaacg agtatgtttg 840
 cagtggtctaa aaagagtcca gaatgtttcg gtcttgtcta tatgtgattt cagggaagac 900
 tggcagacat gggattgtcc aaagaccag gagcatatag aagaaagcag aactggatgg 960
 gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc atactacaaa 1020
 atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgttgaaaat 1080

eolf-seql

gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat	1140
tcactgtttt attctagcaa tgaatttgaa gattaccctg gaagaagaaa catctacaga	1200
attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa	1260
aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc	1320
tatggcccag gcatcccat ttccaccctt catgacggac gcactgatca agaaattaa	1380
atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag	1440
gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct	1500
caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt	1560
cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg	1620
atggctcattg ccttggtgga tggtcgggga acagctttcc aagggtgaca actcctgtat	1680
gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa	1740
ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga	1800
ggatatgttt catcactggc ccttgcatct ggaactggtc ttttcaaagtg tgggatagca	1860
gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt	1920
ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca	1980
gaatatattca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac	2040
tttcaaaact cagcacagat tgctaaagct ctggttaatg cacaagtgga tttccaggca	2100
atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc	2160
cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa	2220
aagggccacc accatcacca tcac	2244

<210> 28
 <211> 702
 <212> PRT
 <213> Homo sapiens
 <400> 28

eolf-seql

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
130 135 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145 150 155 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
165 170 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190

eolf-seq1

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
195 200 205

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

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225 230 235 240

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
245 250 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
260 265 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
290 295 300

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305 310 315 320

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
325 330 335

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
340 345 350

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
355 360 365

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
370 375 380

eolf-seql

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Lys Leu Ser
385 390 395 400

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
405 410 415

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
420 425 430

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
435 440 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
450 455 460

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465 470 475 480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
485 490 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
500 505 510

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
515 520 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
530 535 540

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545 550 555 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
565 570 575

eolf-seq1

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
580 585 590

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
595 600 605

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
610 615 620

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625 630 635 640

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
645 650 655

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
660 665 670

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
675 680 685

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
690 695 700

<210> 29
<211> 2322
<212> PRT
<213> Homo sapiens

<400> 29

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

Ala Leu Thr Leu Thr Met Leu Ala Arg Leu Ala Ser Ala Ala Ser Phe
20 25 30

Phe Gly Glu Asn His Leu Glu Val Pro Val Ala Thr Ala Leu Thr Asp

eolf-seql

35

40

45

Ile Asp Leu Gln Leu Gln Phe Ser Thr Ser Gln Pro Glu Ala Leu Leu
 50 55 60

Leu Leu Ala Ala Gly Pro Ala Asp His Leu Leu Leu Gln Leu Tyr Ser
 65 70 75 80

Gly Arg Leu Gln Val Arg Leu Val Leu Gly Gln Glu Glu Leu Arg Leu
 85 90 95

Gln Thr Pro Ala Glu Thr Leu Leu Ser Asp Ser Ile Pro His Thr Val
 100 105 110

Val Leu Thr Val Val Glu Gly Trp Ala Thr Leu Ser Val Asp Gly Phe
 115 120 125

Leu Asn Ala Ser Ser Ala Val Pro Gly Ala Pro Leu Glu Val Pro Tyr
 130 135 140

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

Gly Thr Ser Arg Pro Leu Arg Gly Cys Leu His Ala Ala Thr Leu Asn
 165 170 175

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

Ala Glu Glu Phe Ser Ala Ser Asp Asp Val Ala Leu Gly Phe Ser Gly
 195 200 205

Pro His Ser Leu Ala Ala Phe Pro Ala Trp Gly Thr Gln Asp Glu Gly
 210 215 220

Thr Leu Glu Phe Thr Leu Thr Thr Gln Ser Arg Gln Ala Pro Leu Ala

eolf-seql

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

eolf-seql

420

425

430

Thr Ile Ser Pro Leu Val Val Ala Glu Gly Gly Thr Ala Trp Leu Glu
435 440 445

Trp Arg His Val Gln Pro Thr Leu Asp Leu Met Glu Ala Glu Leu Arg
450 455 460

Lys Ser Gln Val Leu Phe Ser Val Thr Arg Gly Ala Arg His Gly Glu
465 470 475 480

Leu Glu Leu Asp Ile Pro Gly Ala Gln Ala Arg Lys Met Phe Thr Leu
485 490 495

Leu Asp Val Val Asn Arg Lys Ala Arg Phe Ile His Asp Gly Ser Glu
500 505 510

Asp Thr Ser Asp Gln Leu Val Leu Glu Val Ser Val Thr Ala Arg Val
515 520 525

Pro Met Pro Ser Cys Leu Arg Arg Gly Gln Thr Tyr Leu Leu Pro Ile
530 535 540

Gln Val Asn Pro Val Asn Asp Pro Pro His Ile Ile Phe Pro His Gly
545 550 555 560

Ser Leu Met Val Ile Leu Glu His Thr Gln Lys Pro Leu Gly Pro Glu
565 570 575

Val Phe Gln Ala Tyr Asp Pro Asp Ser Ala Cys Glu Gly Leu Thr Phe
580 585 590

Gln Val Leu Gly Thr Ser Ser Gly Leu Pro Val Glu Arg Arg Asp Gln
595 600 605

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

eolf-seql

610

615

620

Ser Leu Val Tyr Val His Arg Gly Gly Pro Ala Gln Asp Leu Thr Phe
 625 630 635 640

Arg Val Ser Asp Gly Leu Gln Ala Ser Pro Pro Ala Thr Leu Lys Val
 645 650 655

Val Ala Ile Arg Pro Ala Ile Gln Ile His Arg Ser Thr Gly Leu Arg
 660 665 670

Leu Ala Gln Gly Ser Ala Met Pro Ile Leu Pro Ala Asn Leu Ser Val
 675 680 685

Glu Thr Asn Ala Val Gly Gln Asp Val Ser Val Leu Phe Arg Val Thr
 690 695 700

Gly Ala Leu Gln Phe Gly Glu Leu Gln Lys Gln Gly Ala Gly Gly Val
 705 710 715 720

Glu Gly Ala Glu Trp Trp Ala Thr Gln Ala Phe His Gln Arg Asp Val
 725 730 735

Glu Gln Gly Arg Val Arg Tyr Leu Ser Thr Asp Pro Gln His His Ala
 740 745 750

Tyr Asp Thr Val Glu Asn Leu Ala Leu Glu Val Gln Val Gly Gln Glu
 755 760 765

Ile Leu Ser Asn Leu Ser Phe Pro Val Thr Ile Gln Arg Ala Thr Val
 770 775 780

Trp Met Leu Arg Leu Glu Pro Leu His Thr Gln Asn Thr Gln Gln Glu
 785 790 795 800

Thr Leu Thr Thr Ala His Leu Glu Ala Thr Leu Glu Glu Ala Gly Pro

eolf-seql

805

810

815

Ser Pro Pro Thr Phe His Tyr Glu Val Val Gln Ala Pro Arg Lys Gly
820 825 830

Asn Leu Gln Leu Gln Gly Thr Arg Leu Ser Asp Gly Gln Gly Phe Thr
835 840 845

Gln Asp Asp Ile Gln Ala Gly Arg Val Thr Tyr Gly Ala Thr Ala Arg
850 855 860

Ala Ser Glu Ala Val Glu Asp Thr Phe Arg Phe Arg Val Thr Ala Pro
865 870 875 880

Pro Tyr Phe Ser Pro Leu Tyr Thr Phe Pro Ile His Ile Gly Gly Asp
885 890 895

Pro Asp Ala Pro Val Leu Thr Asn Val Leu Leu Val Val Pro Glu Gly
900 905 910

Gly Glu Gly Val Leu Ser Ala Asp His Leu Phe Val Lys Ser Leu Asn
915 920 925

Ser Ala Ser Tyr Leu Tyr Glu Val Met Glu Arg Pro Arg His Gly Arg
930 935 940

Leu Ala Trp Arg Gly Thr Gln Asp Lys Thr Thr Met Val Thr Ser Phe
945 950 955 960

Thr Asn Glu Asp Leu Leu Arg Gly Arg Leu Val Tyr Gln His Asp Asp
965 970 975

Ser Glu Thr Thr Glu Asp Asp Ile Pro Phe Val Ala Thr Arg Gln Gly
980 985 990

Glu Ser Ser Gly Asp Met Ala Trp Glu Glu Val Arg Gly Val Phe Arg

eolf-seql

995

1000

1005

Val Ala Ile Gln Pro Val Asn Asp His Ala Pro Val Gln Thr Ile
 1010 1015 1020

Ser Arg Ile Phe His Val Ala Arg Gly Gly Arg Arg Leu Leu Thr
 1025 1030 1035

Thr Asp Asp Val Ala Phe Ser Asp Ala Asp Ser Gly Phe Ala Asp
 1040 1045 1050

Ala Gln Leu Val Leu Thr Arg Lys Asp Leu Leu Phe Gly Ser Ile
 1055 1060 1065

Val Ala Val Asp Glu Pro Thr Arg Pro Ile Tyr Arg Phe Thr Gln
 1070 1075 1080

Glu Asp Leu Arg Lys Arg Arg Val Leu Phe Val His Ser Gly Ala
 1085 1090 1095

Asp Arg Gly Trp Ile Gln Leu Gln Val Ser Asp Gly Gln His Gln
 1100 1105 1110

Ala Thr Ala Leu Leu Glu Val Gln Ala Ser Glu Pro Tyr Leu Arg
 1115 1120 1125

Val Ala Asn Gly Ser Ser Leu Val Val Pro Gln Gly Gly Gln Gly
 1130 1135 1140

Thr Ile Asp Thr Ala Val Leu His Leu Asp Thr Asn Leu Asp Ile
 1145 1150 1155

Arg Ser Gly Asp Glu Val His Tyr His Val Thr Ala Gly Pro Arg
 1160 1165 1170

Trp Gly Gln Leu Val Arg Ala Gly Gln Pro Ala Thr Ala Phe Ser

eolf-seql

1175

1180

1185

Gln Gln Asp Leu Leu Asp Gly Ala Val Leu Tyr Ser His Asn Gly
1190 1195 1200

Ser Leu Ser Pro Arg Asp Thr Met Ala Phe Ser Val Glu Ala Gly
1205 1210 1215

Pro Val His Thr Asp Ala Thr Leu Gln Val Thr Ile Ala Leu Glu
1220 1225 1230

Gly Pro Leu Ala Pro Leu Lys Leu Val Arg His Lys Lys Ile Tyr
1235 1240 1245

Val Phe Gln Gly Glu Ala Ala Glu Ile Arg Arg Asp Gln Leu Glu
1250 1255 1260

Ala Ala Gln Glu Ala Val Pro Pro Ala Asp Ile Val Phe Ser Val
1265 1270 1275

Lys Ser Pro Pro Ser Ala Gly Tyr Leu Val Met Val Ser Arg Gly
1280 1285 1290

Ala Leu Ala Asp Glu Pro Pro Ser Leu Asp Pro Val Gln Ser Phe
1295 1300 1305

Ser Gln Glu Ala Val Asp Thr Gly Arg Val Leu Tyr Leu His Ser
1310 1315 1320

Arg Pro Glu Ala Trp Ser Asp Ala Phe Ser Leu Asp Val Ala Ser
1325 1330 1335

Gly Leu Gly Ala Pro Leu Glu Gly Val Leu Val Glu Leu Glu Val
1340 1345 1350

Leu Pro Ala Ala Ile Pro Leu Glu Ala Gln Asn Phe Ser Val Pro

eolf-seql

1355

1360

1365

Glu Gly Gly Ser Leu Thr Leu Ala Pro Pro Leu Leu Arg Val Ser
1370 1375 1380

Gly Pro Tyr Phe Pro Thr Leu Leu Gly Leu Ser Leu Gln Val Leu
1385 1390 1395

Glu Pro Pro Gln His Gly Ala Leu Gln Lys Glu Asp Gly Pro Gln
1400 1405 1410

Ala Arg Thr Leu Ser Ala Phe Ser Trp Arg Met Val Glu Glu Gln
1415 1420 1425

Leu Ile Arg Tyr Val His Asp Gly Ser Glu Thr Leu Thr Asp Ser
1430 1435 1440

Phe Val Leu Met Ala Asn Ala Ser Glu Met Asp Arg Gln Ser His
1445 1450 1455

Pro Val Ala Phe Thr Val Thr Val Leu Pro Val Asn Asp Gln Pro
1460 1465 1470

Pro Ile Leu Thr Thr Asn Thr Gly Leu Gln Met Trp Glu Gly Ala
1475 1480 1485

Thr Ala Pro Ile Pro Ala Glu Ala Leu Arg Ser Thr Asp Gly Asp
1490 1495 1500

Ser Gly Ser Glu Asp Leu Val Tyr Thr Ile Glu Gln Pro Ser Asn
1505 1510 1515

Gly Arg Val Val Leu Arg Gly Ala Pro Gly Thr Glu Val Arg Ser
1520 1525 1530

Phe Thr Gln Ala Gln Leu Asp Gly Gly Leu Val Leu Phe Ser His

eolf-seql

1535

1540

1545

Arg Gly Thr Leu Asp Gly Gly Phe Arg Phe Arg Leu Ser Asp Gly
 1550 1555 1560

Glu His Thr Ser Pro Gly His Phe Phe Arg Val Thr Ala Gln Lys
 1565 1570 1575

Gln Val Leu Leu Ser Leu Lys Gly Ser Gln Thr Leu Thr Val Cys
 1580 1585 1590

Pro Gly Ser Val Gln Pro Leu Ser Ser Gln Thr Leu Arg Ala Ser
 1595 1600 1605

Ser Ser Ala Gly Thr Asp Pro Gln Leu Leu Leu Tyr Arg Val Val
 1610 1615 1620

Arg Gly Pro Gln Leu Gly Arg Leu Phe His Ala Gln Gln Asp Ser
 1625 1630 1635

Thr Gly Glu Ala Leu Val Asn Phe Thr Gln Ala Glu Val Tyr Ala
 1640 1645 1650

Gly Asn Ile Leu Tyr Glu His Glu Met Pro Pro Glu Pro Phe Trp
 1655 1660 1665

Glu Ala His Asp Thr Leu Glu Leu Gln Leu Ser Ser Pro Pro Ala
 1670 1675 1680

Arg Asp Val Ala Ala Thr Leu Ala Val Ala Val Ser Phe Glu Ala
 1685 1690 1695

Ala Cys Pro Gln Arg Pro Ser His Leu Trp Lys Asn Lys Gly Leu
 1700 1705 1710

Trp Val Pro Glu Gly Gln Arg Ala Arg Ile Thr Val Ala Ala Leu

eolf-seql

1715

1720

1725

Asp Ala Ser Asn Leu Leu Ala Ser Val Pro Ser Pro Gln Arg Ser
1730 1735 1740

Glu His Asp Val Leu Phe Gln Val Thr Gln Phe Pro Ser Arg Gly
1745 1750 1755

Gln Leu Leu Val Ser Glu Glu Pro Leu His Ala Gly Gln Pro His
1760 1765 1770

Phe Leu Gln Ser Gln Leu Ala Ala Gly Gln Leu Val Tyr Ala His
1775 1780 1785

Gly Gly Gly Gly Thr Gln Gln Asp Gly Phe His Phe Arg Ala His
1790 1795 1800

Leu Gln Gly Pro Ala Gly Ala Ser Val Ala Gly Pro Gln Thr Ser
1805 1810 1815

Glu Ala Phe Ala Ile Thr Val Arg Asp Val Asn Glu Arg Pro Pro
1820 1825 1830

Gln Pro Gln Ala Ser Val Pro Leu Arg Leu Thr Arg Gly Ser Arg
1835 1840 1845

Ala Pro Ile Ser Arg Ala Gln Leu Ser Val Val Asp Pro Asp Ser
1850 1855 1860

Ala Pro Gly Glu Ile Glu Tyr Glu Val Gln Arg Ala Pro His Asn
1865 1870 1875

Gly Phe Leu Ser Leu Val Gly Gly Gly Leu Gly Pro Val Thr Arg
1880 1885 1890

Phe Thr Gln Ala Asp Val Asp Ser Gly Arg Leu Ala Phe Val Ala

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1895

1900

1905

Asn Gly Ser Ser Val Ala Gly Ile Phe Gln Leu Ser Met Ser Asp
1910 1915 1920

Gly Ala Ser Pro Pro Leu Pro Met Ser Leu Ala Val Asp Ile Leu
1925 1930 1935

Pro Ser Ala Ile Glu Val Gln Leu Arg Ala Pro Leu Glu Val Pro
1940 1945 1950

Gln Ala Leu Gly Arg Ser Ser Leu Ser Gln Gln Gln Leu Arg Val
1955 1960 1965

Val Ser Asp Arg Glu Glu Pro Glu Ala Ala Tyr Arg Leu Ile Gln
1970 1975 1980

Gly Pro Gln Tyr Gly His Leu Leu Val Gly Gly Arg Pro Thr Ser
1985 1990 1995

Ala Phe Ser Gln Phe Gln Ile Asp Gln Gly Glu Val Val Phe Ala
2000 2005 2010

Phe Thr Asn Phe Ser Ser Ser His Asp His Phe Arg Val Leu Ala
2015 2020 2025

Leu Ala Arg Gly Val Asn Ala Ser Ala Val Val Asn Val Thr Val
2030 2035 2040

Arg Ala Leu Leu His Val Trp Ala Gly Gly Pro Trp Pro Gln Gly
2045 2050 2055

Ala Thr Leu Arg Leu Asp Pro Thr Val Leu Asp Ala Gly Glu Leu
2060 2065 2070

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

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2075

2080

2085

Pro Arg His Gly Arg Val Val Arg Val Pro Arg Ala Arg Thr Glu
 2090 2095 2100

Pro Gly Gly Ser Gln Leu Val Glu Gln Phe Thr Gln Gln Asp Leu
 2105 2110 2115

Glu Asp Gly Arg Leu Gly Leu Glu Val Gly Arg Pro Glu Gly Arg
 2120 2125 2130

Ala Pro Gly Pro Ala Gly Asp Ser Leu Thr Leu Glu Leu Trp Ala
 2135 2140 2145

Gln Gly Val Pro Pro Ala Val Ala Ser Leu Asp Phe Ala Thr Glu
 2150 2155 2160

Pro Tyr Asn Ala Ala Arg Pro Tyr Ser Val Ala Leu Leu Ser Val
 2165 2170 2175

Pro Glu Ala Ala Arg Thr Glu Ala Gly Lys Pro Glu Ser Ser Thr
 2180 2185 2190

Pro Thr Gly Glu Pro Gly Pro Met Ala Ser Ser Pro Glu Pro Ala
 2195 2200 2205

Val Ala Lys Gly Gly Phe Leu Ser Phe Leu Glu Ala Asn Met Phe
 2210 2215 2220

Ser Val Ile Ile Pro Met Cys Leu Val Leu Leu Leu Leu Ala Leu
 2225 2230 2235

Ile Leu Pro Leu Leu Phe Tyr Leu Arg Lys Arg Asn Lys Thr Gly
 2240 2245 2250

Lys His Asp Val Gln Val Leu Thr Ala Lys Pro Arg Asn Gly Leu

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2255 2260 2265

Ala Gly Asp Thr Glu Thr Phe Arg Lys Val Glu Pro Gly Gln Ala
2270 2275 2280

Ile Pro Leu Thr Ala Val Pro Gly Gln Gly Pro Pro Pro Gly Gly
2285 2290 2295

Gln Pro Asp Pro Glu Leu Leu Gln Phe Cys Arg Thr Pro Asn Pro
2300 2305 2310

Ala Leu Lys Asn Gly Gln Tyr Trp Val
2315 2320

<210> 30
<211> 1210
<212> PRT
<213> Homo sapiens

<400> 30

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

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

eolf-seql

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

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

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

eolf-seql

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

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

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

eolf-seql

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

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Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850 855 860

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Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
1040 1045 1050

eolf-seql

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
1205 1210

<210> 31
<211> 556

eolf-seql

<212> PRT

<213> Homo sapiens

<400> 31

Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
1 5 10 15

Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
20 25 30

Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
35 40 45

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
50 55 60

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
65 70 75 80

Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
85 90 95

Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
100 105 110

Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
115 120 125

Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
130 135 140

Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
145 150 155 160

Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro
165 170 175

eolf-seql

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
180 185 190

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
195 200 205

Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser
210 215 220

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
225 230 235 240

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
245 250 255

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
260 265 270

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
275 280 285

Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu
290 295 300

Cys Ser Leu Val Gly Ile Leu His Leu Gln Arg Ala Leu Val Leu Arg
305 310 315 320

Arg Lys Arg Lys Arg Met Thr Asp Pro Thr Arg Arg Phe Phe Lys Val
325 330 335

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

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
355 360 365

eolf-seql

Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
370 375 380

Val Gln Ala Asp Gly Ala Leu Gly Ser Arg Ser Pro Pro Gly Val Gly
385 390 395 400

Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
405 410 415

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
420 425 430

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
435 440 445

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
450 455 460

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
465 470 475 480

Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
485 490 495

Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
500 505 510

Leu Arg Ser Ile Arg Gly Gln Pro Gly Pro Asn His Glu Glu Asp Ala
515 520 525

Asp Ser Tyr Glu Asn Met Asp Asn Pro Asp Gly Pro Asp Pro Ala Trp
530 535 540

Gly Gly Gly Gly Arg Met Gly Thr Trp Ser Thr Arg
545 550 555

eolf-seql

<210> 32
 <211> 297
 <212> PRT
 <213> Homo sapiens

<400> 32

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
 1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
 20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
 35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
 50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
 65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
 85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
 100 105 110

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

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
 130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
 145 150 155 160

eolf-seql

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
290 295

<210> 33
<211> 364
<212> PRT
<213> Homo sapiens

<400> 33

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1 5 10 15

Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln

eolf-seql

20

25

30

Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro
35 40 45

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

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

Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro
85 90 95

Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp
100 105 110

Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser
115 120 125

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

Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn
145 150 155 160

Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile
165 170 175

Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr
180 185 190

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

Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu

eolf-seql

210

215

220

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr
225 230 235 240

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

Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala
260 265 270

Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys
275 280 285

Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly
290 295 300

Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr
305 310 315 320

Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu
325 330 335

Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys
340 345 350

Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
355 360

<210> 34
<211> 205
<212> PRT
<213> Homo sapiens

<400> 34

Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
1 5 10 15

eolf-seql

Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
20 25 30

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

Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
50 55 60

Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
65 70 75 80

Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
85 90 95

Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
100 105 110

Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro
115 120 125

Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
130 135 140

His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
145 150 155 160

Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
165 170 175

Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
180 185 190

Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
195 200 205

eolf-seql

<210> 35
 <211> 233
 <212> PRT
 <213> Homo sapiens
 <400> 35

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 100 105 110

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

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 145 150 155 160

eolf-seql

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
225 230

<210> 36
<211> 244
<212> PRT
<213> Homo sapiens

<400> 36

Met Gly Ala Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg
1 5 10 15

Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
20 25 30

Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
35 40 45

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

Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
65 70 75 80

eolf-seql

Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
85 90 95

Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
100 105 110

Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
115 120 125

Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg
130 135 140

Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg
145 150 155 160

Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu
165 170 175

Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala
180 185 190

Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly
195 200 205

Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn Ile Ser
210 215 220

His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe Gly Ala
225 230 235 240

Val Met Val Gly

<210> 37
<211> 183
<212> PRT
<213> Homo sapiens

eolf-seql

<400> 37

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

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

Gly Leu Gly Leu Leu Leu Cys Phe Thr Tyr Ile Cys Leu His Phe Ser
35 40 45

Ala Leu Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val
50 55 60

Gln Phe Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln
65 70 75 80

Lys Glu Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn
85 90 95

Cys Asp Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu
100 105 110

Val Asn Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln
115 120 125

Leu Lys Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr
130 135 140

Tyr Lys Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu
145 150 155 160

Asp Asp Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn
165 170 175

Pro Gly Glu Phe Cys Val Leu

eolf-seql

180

<210> 38
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 38

Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
 1 5 10 15

Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
 35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 50 55 60

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 85 90 95

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 100 105 110

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 115 120 125

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 130 135 140

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 145 150 155 160

eolf-seql

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
165 170 175

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
180 185 190

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
195 200 205

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
210 215 220

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
225 230 235 240

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
245 250 255

Gly Leu Leu Lys Leu
260

<210> 39
<211> 281
<212> PRT
<213> Homo sapiens

<400> 39

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
1 5 10 15

Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
20 25 30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
35 40 45

eolf-seql

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

eolf-seql

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
245 250 255

Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
260 265 270

Gln Thr Phe Phe Gly Leu Tyr Lys Leu
275 280

<210> 40

<211> 193

<212> PRT

<213> Homo sapiens

<400> 40

Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly
1 5 10 15

Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile
20 25 30

Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Gln Gln Gln Leu
35 40 45

Pro Leu Glu Ser Leu Gly Trp Asp Val Ala Glu Leu Gln Leu Asn His
50 55 60

Thr Gly Pro Gln Gln Asp Pro Arg Leu Tyr Trp Gln Gly Gly Pro Ala
65 70 75 80

Leu Gly Arg Ser Phe Leu His Gly Pro Glu Leu Asp Lys Gly Gln Leu
85 90 95

Arg Ile His Arg Asp Gly Ile Tyr Met Val His Ile Gln Val Thr Leu
100 105 110

eolf-seql

Ala Ile Cys Ser Ser Thr Thr Ala Ser Arg His His Pro Thr Thr Leu
115 120 125

Ala Val Gly Ile Cys Ser Pro Ala Ser Arg Ser Ile Ser Leu Leu Arg
130 135 140

Leu Ser Phe His Gln Gly Cys Thr Ile Ala Ser Gln Arg Leu Thr Pro
145 150 155 160

Leu Ala Arg Gly Asp Thr Leu Cys Thr Asn Leu Thr Gly Thr Leu Leu
165 170 175

Pro Ser Arg Asn Thr Asp Glu Thr Phe Phe Gly Val Gln Trp Val Arg
180 185 190

Pro

<210> 41
<211> 234
<212> PRT
<213> Homo sapiens

<400> 41

Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly
1 5 10 15

Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly
20 25 30

Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu
35 40 45

Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg
50 55 60

Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly

eolf-seql																
65				70				75				80				
Asn	Cys	Ser	Glu	Asp	Leu	Leu	Cys	Ile	Leu	Lys	Arg	Ala	Pro	Phe	Lys	
				85					90					95		
Lys	Ser	Trp	Ala	Tyr	Leu	Gln	Val	Ala	Lys	His	Leu	Asn	Lys	Thr	Lys	
				100					105					110		
Leu	Ser	Trp	Asn	Lys	Asp	Gly	Ile	Leu	His	Gly	Val	Arg	Tyr	Gln	Asp	
				115					120					125		
Gly	Asn	Leu	Val	Ile	Gln	Phe	Pro	Gly	Leu	Tyr	Phe	Ile	Ile	Cys	Gln	
				130					135					140		
Leu	Gln	Phe	Leu	Val	Gln	Cys	Pro	Asn	Asn	Ser	Val	Asp	Leu	Lys	Leu	
				145					150					155		
Glu	Leu	Leu	Ile	Asn	Lys	His	Ile	Lys	Lys	Gln	Ala	Leu	Val	Thr	Val	
				165					170					175		
Cys	Glu	Ser	Gly	Met	Gln	Thr	Lys	His	Val	Tyr	Gln	Asn	Leu	Ser	Gln	
				180					185					190		
Phe	Leu	Leu	Asp	Tyr	Leu	Gln	Val	Asn	Thr	Thr	Ile	Ser	Val	Asn	Val	
				195					200					205		
Asp	Thr	Phe	Gln	Tyr	Ile	Asp	Thr	Ser	Thr	Phe	Pro	Leu	Glu	Asn	Val	
				210					215					220		
Leu	Ser	Ile	Phe	Leu	Tyr	Ser	Asn	Ser	Asp							
				225					230							

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eolf-seql

<400> 42

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
1 5 10 15

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
50 55 60

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
85 90 95

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
100 105 110

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
115 120 125

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
130 135 140

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
165 170 175

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

eolf-seql

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
 195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
 210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
 225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
 245 250

<210> 43
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 43

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

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
 20 25 30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
 35 40 45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
 50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
 65 70 75 80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
 85 90 95

eolf-seql

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
130 135 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
165 170 175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
245 250 255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

eolf-seql

<210> 44
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 44

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

Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
 20 25 30

Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 35 40 45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65 70 75 80

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

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160

eolf-seql

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
210 215 220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225 230 235 240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
275 280 285

Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
290 295 300

Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315

<210> 45
<211> 249
<212> PRT
<213> Homo sapiens

<400> 45

Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg Gly Glu Pro

eolf-seql

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

eolf-seql

195

200

205

Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly Ser Ser Leu
210 215 220

Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe Leu
225 230 235 240

Thr Tyr Phe Gly Leu Phe Gln Val His
245

<210> 46
<211> 250
<212> PRT
<213> Homo sapiens

<400> 46

Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
1 5 10 15

Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
20 25 30

Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
35 40 45

Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg
50 55 60

Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp
65 70 75 80

Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn
85 90 95

Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys
100 105 110

eolf-seql

Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys
 115 120 125

Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
 130 135 140

Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala
 145 150 155 160

Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
 165 170 175

Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr
 180 185 190

Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr
 195 200 205

Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile
 210 215 220

Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
 225 230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
 245 250

<210> 47
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 47

Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
 1 5 10 15

eolf-seql

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
35 40 45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
50 55 60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
65 70 75 80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
85 90 95

Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
100 105 110

Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
115 120 125

Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
130 135 140

Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
145 150 155 160

Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
165 170 175

Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
180 185 190

Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
195 200 205

eolf-seql

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
210 215 220

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225 230 235 240

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
245 250 255

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

Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
275 280 285

<210> 48
<211> 240
<212> PRT
<213> Homo sapiens

<400> 48

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

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

Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Met Gly
35 40 45

Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
50 55 60

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

eolf-seql

Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
85 90 95

His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
100 105 110

Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
115 120 125

His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
130 135 140

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

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

Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
180 185 190

Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
195 200 205

Leu Glu Ala Gly Glu Lys Val Val Val Arg Val Leu Asp Glu Arg Leu
210 215 220

Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
225 230 235 240

<210> 49
<211> 251
<212> PRT
<213> Homo sapiens

<400> 49

Met Ala Glu Asp Leu Gly Leu Ser Phe Gly Glu Thr Ala Ser Val Glu

eolf-seql

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

eolf-seql

195

200

205

Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln Glu Gly Asp
210 215 220

Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
225 230 235 240

Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
245 250

<210> 50

<211> 199

<212> PRT

<213> Homo sapiens

<400> 50

Met Thr Leu His Pro Ser Pro Ile Thr Cys Glu Phe Leu Phe Ser Thr
1 5 10 15

Ala Leu Ile Ser Pro Lys Met Cys Leu Ser His Leu Glu Asn Met Pro
20 25 30

Leu Ser His Ser Arg Thr Gln Gly Ala Gln Arg Ser Ser Trp Lys Leu
35 40 45

Trp Leu Phe Cys Ser Ile Val Met Leu Leu Phe Leu Cys Ser Phe Ser
50 55 60

Trp Leu Ile Phe Ile Phe Leu Gln Leu Glu Thr Ala Lys Glu Pro Cys
65 70 75 80

Met Ala Lys Phe Gly Pro Leu Pro Ser Lys Trp Gln Met Ala Ser Ser
85 90 95

Glu Pro Pro Cys Val Asn Lys Val Ser Asp Trp Lys Leu Glu Ile Leu
100 105 110

eolf-seql

Gln Asn Gly Leu Tyr Leu Ile Tyr Gly Gln Val Ala Pro Asn Ala Asn
 115 120 125

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

Met Ile Gln Thr Leu Thr Asn Lys Ser Lys Ile Gln Asn Val Gly Gly
 145 150 155 160

Thr Tyr Glu Leu His Val Gly Asp Thr Ile Asp Leu Ile Phe Asn Ser
 165 170 175

Glu His Gln Val Leu Lys Asn Asn Thr Tyr Trp Gly Ile Ile Leu Leu
 180 185 190

Ala Asn Pro Gln Phe Ile Ser
 195

<210> 51
 <211> 391
 <212> PRT
 <213> Homo sapiens

<400> 51

Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
 1 5 10 15

Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
 20 25 30

Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
 35 40 45

Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
 50 55 60

eolf-seql

Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
65 70 75 80

Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
85 90 95

Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
100 105 110

Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
115 120 125

Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
130 135 140

Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145 150 155 160

Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
165 170 175

Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
180 185 190

Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
195 200 205

Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
210 215 220

Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225 230 235 240

Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
245 250 255

eolf-seql

Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
260 265 270

Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
275 280 285

Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
290 295 300

Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
305 310 315 320

Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
325 330 335

Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
340 345 350

Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
355 360 365

Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
370 375 380

Leu Gly Glu Ala Pro Ala Ser
385 390

<210> 52
<211> 205
<212> PRT
<213> Homo sapiens

<400> 52

Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala
1 5 10 15

eolf-seq1

Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro
20 25 30

Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala
35 40 45

Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro
50 55 60

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

Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe
85 90 95

Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val
100 105 110

Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala
115 120 125

Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg
130 135 140

Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly
145 150 155 160

Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala
165 170 175

Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr
180 185 190

Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
195 200 205

eolf-seql

<210> 53
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 53

Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe
 1 5 10 15

Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu
 20 25 30

Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp
 35 40 45

Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn
 50 55 60

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
 65 70 75 80

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
 85 90 95

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp
 100 105 110

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
 115 120 125

Glu Phe Cys Val Leu
 130

<210> 54
 <211> 132
 <212> PRT
 <213> Homo sapiens

eolf-seql

<400> 54

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

Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp
20 25 30

Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly
35 40 45

Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile
50 55 60

Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
65 70 75 80

Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp
85 90 95

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

His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
115 120 125

Phe Cys Val Leu
130

<210> 55

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker (SG4)₂

<400> 55

eolf-seql

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

<210> 56
 <211> 14
 <212> PRT
 <213> Artificial Sequences

<220>
 <223> Peptide linker

<400> 56

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

<210> 57
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker

<400> 57

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

<210> 58
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide linker

<400> 58

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
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Gly Gly Gly Ser
 20

eolf-seql

<210> 59
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 59

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

<210> 60
<211> 8
<212> PRT
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<220>
<223> Peptide Linker

<400> 60

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 61
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 61

Gly Gly Ser Gly Ser Gly
1 5

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> Peptide linker

<400> 62

Gly Gly Ser Gly

1

<210> 63

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 63

Gly Gly Ser Gly Asn Gly Ser Gly

1

5

<210> 64

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Linker

<400> 64

Gly Gly Asn Gly Ser Gly Ser Gly

1

5

<210> 65

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker

<400> 65

eolf-seql

Gly Gly Asn Gly Ser Gly
1 5

<210> 66
<211> 2154
<212> DNA
<213> Artificial Sequence

<220>
<223> dimeric hu 4-1BBL (71-254) -CH1 FC knob chain

<400> 66
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atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac 120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300
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gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420
aggctgggag tgcattctga cacagaggcc agggctagac acgcctggca gctgacacag 480
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catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 1080

eolf-seq1

ctgttttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaagggggc	1140
ggaggaagcg gagggggagg aagtgctagc accaagggcc ctagcgtgtt ccctctggcc	1200
cctagcagca agagcacaag tggaggaaca gccgccctgg gctgcctggc caaggactac	1260
ttccccgagc ccgtgaccgt gtcctggaat tctggcgccc tgacaagcgg cgtgcacaca	1320
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caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctcggc	1800
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ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	2100
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa	2154

<210> 67

<211> 903

<212> DNA

<213> Artificial Sequence

<220>

<223> monomeric hu 4-1BBL(71-254) -CL

<400> 67

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eolf-seql

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aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	360
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
aggctgggag tgcattctga cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagt acccccgaga ttccagccgg cctgccttct	540
ccaagaagcg aaggcggagg cggatctggc ggccggaggat ctctacggg ggctgcacca	600
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tgctgtctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc	720
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac	780
agcctcagca gcacctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc	840
tgcaagtca cccatcaggg cctgagctcg cccgtcaca agagcttcaa caggggagag	900
tgt	903

<210> 68

<211> 1338

<212> DNA

<213> Artificial Sequence

<220>

<223> FAP(28H1) Fc hole heavy chain

<400> 68

gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg	60
tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct	120
cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc	180
gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg	240

eolf-seql

cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca	gggctggctg	300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc	tagcaccaag	360
ggccccctccg tgttccccct ggccccccagc agcaagagca ccagcggcgg	cacagccgct	420
ctgggctgcc tggtaagga ctacttcccc gagcccgtga ccgtgtcctg	gaacagcgga	480
gccctgacct ccggcgtgca caccttcccc gccgtgctgc agagttctgg	cctgtatagc	540
ctgagcagcg tggtcaccgt gccttctagc agcctgggca cccagaccta	catctgcaac	600
gtgaaccaca agcccagcaa caccaagggtg gacaagaagg tggagcccaa	gagctgcgac	660
aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc	gtcagtcttc	720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga	ggtcacatgc	780
gtgggtgggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta	cgtggacggc	840
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gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga	gtacaagtgc	960
aaggctctcca acaaagccct cggcgcccc atcgagaaaa ccatctcca	agccaaaggg	1020
cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct	gaccaagaac	1080
caggtcagcc tctcgtgcgc agtcaaaggc ttctatcca gcgacatcg	cgtggagtgg	1140
gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct	ggactccgac	1200
ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca	gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca	gaagagcctc	1320
tccctgtctc cgggtaaa		1338

<210> 69

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> FAP(28H1) light chain

eolf-seql

```

<400> 69
gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc      60
ctgtcctgca gagcctccca gtccgtgtcc cggctcctacc tcgcctggta tcagcagaag      120
cccgccagg cccctcggct gctgatcatc ggcgcttcta ccagagccac cggcatccct      180
gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa      240
cccgaggact tcgccgtgta ctactgccag cagggccagg tcatccctcc cacctttggc      300
cagggcacca aggtggaaat caagcgtacg gtggctgcac catctgtctt catcttcccg      360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420
tatcccagag aggccaaagt acagtggaaag gtggataacg ccctccaatc gggtaaactcc      480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt                        645

```

```

<210> 70
<211> 309
<212> PRT
<213> Mus musculus

```

<400> 70

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Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
1           5           10          15

```

```

Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
          20          25          30

```

```

Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
          35          40          45

```

```

Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
          50          55          60

```

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Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His

```

eolf-seql

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

eolf-seql

260

265

270

Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
275 280 285

Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
290 295 300

Asp Asn Pro Trp Glu
305

<210> 71
<211> 2298
<212> DNA
<213> Artificial sequence

<220>
<223> dimeric 4-1BBL(71-254) -CH1-Fc knob chain

<400> 71
agaaccgagc ccagacccgc cctgaccatc accaccagcc ctaacctggg caccagagag 60
aacaacgccg accaagtgac ccccggtgtcc cacatcggca gcccgaatac cacacagcag 120
ggcagccctg tgttcgccaa gctgctggcc aagaaccagg ccagcctgag caacaccacc 180
ctgaactggc acagccagga tggcgccgga agcagctatc tgagccaggg cctgagatac 240
gaagaggaca agaaagaact ggtggtggac agccctggcc tgtactacgt gttcctggaa 300
ctgaagctga gcccacctt caccaacacc ggccacaagg tgcagggctg ggtgtcactg 360
gtgctgcagg ccaaacccca ggtggacgac ttcgacaacc tggccctgac cgtggaactg 420
ttccccagca gcatggaaaa caagctggtg gatcggagct ggtcccagct tctgctgctg 480
aaggccggac acagactgag cgtgggcctg agggcttatc tgcacggcgc ccaggacgcc 540
tacagagact gggagctgag ctaccccaac acaaccagct tcggcctggt cctcgtgaag 600
cccgacaacc cttgggaagg cggcggagga tctggcggag gcggatctag aacagagcct 660
cggcctgccc tgacaattac cacatcccc aatctgggca cccgggaaaa caatgcagat 720

eolf-seq1

caagtgcacac ctgtgtctca tattggctcc ccaaacta cccagcaggg ctccccgtg	780
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aaagaactgg tgggtggattc ccccgactg tactatgtgt ttctggaact gaaactgtcc	960
cctaccttta caaataccgg gcacaaagt cagggatggg tgtccctggg gctgcaggct	1020
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atggaaaaca agctggtgga cagaagctgg tcccagctcc tgctgctgaa ggccggacac	1140
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cagtggaacg gccagcccg cagaactac gacaacaccc agcctatcat ggacaccgac	2160

eolf-seql

ggctcctact tcgtgtacag cgacctgaac gtgcagaagt ccaactggga ggccggcaac	2220
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tcccacagcc ctggcaag	2298

<210> 72
 <211> 954
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Monomeric mu 4-1BBL(71-254) -CL fusion

<400> 72	
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tacagagact gggagctgag ctacccaac acaaccagct tcggcctgtt cctcgtgaag	600
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eolf-seql

<210> 73
<211> 1320
<212> DNA
<213> Artificial sequence

<220>
<223> FAP Fc KK heavy chain

<400> 73
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gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
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aagccctgca tctgcaccgt gcccgaggtg tccagcgtgt tcatcttccc acccaagccc 720
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atgatcacca actttttccc cgaggacatc accgtggagt ggcagtggaa tggccagccc 1140

eolf-seql

gccgagaact acaagaacac ccagcccatc atgaagaccg acggcagcta cttcgtgtac 1200
agcaagctga acgtgcagaa gtccaactgg gaggccggca acaccttcac ctgtagcgtg 1260
ctgcacgagg gcctgcacaa ccaccacacc gagaagtccc tgagccactc ccccggaag 1320

<210> 74
<211> 645
<212> DNA
<213> Artificial sequence

<220>
<223> FAP light chain

<400> 74
gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60
ctgtcctgca gagcctccca gtccgtgtcc cggctctacc tcgcctggta tcagcagaag 120
cccgccagg cccctcggct gctgatcatc ggcgctcta ccagagccac cggcatccct 180
gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240
cccgaggact tcgccgtgta ctactgccag cagggccagg tcatccctcc cacctttggc 300
cagggcacca aggtggaaat caagcgtgcc gatgctgcac caactgtatc gattttccca 360
ccatccagtg agcagttaac atctggaggt gcctcagtcg tgtgcttctt gaacaacttc 420
taccccaaag acatcaatgt caagtggaaag attgatggca gtgaacgaca aaatggcgtc 480
ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc 540
acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag 600
acatcaactt caccattgt caagagcttc aacaggaatg agtgt 645

<210> 75
<211> 766
<212> PRT
<213> Artificial sequence

<220>
<223> dimeric mu 4-1BBL(71-254)-CH1-Fc DD heavy chain

<400> 75

eolf-seql

Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile Thr Thr Ser Pro Asn Leu
1 5 10 15

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

Gly Ser Pro Asn Thr Thr Gln Gln Gly Ser Pro Val Phe Ala Lys Leu
35 40 45

Leu Ala Lys Asn Gln Ala Ser Leu Ser Asn Thr Thr Leu Asn Trp His
50 55 60

Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser Gln Gly Leu Arg Tyr
65 70 75 80

Glu Glu Asp Lys Lys Glu Leu Val Val Asp Ser Pro Gly Leu Tyr Tyr
85 90 95

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

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

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

Met Glu Asn Lys Leu Val Asp Arg Ser Trp Ser Gln Leu Leu Leu Leu
145 150 155 160

Lys Ala Gly His Arg Leu Ser Val Gly Leu Arg Ala Tyr Leu His Gly
165 170 175

Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu Ser Tyr Pro Asn Thr Thr
180 185 190

eolf-seql

Ser Phe Gly Leu Phe Leu Val Lys Pro Asp Asn Pro Trp Glu Gly Gly
195 200 205

Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr Glu Pro Arg Pro Ala Leu
210 215 220

Thr Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp
225 230 235 240

Gln Val Thr Pro Val Ser His Ile Gly Ser Pro Asn Thr Thr Gln Gln
245 250 255

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

Ser Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser
275 280 285

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

Val Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser
305 310 315 320

Pro Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu
325 330 335

Val Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu
340 345 350

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

Ser Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val
370 375 380

eolf-seql

Gly Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp
385 390 395 400

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

Pro Asp Asn Pro Trp Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
420 425 430

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
435 440 445

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
450 455 460

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
465 470 475 480

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
485 490 495

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
500 505 510

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
515 520 525

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Val Pro Arg Asp Cys
530 535 540

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
545 550 555 560

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
565 570 575

eolf-seql

Lys Val Thr Cys Val Val Val Ala Ile Ser Lys Asp Asp Pro Glu Val
580 585 590

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
595 600 605

Lys Pro Arg Glu Glu Gln Ile Asn Ser Thr Phe Arg Ser Val Ser Glu
610 615 620

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
625 630 635 640

Arg Val Asn Ser Ala Ala Phe Gly Ala Pro Ile Glu Lys Thr Ile Ser
645 650 655

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
660 665 670

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
675 680 685

Thr Asn Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
690 695 700

Gln Pro Ala Glu Asn Tyr Asp Asn Thr Gln Pro Ile Met Asp Thr Asp
705 710 715 720

Gly Ser Tyr Phe Val Tyr Ser Asp Leu Asn Val Gln Lys Ser Asn Trp
725 730 735

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
740 745 750

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
755 760 765

eolf-seql

<210> 76
 <211> 318
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Monomeric mu 4-1BBL(71-254) -CL fusion

<400> 76

Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile Thr Thr Ser Pro Asn Leu
 1 5 10 15

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

Gly Ser Pro Asn Thr Thr Gln Gln Gly Ser Pro Val Phe Ala Lys Leu
 35 40 45

Leu Ala Lys Asn Gln Ala Ser Leu Ser Asn Thr Thr Leu Asn Trp His
 50 55 60

Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser Gln Gly Leu Arg Tyr
 65 70 75 80

Glu Glu Asp Lys Lys Glu Leu Val Val Asp Ser Pro Gly Leu Tyr Tyr
 85 90 95

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

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

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

Met Glu Asn Lys Leu Val Asp Arg Ser Trp Ser Gln Leu Leu Leu Leu

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

<210> 77
 <211> 440
 <212> PRT
 <213> Artificial sequence

eolf-seql

<220>

<223> anti-FAP Fc KK heavy chain

<400> 77

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

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

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala
115 120 125

Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu
130 135 140

Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
145 150 155 160

Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp
165 170 175

eolf-seql

Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro
180 185 190

Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys
195 200 205

Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile
210 215 220

Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
225 230 235 240

Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
245 250 255

Val Ala Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val
260 265 270

Asp Asp Val Glu Val His Thr Ala Gln Thr Lys Pro Arg Glu Glu Gln
275 280 285

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

Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
305 310 315 320

Phe Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
325 330 335

Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Lys Gln Met Ala
340 345 350

Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asn Phe Phe Pro Glu
355 360 365

eolf-seql

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

Lys Asn Thr Gln Pro Ile Met Lys Thr Asp Gly Ser Tyr Phe Val Tyr
385 390 395 400

Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
405 410 415

Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys
420 425 430

Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> 78
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-FAP light chain

<400> 78

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

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

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

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

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

eolf-seql

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

<210> 79
 <211> 1335
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47 Fc hole heavy chain

<400> 79

eolf-seql

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccatcggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg	420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgcgtggaa ctcaggcgcc	480
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc	540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	600
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa	660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	780
gtgggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag	960
gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagaac cacaggtgtg caccctgccc ccatcccggt atgagctgac caagaaccag	1080
gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1200
tccttcttcc tcgtgagcaa gtcaccgtg gacaagagca ggtggcagca ggggaacgtc	1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc	1320
ctgtctccgg gtaaa	1335

eolf-seql

<211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47 light chain

<400> 80
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgtagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgct gacgttcggc 300
 caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
 ggcttgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 81
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47 Fc hole heavy chain

<400> 81

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

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

eolf-seql

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

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

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

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

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

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

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

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

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

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

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

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

eolf-seql

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

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

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

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

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

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

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

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

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

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

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

eolf-seql

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 82
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DP47 light chain

<400> 82

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

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

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

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

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

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

Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110

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

eolf-seql

115

120

125

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 83
<211> 163
<212> PRT
<213> Homo sapiens

<400> 83

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

eolf-seql

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
130 135 140

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

Ser Pro Gln

<210> 84

<211> 163

<212> PRT

<213> Cynomolgus

<400> 84

Leu Gln Asp Leu Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Ser Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

eolf-seql

Phe Lys Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

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

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
130 135 140

Gly Ala Ser Ser Ala Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145 150 155 160

Ser Pro Gln

<210> 85
<211> 164
<212> PRT
<213> Mus musculus

<400> 85

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
1 5 10 15

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

eolf-seql

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
35 40 45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
50 55 60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
65 70 75 80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys
85 90 95

Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr
115 120 125

Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe Ser Pro
130 135 140

Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly His Ser
145 150 155 160

Leu Gln Val Leu

<210> 86
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc hole chain

<400> 86
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 60
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

eolf-seql

tgctgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	180
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	240
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	300
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	360
gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag	420
aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag	480
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	540
gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg	600
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	660
ctctccctgt ctccgggtaa a	681

<210> 87
 <211> 1266
 <212> DNA
 <213> Artificial sequence

<220>
 <223> hu 4-1BB Fc knob fusion

<400> 87	
ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag	60
atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac	120
atctgcagac agtgcaaggg cgtgttcaga acccggaag agtgcagcag caccagcaac	180
gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag	240
caggactgca agcagggcca ggaactgacc aagaagggt gcaaggactg ctgcttcggc	300
accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc	360
aagagcgtgc tgggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct	420
gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac	480
tctcctcagg tcgacgaaca gttatatttt cagggcggct caccctaatc tgcagacaaa	540

eolf-seql

actcacacat gccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc	600
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	660
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	720
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	780
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag	840
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag	900
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag	960
gtcagcctgt ggtgcctggg caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1020
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1080
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc	1140
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc	1200
ctgtctccgg gtaaatccgg aggcctgaac gacatcttcg aggcccagaa gattgaatgg	1260
cacgag	1266

<210> 88
 <211> 1266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Cynomolgus 4-1BB Fc knob fusion

<400> 88	
ttgcaggatc tgtgtagtaa ctgcccagct ggtacattct gtgataataa caggagtcag	60
atttgcagtc cctgtcctcc aaatagtttc tccagcgcag gtggacaaag gacctgtgac	120
atatgcaggc agtgtaaagg tgttttcaag accaggaagg agtgttcctc caccagcaat	180
gcagagtgtg actgcatttc agggatatcac tgcctggggg cagagtgcag catgtgtgaa	240
caggattgta aacaagggtca agaattgaca aaaaaagggt gtaaagactg ttgctttggg	300
acatttaatg accagaaacg tggcatctgt cgcccctgga caaactgttc tttggatgga	360

eolf-seql

aagtctgtgc ttgtgaatgg gacgaaggag agggacgtgg tctgcggacc atctccagcc	420
gacctctctc caggagcatc ctctgcgacc ccgcctgccc ctgcgagaga gccaggacac	480
tctccgcagg tcgacgaaca gttatatattt cagggcggct cacccaaadc tgcagacaaa	540
actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc	600
ttccccccaa aacccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg	660
gtgggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	720
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	780
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag	840
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag	900
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag	960
gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1020
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1080
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc	1140
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc	1200
ctgtctccgg gtaaattccg aggctgaac gacatcttcg agggccagaa gattgaatgg	1260
cacgag	1266

<210> 89

<211> 1269

<212> DNA

<213> Artificial Sequence

<220>

<223> murine 4-1BB Fc knob fusion

<400> 89

gtgcagaaca gctgcgacaa ctgccagccc ggcaccttct gccggaagta caaccccggtg	60
tgcaagagct gcccccccag caccttcagc agcatcggcg gccagcccaa ctgcaacatc	120
tgcagagtgt gcgccggcta cttccggttc aagaagttct gcagcagcac ccacaacgcc	180

eolf-seql

gagtgcgagt gcatcgaggg cttccactgc ctgggcccc agtgcaccag atgcgagaag	240
gactgcagac ccggccagga actgaccaag cagggtgtga agacctgcag cctgggcacc	300
ttcaacgacc agaacgggac cggcgtgtgc cggccttgga ccaattgcag cctggacggg	360
agaagcgtgc tgaaaaccgg caccaccgag aaggacgtcg tgtgcggccc tcccgtggtg	420
tccttcagcc ctagcaccac catcagcgtg acccctgaag gcggccctgg cggacactct	480
ctgcagggtcc tggctgcacga acagttatat tttcaggggcg gctcacccaa atctgcagac	540
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc	600
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc	660
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	720
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt	780
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	840
aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg	900
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac	960
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg	1020
gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	1080
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1140
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1200
tccctgtctc cgggtaaatc cggaggcctg aacgacatct tcgaggccca gaagattgaa	1260
tggcacgag	1269

<210> 90
 <211> 227
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Fc hole chain

eolf-seql

<400> 90

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

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

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

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

eolf-seql

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

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

Pro Gly Lys
225

<210> 91
<211> 422
<212> PRT
<213> Artificial sequence

<220>
<223> human 4-1BB Fc knob fusion

<400> 91

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

eolf-seql

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
130 135 140

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

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
165 170 175

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
180 185 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
195 200 205

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
210 215 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
225 230 235 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
245 250 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
260 265 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
275 280 285

eolf-seq1

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
290 295 300

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
305 310 315 320

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
325 330 335

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
340 345 350

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
355 360 365

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
370 375 380

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
385 390 395 400

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
405 410 415

Lys Ile Glu Trp His Glu
420

<210> 92

<211> 422

<212> PRT

<213> Artificial sequence

<220>

<223> cynomolgus 4-1BB Fc knob fusion

<400> 92

Leu Gln Asp Leu Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

eolf-seql

Asn Arg Ser Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Lys Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

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

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
130 135 140

Gly Ala Ser Ser Ala Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145 150 155 160

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
165 170 175

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
180 185 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
195 200 205

eolf-seql

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 210 215 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 225 230 235 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 245 250 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 260 265 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 275 280 285

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 290 295 300

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
 305 310 315 320

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 325 330 335

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 340 345 350

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 355 360 365

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 370 375 380

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 385 390 395 400

eolf-seql

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
 405 410 415

Lys Ile Glu Trp His Glu
 420

<210> 93
 <211> 423
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> murine 4-1BB Fc knob fusion

<400> 93

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
 1 5 10 15

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

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
 35 40 45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
 50 55 60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
 65 70 75 80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys
 85 90 95

Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro
 100 105 110

eolf-seq1

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

eolf-seql

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
305 310 315 320

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
325 330 335

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
340 345 350

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
355 360 365

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
370 375 380

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
385 390 395 400

Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala
405 410 415

Gln Lys Ile Glu Trp His Glu
420

<210> 94

<211> 594

<212> DNA

<213> Artificial sequence

<220>

<223> human 4-1BB His-tagged

<400> 94

ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag 60

atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac 120

atctgcagac agtgcaaggg cgtgttcaga acccggaag agtgcagcag caccagcaac 180

gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag 240

eolf-seql

caggactgca agcagggcca ggaactgacc aagaagggt gcaaggactg ctgcttcggc 300
 accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc 360
 aagagcgtgc tgggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct 420
 gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac 480
 tctcctcagg tcgacgaaca gttatatattt cagggcggct caggcctgaa cgacatcttc 540
 gaggcccaga agatcgagtg gcacgaggct cgagctcacc accatcacca tcac 594

<210> 95
 <211> 198
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human 4-1BB His-tagged

<400> 95

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
 1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
 20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
 35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
 50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
 65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
 85 90 95

eolf-seql

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
130 135 140

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

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Gly Leu
165 170 175

Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Ala Arg Ala
180 185 190

His His His His His His
195

<210> 96
<211> 178
<212> PRT
<213> Homo sapiens

<400> 96

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val

eolf-seql

50

55

60

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu

<210> 97

<211> 366

<212> PRT

<213> Artificial Sequence

<220>

<223> dimeric hu 4-1BBL connected by (G4S)₂

<400> 97

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

eolf-seql

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
180 185 190

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
195 200 205

eolf-seql

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
 210 215 220

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 225 230 235 240

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
 245 250 255

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

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
 275 280 285

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
 290 295 300

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
 305 310 315 320

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

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
 340 345 350

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
 355 360 365

<210> 98

<211> 360

<212> PRT

<213> Artificial Sequence

<220>

<223> dimeric hu 4-1BBL (80-254) connected by (G4S)₂ linker

eolf-seql

<400> 98

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
1 5 10 15

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
20 25 30

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
35 40 45

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
50 55 60

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
65 70 75 80

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
85 90 95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
145 150 155 160

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gly Leu Leu Asp

eolf-seql

180

185

190

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
 195 200 205

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
 210 215 220

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
 225 230 235 240

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
 245 250 255

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
 260 265 270

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
 275 280 285

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
 290 295 300

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 305 310 315 320

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 325 330 335

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
 340 345 350

Gly Leu Pro Ser Pro Arg Ser Glu
 355 360

<210> 99

eolf-seql

<211> 416

<212> PRT

<213> Artificial Sequence

<220>

<223> dimeric hu 4-1BBL (52-254) connected by (G4S)₂ linker

<400> 99

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
1 5 10 15

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
20 25 30

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
35 40 45

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
50 55 60

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

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
85 90 95

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
100 105 110

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
115 120 125

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
130 135 140

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
145 150 155 160

eolf-seql

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
165 170 175

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
180 185 190

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser
195 200 205

Gly Gly Gly Gly Ser Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro
210 215 220

Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro
225 230 235 240

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
245 250 255

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

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
275 280 285

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
290 295 300

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
305 310 315 320

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

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
340 345 350

eolf-seql

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
 355 360 365

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
 370 375 380

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
 385 390 395 400

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

<210> 100
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) CDR-H1

<400> 100

Ser Tyr Ala Met Ser
 1 5

<210> 101
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) CDR-H2

<400> 101

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

Gly

eolf-seql

<210> 102
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-H3

<400> 102

Gly Trp Phe Gly Gly Phe Asn Tyr
1 5

<210> 103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-L1

<400> 103

Arg Ala Ser Gln Ser Val Thr Ser Ser Tyr Leu Ala
1 5 10

<210> 104
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> FAP(4B9) CDR-L2

<400> 104

Val Gly Ser Arg Arg Ala Thr
1 5

<210> 105
<211> 9
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> FAP(4B9) CDR-L3

<400> 105

Gln Gln Gly Ile Met Leu Pro Pro Thr
1 5

<210> 106

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> FAP(4B9) VH

<400> 106

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

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

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

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

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser

eolf-seql

115

<210> 107
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FAP(4B9) VL

<400> 107

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

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile Met Leu Pro
 85 90 95

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

<210> 108
 <211> 718
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dimeric hu 4-1BBL (71-254) - CH1* Fc knob chain

eolf-seql

<400> 108

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly

eolf-seql

180

185

190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
 195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
 210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
 225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
 245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
 260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
 275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
 290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
 305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
 325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
 340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
 355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly

eolf-seql

370

375

380

Gly Gly Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
385 390 395 400

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
405 410 415

Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
420 425 430

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
435 440 445

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
450 455 460

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
465 470 475 480

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
500 505 510

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
515 520 525

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
530 535 540

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
545 550 555 560

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val

eolf-seql

565

570

575

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
580 585 590

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
595 600 605

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
610 615 620

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
625 630 635 640

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
645 650 655

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
660 665 670

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
675 680 685

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
690 695 700

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
705 710 715

<210> 109

<211> 301

<212> PRT

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (71-254) -CL*

<400> 109

eolf-seql

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

eolf-seql

Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
195 200 205

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

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
225 230 235 240

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
245 250 255

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
260 265 270

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
275 280 285

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
290 295 300

<210> 110
<211> 296
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-254) -(G4S)1- CL*

<400> 110

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val

eolf-seql

35

40

45

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
 65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
 85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
 100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
 115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Ser Arg Thr Val
 180 185 190

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Arg Lys Leu Lys
 195 200 205

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 210 215 220

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn

										eolf-seql				
225				230						235				240
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr
				245					250					255
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His
				260				265					270	
Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val
		275					280					285		Thr
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
	290					295								
<210> 111														
<211> 756														
<212> PRT														
<213> Artificial Sequence														
<220>														
<223> Dimeric hu 4-1BBL (52-254) - CH1* Fc knob chain														
<400> 111														
Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	Ser	Ala	Ala
1				5					10					15
Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp	Pro	Ala
			20					25					30	Gly
Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	Val	Ala	Gln
		35					40					45		Asn
Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	Asp	Pro	Gly
	50					55					60			Leu
Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	Glu	Asp	Thr
65					70					75				80

eolf-seql

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
85 90 95

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
100 105 110

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
115 120 125

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
130 135 140

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
145 150 155 160

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
165 170 175

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
180 185 190

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser
195 200 205

Gly Gly Gly Gly Ser Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro
210 215 220

Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro
225 230 235 240

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
245 250 255

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

eolf-seql

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
275 280 285

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
290 295 300

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
305 310 315 320

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

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
340 345 350

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
355 360 365

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
370 375 380

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
385 390 395 400

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Thr Lys Gly Pro
420 425 430

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
435 440 445

Ala Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro Val Thr
450 455 460

eolf-seql

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
465 470 475 480

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
485 490 495

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
500 505 510

His Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro Lys Ser
515 520 525

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
530 535 540

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
545 550 555 560

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
565 570 575

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
580 585 590

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
595 600 605

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
610 615 620

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
625 630 635 640

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
645 650 655

eolf-seql

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
660 665 670

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
675 680 685

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
690 695 700

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
705 710 715 720

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
725 730 735

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
740 745 750

Ser Pro Gly Lys
755

<210> 112
<211> 320
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (52-254) -CL*

<400> 112

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
1 5 10 15

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
20 25 30

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn

eolf-seql

35

40

45

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
 50 55 60

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

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
 85 90 95

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
 100 105 110

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
 115 120 125

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
 130 135 140

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
 145 150 155 160

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
 165 170 175

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
 180 185 190

Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser
 195 200 205

Gly Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 210 215 220

Pro Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala Ser Val Val Cys

eolf-seql

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

<210> 113
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dimeric hu 4-1BBL (80-254) - CH1* Fc knob chain

<400> 113

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
1 5 10 15

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
20 25 30

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
35 40 45

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
50 55 60

eolf-seql

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
65 70 75 80

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
85 90 95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
145 150 155 160

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Ala Gly Leu Leu Asp
180 185 190

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
195 200 205

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
210 215 220

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
225 230 235 240

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
245 250 255

eolf-seql

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
260 265 270

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
275 280 285

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
290 295 300

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
305 310 315 320

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
325 330 335

Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala
340 345 350

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
355 360 365

Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
370 375 380

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Glu
385 390 395 400

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
405 410 415

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
420 425 430

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
435 440 445

eolf-seql

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
450 455 460

Asp Glu Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
465 470 475 480

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
485 490 495

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
500 505 510

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
515 520 525

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
530 535 540

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
565 570 575

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
580 585 590

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
595 600 605

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
610 615 620

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
625 630 635 640

eolf-seql

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
645 650 655

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
660 665 670

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
675 680 685

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
690 695 700

<210> 114

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (80-254) -CL*

<400> 114

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
1 5 10 15

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
20 25 30

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
35 40 45

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
50 55 60

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
65 70 75 80

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly

eolf-seql

85

90

95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
 100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 145 150 155 160

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser
 180 185 190

Val Phe Ile Phe Pro Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala
 195 200 205

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
 210 215 220

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
 225 230 235 240

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
 245 250 255

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
 260 265 270

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn

eolf-seql

275

280

285

Arg Gly Glu Cys
290

<210> 115

<211> 722

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-254) - CL* Fc knob chain

<400> 115

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

eolf-seql

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
305 310 315 320

eolf-seql

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
385 390 395 400

Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
405 410 415

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
420 425 430

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
435 440 445

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
450 455 460

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
465 470 475 480

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp
485 490 495

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
500 505 510

eolf-seql

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
515 520 525

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
530 535 540

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
545 550 555 560

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
565 570 575

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
580 585 590

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
595 600 605

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
610 615 620

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
625 630 635 640

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
645 650 655

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
660 665 670

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
675 680 685

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
690 695 700

eolf-seql

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
705 710 715 720

Gly Lys

<210> 116
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-254) -CH1*

<400> 116

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

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

eolf-seql

115

120

125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
 180 185 190

Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 195 200 205

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Glu
 210 215 220

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 225 230 235 240

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 245 250 255

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 260 265 270

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 275 280 285

Asp Glu Lys Val Glu Pro Lys Ser Cys
 290 295

<210> 117

eolf-seql

<211> 722

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-254) - CL Fc knob chain

<400> 117

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

eolf-seql

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
340 345 350

eolf-seql

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
385 390 395 400

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
405 410 415

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
420 425 430

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
435 440 445

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
450 455 460

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
465 470 475 480

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp
485 490 495

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
500 505 510

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
515 520 525

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
530 535 540

eolf-seql

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
545 550 555 560

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
565 570 575

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
580 585 590

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
595 600 605

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
610 615 620

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
625 630 635 640

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
645 650 655

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
660 665 670

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
675 680 685

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
690 695 700

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
705 710 715 720

Gly Lys

eolf-seql

<210> 118
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-254) - CH1

<400> 118

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln

eolf-seql

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
180 185 190

eolf-seql

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
 195 200 205

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
 210 215 220

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 225 230 235 240

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
 245 250 255

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

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
 275 280 285

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
 290 295 300

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
 305 310 315 320

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

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
 340 345 350

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val
 370 375 380

eolf-seql

Phe Ile Phe Pro Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala Ser
385 390 395 400

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
405 410 415

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
435 440 445

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
450 455 460

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
465 470 475 480

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
485 490 495

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
500 505 510

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
515 520 525

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
530 535 540

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
545 550 555 560

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
565 570 575

eolf-seql

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
580 585 590

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
595 600 605

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
610 615 620

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
625 630 635 640

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
645 650 655

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
660 665 670

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
675 680 685

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
690 695 700

Ser Leu Ser Pro Gly Lys
705 710

<210> 120
<211> 291
<212> PRT
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-248) - CH1*

<400> 120

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp

eolf-seql

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

eolf-seql

195

200

205

Gly Thr Ala Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe Pro Glu Pro
210 215 220

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
225 230 235 240

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
245 250 255

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
260 265 270

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Glu Lys Val Glu Pro
275 280 285

Lys Ser Cys
290

<210> 121

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FAP (28H1) Fc hole chain fused to dimeric hu 4-1BBL (71-254)

<400> 121

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

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

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

eolf-seql

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

eolf-seql

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 His Glu Asp Pro Glu Val
260 265 270

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

Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala 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 Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

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

eolf-seql

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

Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp
450 455 460

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
465 470 475 480

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
485 490 495

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
500 505 510

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
515 520 525

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
530 535 540

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
545 550 555 560

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
565 570 575

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
580 585 590

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
595 600 605

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
610 615 620

eolf-seql

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly
625 630 635 640

Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser
645 650 655

Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala
660 665 670

Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp
675 680 685

Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser
690 695 700

Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr
705 710 715 720

Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly
725 730 735

Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala
740 745 750

Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser
755 760 765

Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His
770 775 780

Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg
785 790 795 800

Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu
805 810 815

eolf-seql

Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser
820 825 830

Glu

<210> 122
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-FAP (28H1) Fc knob chain fused to monomeric hu 4-1BBL
(71-254)

<400> 122

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

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

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

eolf-seql

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 His Glu Asp Pro Glu Val
260 265 270

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

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

eolf-seq1

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 Ala Leu Gly Ala Pro 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

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp 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 Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln 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 Pro Gly Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp
450 455 460

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
465 470 475 480

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
485 490 495

eolf-seq1

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
500 505 510

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
515 520 525

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
530 535 540

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
545 550 555 560

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
565 570 575

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
580 585 590

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
595 600 605

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
610 615 620

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
625 630 635

<210> 123

<211> 834

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FAP (4B9) Fc hole chain fused to dimeric hu 4-1BBL (71-254)

<400> 123

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

eolf-seql

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

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

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

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

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

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

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

eolf-seql

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
450 455 460

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
465 470 475 480

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
485 490 495

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
500 505 510

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
515 520 525

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
530 535 540

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
545 550 555 560

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
565 570 575

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
580 585 590

eolf-seql

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
595 600 605

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
610 615 620

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu
645 650 655

Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe
660 665 670

Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser
675 680 685

Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu
690 695 700

Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val
705 710 715 720

Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu
725 730 735

Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser
740 745 750

Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala
755 760 765

Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu
770 775 780

eolf-seql

His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
785 790 795 800

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly
805 810 815

Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg
820 825 830

Ser Glu

<210> 124
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-FAP (4B9) Fc knob chain fused to monomeric hu 4-1BBL
(71-254)

<400> 124

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

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

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

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

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

eolf-seql

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
450 455 460

eolf-seql

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
465 470 475 480

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
485 490 495

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
500 505 510

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
515 520 525

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
530 535 540

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
545 550 555 560

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
565 570 575

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
580 585 590

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
595 600 605

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
610 615 620

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
625 630 635 640

<210> 125
<211> 215
<212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<223> anti-FAP (4B9) light chain

<400> 125

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

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile Met Leu Pro
85 90 95

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

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

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

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

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

eolf-seql

165

170

175

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 126

<211> 822

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FAP (4B9) Fc hole chain fused to dimeric hu 4-1BBL (71-248)

<400> 126

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

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

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

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

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

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

eolf-seql

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
450 455 460

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
465 470 475 480

eolf-seql

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
485 490 495

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
500 505 510

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
515 520 525

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
530 535 540

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
545 550 555 560

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
565 570 575

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
580 585 590

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
595 600 605

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
610 615 620

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly Gly Gly Ser Gly
625 630 635 640

Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
645 650 655

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
660 665 670

eolf-seql

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
675 680 685

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
690 695 700

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
705 710 715 720

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
725 730 735

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
740 745 750

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
755 760 765

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
770 775 780

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
785 790 795 800

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
805 810 815

Glu Ile Pro Ala Gly Leu
820

<210> 127

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-FAP (4B9) Fc knob chain fused to monomeric hu 4-1BBL

eolf-seql

(71-248)

<400> 127

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

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

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

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

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

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

eolf-seq1

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

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

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

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

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

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

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

eolf-seq1

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
450 455 460

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
465 470 475 480

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
485 490 495

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
500 505 510

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
515 520 525

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
530 535 540

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
545 550 555 560

eolf-seql

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
565 570 575

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
580 585 590

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
595 600 605

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
610 615 620

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
625 630

<210> 128
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker G4S

<400> 128

Gly Gly Gly Gly Ser
1 5

<210> 129
<211> 2166
<212> DNA
<213> Artificial Sequence

<220>
<223> Dimeric hu 4-1BBL (71-254) - CL* Fc knob chain

<400> 129
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac 120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

eolf-seq1

aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtgg ccggcgaagg atctggctct gtgtctcttg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	360
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagt acccccgaga ttccagccgg cctgccttct	540
ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctagagaggg acccgaactg	600
tccccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctgggtg	660
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca	720
ggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct	780
aaagctgggg tgtactatgt gttttttcag ctggaactga ggcgggtggt ggctggggag	840
ggctcaggat ctgtgtccct ggctctgcat ctgcagccac tgcgctctgc tgctggcgca	900
gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc	960
ttcgggttcc aaggacgcct gctgcatctg agcgccggac agcgcttggg agtgcattctg	1020
catactgaag ccagagcccc gcatgcttgg cagctgactc agggggcaac tgtgctggga	1080
ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaagggggc	1140
ggagggttccg gagggggagg atctcgtacg gtggctgcac catctgtctt tatcttccca	1200
cccagcgacc ggaagctgaa gtctggcaca gccagcgtcg tgtgcctgct gaataacttc	1260
tacccccgcg aggccaaggt gcagtggaa gtggacaatg ccctgcagag cggcaacagc	1320
caggaaagcg tgaccgagca ggacagcaag gactccacct acagcctgag cagcaccctg	1380
accctgagca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gaccaccag	1440
ggcctgtcta gccccgtgac caagagcttc aaccggggcg agtgcgacaa gaccacacc	1500
tgtcctccat gccctgcccc tgaagctgct ggcgcccta gcgtgttcct gttccccca	1560
aagcccaagg acaccctgat gatcagccgg acccctgaag tgacctgcgt ggtggtggat	1620

eolf-seql

gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac	1680
aatgccaaaga ccaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc	1740
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac	1800
aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaaggga gccccgagaa	1860
ccacaggtgt acaccctgcc cccatgccgg gatgagctga ccaagaacca ggtcagcctg	1920
tggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg	1980
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctctttcttc	2040
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc	2100
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg	2160
ggtaaa	2166

<210> 130
 <211> 891
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Monomeric hu 4-1BBL (71-254) -CH1*

<400> 130	
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc	360
gaggcccga atagcgatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag	420
agactgggag tgcattctgca cacagaggcc agagccaggc acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcttgccgg cctgcctagc	540

eolf-seql

cctagatctg aaggcggcgg aggttccgga ggcggaggat ctgctagcac aaagggcccc	600
agcgtgttcc ctctggcccc tagcagcaag agcacatctg gcggaacagc cgccctgggc	660
tgcttggtgg aagattactt ccccgagccc gtgaccgtgt cctggaattc tggcgccctg	720
acaagcggcg tgcacacctt tccagccgtg ctgcagagca gcggcctgta ctctctgagc	780
agcgtcgtga cagtggccag cagctctctg ggcacccaga cctacatctg caacgtgaac	840
cacaagccca gcaacaccaa ggtggacgag aagggtggaac ccaagtcctg c	891

<210> 131
 <211> 2154
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Dimeric hu 4-1BBL (71-254) - CH1* Fc knob chain

<400> 131	
agagaggggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	360
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
aggctgggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct	540
ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctagagaggg acccgaactg	600
tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctggtg	660
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca	720
ggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct	780

eolf-seql

aaagctgggg	tgtactatgt	gttttttcag	ctggaactga	ggcgggtggt	ggctggggag	840
ggctcaggat	ctgtgtccct	ggctctgcat	ctgcagccac	tgcgctctgc	tgctggcgca	900
gctgcactgg	ctctgactgt	ggacctgcca	ccagcctcta	gcgaggccag	aaacagcgcc	960
ttcgggttcc	aaggacgcct	gctgcatctg	agcgccggac	agcgcttggg	agtgcactctg	1020
catactgaag	ccagagcccc	gcatgcttgg	cagctgactc	agggggcaac	tgtgctggga	1080
ctgtttcgcg	tgacacctga	gatccctgcc	ggactgccaa	gccctagatc	agaagggggc	1140
ggaggaagcg	gagggggagg	aagtgctagc	accaagggcc	cctccgtgtt	ccccctggcc	1200
cccagcagca	agagcaccag	cggcggcaca	gccgctctgg	gctgcctggt	cgaggactac	1260
ttccccgagc	ccgtgaccgt	gtcctggaac	agcggagccc	tgacctccgg	cgtgcacacc	1320
ttccccgccg	tgctgcagag	ttctggcctg	tatagcctga	gcagcgtggt	caccgtgcct	1380
tctagcagcc	tgggcaccca	gacctacatc	tgcaacgtga	accacaagcc	cagcaacacc	1440
aaggtggacg	agaaggtgga	gcccagagc	tgcgacaaaa	ctcacacatg	cccaccgtgc	1500
ccagcacctg	aagctgcagg	gggaccgtca	gtcttcctct	tcccccaaaa	acccaaggac	1560
accctcatga	tctcccgac	ccctgaggtc	acatgcgtgg	tggtggacgt	gagccacgaa	1620
gacctgagg	tcaagttcaa	ctggtacgtg	gacggcgtgg	aggtgcataa	tgccaagaca	1680
aagccgcggg	aggagcagta	caacagcacg	taccgtgtgg	tcagcgtcct	caccgtcctg	1740
caccaggact	ggctgaatgg	caaggagtac	aagtgaagg	tctccaacaa	agccctcggc	1800
gcccccatcg	agaaaaccat	ctccaaagcc	aaagggcagc	cccgagaacc	acaggtgtac	1860
accctgcccc	catgccggga	tgagctgacc	aagaaccagg	tcagcctgtg	gtgcctggtc	1920
aaaggcttct	atcccagcga	catcgccgtg	gagtgggaga	gcaatgggca	gccggagaac	1980
aactacaaga	ccacgcctcc	cgtgctggac	tccgacggct	ccttcttcct	ctacagcaag	2040
ctcaccgtgg	acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	2100
gaggctctgc	acaaccacta	cacgcagaag	agcctctccc	tgtctccggg	taaa	2154

eolf-seql

<210> 132
 <211> 903
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Monomeric hu 4-1BBL (71-254) -CL*

<400> 132
 agagaggggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60
 atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac 120
 agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180
 aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
 agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300
 agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360
 gaggcccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420
 aggctgggag tgcattctga cacagaggcc agggctagac acgcctggca gctgacacag 480
 ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 540
 ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctctacggg ggctgcacca 600
 tctgtcttca tcttcccgcc atctgatcgg aagttgaaat ctggaactgc ctctgttggtg 660
 tgctgtctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 720
 ctccaatcgg gtaactcca ggagagtgtc acagagcagg acagcaagga cagcacctac 780
 agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 840
 tgcgaagtca cccatcaggg cctgagctcg cccgtcacia agagcttcaa caggggagag 900
 tgt 903

<210> 133
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>

eolf-seql

<223> anti-FAP (VHCL) (28H1) Fc hole chain

<400> 133

gaagtgcagc tgctggaatc cggcggaggc ctgggtgcagc ctggcggatc tctgagactg	60
tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt cgcacaggct	120
cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc	180
gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg	240
cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca gggctggctg	300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcg tagcgtggcc	360
gctcccagcg tgttcatctt cccaccagc gacgagcagc tgaagtccgg cacagccagc	420
gtgggtgtgcc tgctgaacaa cttctacccc cgcgaggcca aggtgcagtg gaaggtggac	480
aacgccctgc agagcggcaa cagccaggaa tccgtgaccg agcaggacag caaggactcc	540
acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaagggtg	600
tacgcctgcg aagtgaccca ccagggcctg tccagccccg tgaccaagag cttcaaccgg	660
ggcgagtgcg acaagaccca cacctgtccc ctttgccctg cccctgaagc tgctgggtggc	720
ccttcctgtg tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc	780
gaagtgacct gcgtgggtgt cgatgtgtcc cacgaggacc ctgaagtga gttcaattgg	840
tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggcttc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1020
aaagccaaaag ggagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag	1080
ctgaccaaga accaggctcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcagggtg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtaaa	1350

eolf-seql

<210> 134
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-FAP (VLCH1) (28H1) light chain

<400> 134
 gagatcgtgc tgacccagtc tcccggcacc ctgagcctga gccctggcga gagagccacc 60
 ctgagctgca gagccagcca gagcgtgagc cggagctacc tggcctggta tcagcagaag 120
 cccggccagg cccccagact gctgatcatc ggcgccagca cccgggccac cggcatcccc 180
 gatagattca gcggcagcgg ctccggcacc gacttcaccc tgaccatcag ccggctggaa 240
 cccgaggact tcgccgtgta ctactgccag cagggccagg tgatcccccc caccttcggc 300
 cagggcacca aggtggaaat caagagcagc gcttccacca aaggcccttc cgtgtttcct 360
 ctggctccta gctccaagtc cacctctgga ggcaccgctg ctctcggatg cctcgtgaag 420
 gattattttc ctgagcctgt gacagtgtcc tggaatagcg gagcactgac ctctggagtg 480
 catactttcc ccgctgtgct gcagtcctct ggactgtaca gcctgagcag cgtggtgaca 540
 gtgcccagca gcagcctggg caccagacc tacatctgca acgtgaacca caagcccagc 600
 aacaccaagg tggacaagaa ggtggaaccc aagtcttgt 639

<210> 135
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-FAP (VHCL) (28H1) Fc hole chain

<400> 135

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

eolf-seql

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

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

Gly Lys
450

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

<220>
<223> anti-FAP (VLCH1) (28H1) light chain

<400> 136

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

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

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

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

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

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

eolf-seql

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ala Ser
100 105 110

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

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
145 150 155 160

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
165 170 175

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

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
195 200 205

Glu Pro Lys Ser Cys
210

<210> 137
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Monomeric hu 4-1BBL (71-254) - CH1* Fc knob chain

<400> 137
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac 120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

eolf-seql

aaagaactgg tggtaggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc	360
gaggccccga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag	420
agactgggag tgcatctgca cacagaggcc agagccaggc acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg cctgcctagc	540
cctagatctg aaggcggcgg aggttccgga ggccggaggat ctgctagcac caagggtccc	600
tccgtgttcc ccctggcccc cagcagcaag agcaccagcg gcggcacagc cgctctgggc	660
tgcttggtcg aggactactt ccccgagccc gtgaccgtgt cctggaacag cggagccctg	720
acctccggcg tgcacacctt ccccgccgtg ctgcagagtt ctggcctgta tagcctgagc	780
agcgtggtca ccgtgccttc tagcagcctg ggcacccaga cctacatctg caacgtgaac	840
cacaagcccc gcaacaccaa ggtggacgag aaggtggagc ccaagagctg cgacaaaact	900
cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc	960
ccccaaaaac ccaaggacac cctcatgata tcccggaccc ctgaggtcac atgcgtggtg	1020
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag	1080
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc	1140
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc	1200
tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc	1260
cgagaaccac aggtgtacac cctgccccca tgccgggatg agctgaccaa gaaccaggtc	1320
agcctgtggt gcctgggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc	1380
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc	1440
ttcttctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc	1500
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg	1560
tctccgggta aa	1572

eolf-seql

<210> 138
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Dimeric hu 4-1BBL (71-254) -CL*

<400> 138
agagaggggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac 120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
agagtgggtgg ccggcgaagg atctggctct gtgtctcttg ccctgcatct gcagcctctg 300
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420
aggctggggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 540
ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctagagaggg acccgaactg 600
tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctggtg 660
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca 720
ggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct 780
aaagctgggg tgtactatgt gttttttcag ctggaactga ggcgggtggt ggctggggag 840
ggctcaggat ctgtgtccct ggctctgcat ctgcagccac tgcgctctgc tgctggcgca 900
gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc 960
ttcgggttcc aaggacgcct gctgcatctg agcgccggac agcgctggg agtgcatctg 1020
catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 1080
ctgttttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaagggggc 1140

eolf-seql

```

ggagggttccg gagggggagg atctcgtacg gtggctgcac catctgtctt catcttcccg      1200
ccatctgatc  ggaagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      1260
tatcccagag  aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      1320
caggagagtg  tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccttg      1380
acgctgagca  aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      1440
ggcctgagct  cgcccgtcac aaagagcttc aacagggggag agtgt                          1485

```

<210> 139
 <211> 718
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Monomeric hu 4-1BBL (71-254) - CL* Fc knob chain

<400> 139

```

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1              5              10              15

```

```

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20              25              30

```

```

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

```

```

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

```

```

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65              70              75              80

```

```

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85              90              95

```

eolf-seq1

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

eolf-seq1

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
 290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
 305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
 325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
 340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
 355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
 370 375 380

Gly Gly Gly Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 385 390 395 400

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 405 410 415

Val Glu Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 420 425 430

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 435 440 445

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 450 455 460

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 465 470 475 480

eolf-seql

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
500 505 510

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
515 520 525

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
530 535 540

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
545 550 555 560

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
565 570 575

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
580 585 590

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
595 600 605

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
610 615 620

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
625 630 635 640

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
645 650 655

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
660 665 670

eolf-seq1

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
675 680 685

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
690 695 700

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
705 710 715

<210> 140

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-254) -CL*

<400> 140

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

eolf-seql

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
290 295 300

eolf-seql

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
385 390 395 400

Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
405 410 415

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
420 425 430

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
435 440 445

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
450 455 460

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
465 470 475 480

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
485 490 495

eolf-seql

<210> 141
 <211> 2499
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-FAP (28H1) Fc hole chain fused to dimeric hu 4-1BBL (71-254)

<400> 141
 gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
 tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct 120
 cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180
 gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
 cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca gggctggctg 300
 ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
 ggccccctccg tggtccccct ggcccccagc agcaagagca ccagcggcgg cacagccgct 420
 ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaacagcgga 480
 gccctgacct ccggcgtgca caccttcccc gccgtgctgc agagttctgg cctgtatagc 540
 ctgagcagcg tggtcaccgt gccttctagc agcctgggca cccagaccta catctgcaac 600
 gtgaaccaca agcccagcaa caccaagggtg gacaagaagg tggagcccaa gagctgcgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggagggtgc ataatgcca gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggctctca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac 1080
 caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

eolf-seq1

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	1200
ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1320
tccctgtctc cgggtggagg cggcggaagc ggaggaggag gatccagaga gggccctgag	1380
ctgagccccg atgatacctgc tggactgctg gacctgcggc agggcatgtt tgctcagctg	1440
gtggcccaga acgtgctgct gatcgatggc cccctgtcct ggtacagcga tcctggactg	1500
gctggcgtgt cactgacagg cggcctgagc tacaagagg acaccaaaga actggtggtg	1560
gccaaggccg gcgtgtacta cgtgttcttt cagctggaac tgcggagagt ggtggccggc	1620
gaaggatctg gctctgtgtc tctggccctg catctgcagc ctctgagaag cgctgctggc	1680
gctgcagctc tggcactgac agtggatctg cctcctgcca gctccgaggc ccggaatagc	1740
gcatttgggt ttcaaggcag gctgctgcac ctgtctgccg gccagaggct gggagtgcac	1800
ctgcacacag aggccagggc tagacacgcc tggcagctga cacaggcgcc tacagtgtg	1860
ggcctgttca gagtgacccc cgagattcca gccggcctgc cttctccaag aagcgaaggc	1920
ggaggcggat ctggcggcgg aggatctaga gagggacccg aactgtcccc tgacgatcca	1980
gccgggctgc tggatctgag acagggaatg ttcgcccagc tgggtggtca gaatgtgtg	2040
ctgattgacg gacctctgag ctggtactcc gaccagggc tggcaggggt gtccctgact	2100
gggggactgt cctacaaaga agatacaaaa gaactggtgg tggctaaagc tggggtgtac	2160
tatgtgtttt ttcagctgga actgaggcgg gtggtggctg gggagggtc aggatctgtg	2220
tccctggctc tgcatctgca gccactgcgc tctgctgtg gcgcagctgc actggctctg	2280
actgtggacc tgccaccagc ctctagcgag gccagaaaca gcgccttcgg gttccaagga	2340
cgctgctgc atctgagcgc cggacagcgc ctgggagtgc atctgcatac tgaagccaga	2400
gcccggcatg cttggcagct gactcagggg gcaactgtgc tgggactgtt tcgctgaca	2460
cctgagatcc ctgccggact gccaaagccct agatcagaa	2499

eolf-seql

<210> 142
 <211> 1917
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-FAP (28H1) Fc knob chain fused to monomeric hu 4-1BBL
 (71-254)

<400> 142
 gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
 tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct 120
 cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180
 gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
 cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca gggctggctg 300
 ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
 ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggagggtgc ataattgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctcaa agccaaaggg 1020
 cagccccgag aaccacaggt gtacaccctg cccccctgca gagatgagct gaccaagaac 1080
 cagggtgtccc tgtggtgtct ggtcaagggc ttctaccca gcgatatcgc cgtggagtgg 1140

eolf-seql

gagagcaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggacagcgac	1200
ggcagcttct tcctgtactc caaactgacc gtggacaaga gccggtggca gcagggcaac	1260
gtgttcagct gcagcgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg	1320
agcctgagcc ccggcggagg cggcgggaagc ggaggaggag gatccagaga gggccctgag	1380
ctgagccccg atgatcctgc tggactgctg gacctgcggc agggcatgtt tgctcagctg	1440
gtggcccaga acgtgctgct gatcgatggc cccctgtcct ggtacagcga tcctggactg	1500
gctggcgtgt cactgacagg cggcctgagc taaaaagagg acaccaaaga actggtgggtg	1560
gccaaggccg gcgtgtacta cgtgttcttt cagctggaac tgcggagagt ggtggccggc	1620
gaaggatctg gctctgtgtc tctggccctg catctgcagc ctctgagaag cgctgctggc	1680
gctgcagctc tggcactgac agtggatctg cctcctgcca gctccgaggc ccggaatagc	1740
gcatttgggt ttcaaggcag gctgctgcac ctgtctgccg gccagaggct gggagtgcac	1800
ctgcacacag aggccagggc tagacacgcc tggcagctga cacaggcgcc tacagtgtg	1860
ggcctgttca gagtgacccc cgagattcca gccggcctgc cttctccaag aagcgaa	1917

<210> 143

<211> 888

<212> DNA

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (71-254) -(G4S)1- CL*

<400> 143

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	360

eolf-seql

gaggccccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct	540
ccaagaagcg aaggcggagg cggatctcgt acggtggctg caccatctgt cttcatcttc	600
ccgccatctg atcggaagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac	660
ttctatccca gagaggccaa agtacagtgg aaggctggata acgccctcca atcgggtaac	720
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc	780
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat	840
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgt	888

<210> 144
 <211> 2028
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> [anti-FAP (28H1)]2 Fc hole chain

<400> 144	
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg	60
tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct	120
cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc	180
gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg	240
cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcaa gggctggctg	300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcg tagcacaaag	360
ggacctagcg tgttccccct ggccccagc agcaagtcta catctggcgg aacagccgcc	420
ctgggctgcc tcgtgaagga ctactttccc gagcccgtga ccgtgtcctg gaactctggc	480
gctctgacaa gcggcgtgca cacctttcca gccgtgctgc agagcagcgg cctgtactct	540
ctgagcagcg tcgtgacagt gcccagcagc tctctgggca cccagacct catctgcaac	600

eolf-seql

gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggaacccaa gagctgcgac	660
ggcggagggg gatctggcgg cggaggatcc gaagtgcagc tgctggaatc cggcggaggc	720
ctggtgcagc ctggcggatc tctgagactg tcctgcgccg cctccggctt caccttctcc	780
tcccacgcca tgtcctgggt ccgacaggct cctggcaaag gcctggaatg ggtgtccgcc	840
atctgggcct ccggcgagca gtactacgcc gactctgtga agggccggtt caccatctcc	900
cgggacaact ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc	960
gccgtgtact actgtgcca gggctggctg ggcaacttcg actactgggg acagggcacc	1020
ctggtcaccg tgtccagcg tagcaccaag ggccccctcg tgttccccct ggccccagc	1080
agcaagagca ccagcggcgg cacagccgct ctgggctgcc tggtaagga ctacttcccc	1140
gagcccgtga ccgtgtcctg gaacagcggg gccctgacct ccggcgtgca caccttcccc	1200
gccgtgctgc agagtcttg cctgtatagc ctgagcagcg tggtcaccgt gccttctagc	1260
agcctgggca cccagacct catctgcaac gtgaaccaca agcccagcaa caccaaggtg	1320
gacaagaagg tggagcccaa gagctgcgac aaaactcaca catgcccacc gtgcccagca	1380
cctgaagctg cagggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc	1440
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct	1500
gaggtcaagt tcaactggta cgtggacggc gtggagggtc ataatgcca gacaaagccg	1560
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag	1620
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cggcgcccc	1680
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtgcaccctg	1740
ccccatccc gggatgagct gaccaagaac caggtcagcc tctcgtgcgc agtcaaaggc	1800
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac	1860
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctcgtgag caagctcacc	1920
gtggacaaga gcagggtggc gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1980
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa	2028

eolf-seql

<210> 145
<211> 676
<212> PRT
<213> Artificial Sequence

<220>
<223> [anti-FAP (28H1)]2 Fc hole chain

<400> 145

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

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

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly

eolf-seql

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

eolf-seq1

340

345

350

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

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

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

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

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

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

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

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 485 490 495

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

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

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

eolf-seql

530

535

540

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
 675

<210> 146
 <211> 2514
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Dimeric hu 4-1BBL (71-254) - FAP (VHCL*) Fc knob chain

<400> 146

eolf-seq1

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atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	360
gaggcccga atagcgcat tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
aggctgggag tgcacttgca cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagt acccccgaga ttccagccgg cctgccttct	540
ccaagaagcg aaggcggagg cggatctggc ggccggaggat ctagagaggg acccgaactg	600
tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctggtg	660
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca	720
ggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct	780
aaagctgggg tgtactatgt gttttttcag ctggaactga ggccgggtggg ggctggggag	840
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gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc	960
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catactgaag ccagagcccc gcatgcttgg cagctgactc agggggcaac tgtgctggga	1080
ctgtttcgcg tgacacctga gatccctgcc ggactgcaa gccctagatc agaagggggc	1140
ggaggttccg gaggcggagg atctgagggtg cagctgctgg aatccggcgg aggcctggtg	1200
cagcctggcg gatctctgag actgtcctgc gccgcctccg gcttcacctt ctctccccc	1260
gccatgtcct ggggtccgaca ggctcctggc aaaggcctgg aatgggtgtc cgccatctgg	1320
gcctccggcg agcagtacta cgccgactct gtgaagggcc ggttcaccat ctcccgggac	1380
aactccaaga acaccctgta cctgcagatg aactccctgc gggccgagga caccgccgtg	1440

eolf-seql

tactactgtg ccaagggctg gctgggcaac ttcgactact ggggccaggg caccctggtc	1500
accgtgtcca gcgctagcgt ggctgcacca tctgtcttta tcttcccacc cagcgaccgg	1560
aagctgaagt ctggcacagc cagcgtcgtg tgcctgctga ataacttcta cccccgcgag	1620
gccaaggtgc agtggaaagg ggacaatgcc ctgcagagcg gcaacagcca ggaaagcgtg	1680
accgagcagg acagcaagga ctccacctac agcctgagca gcaccctgac cctgagcaag	1740
gccgactacg agaagcaciaa ggtgtacgcc tgcgaagtga cccaccaggg cctgtctagc	1800
cccgtgacca agagcttcaa ccggggcgag tgcgacaaga cccacacctg tcctccatgc	1860
cctgccccctg aagctgctgg cggccctagc gtgttcctgt tcccccaaa gccaaggac	1920
accctgatga tcagccggac ccctgaagtg acctgcgtgg tggatgatgt gtcccacgag	1980
gacctgaag tgaagttaa ttggtacgtg gacggcgtgg aagtgcacia tgccaagacc	2040
aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg	2100
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacia agccctcggc	2160
gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	2220
accctgcccc catgccggga tgagctgacc aagaaccagg tcagcctgtg gtgcctggtc	2280
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC	2340
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttctt ctacagcaag	2400
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	2460
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa	2514

<210> 147
 <211> 1221
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Monomeric hu 4-1BBL (71-254) -FAP (VLCH1*)

<400> 147	
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60

eolf-seql

atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc	360
gaggccccga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag	420
agactgggag tgcattctga cacagaggcc agagccaggc acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagt acccccgaga ttcctgccgg cctgcctagc	540
cctagatctg aaggcggcgg aggttccgga ggccggaggat ctgagatcgt gctgaccag	600
tctcccgga ccctgagcct gagccctggc gagagagcca ccctgagctg cagagccagc	660
cagagcgtga gccggagcta cctggcctgg tatcagcaga agcccgcca ggccccaga	720
ctgctgatca tcggcgccag caccgggcc accggcatcc ccgatagatt cagcggcagc	780
ggctccggca ccgacttcac cctgaccatc agccggctgg aaccgagga cttcgccgtg	840
tactactgcc agcagggcc ggtgatcccc cccaccttcg gccagggcac caaggtggaa	900
atcaagtcct ctgctagcac aaagggtccc agcgtgttcc ctctggcccc tagcagcaag	960
agcacatctg gcggaacagc cgccctgggc tgcctgggtg aagattactt ccccagagcc	1020
gtgaccgtgt cctggaattc tggcgccctg acaagcggcg tgcacacctt tccagccgtg	1080
ctgcagagca gcggcctgta ctctctgagc agcgtcgtga cagtggccag cagctctctg	1140
ggcaccaga cctacatctg caacgtgaac cacaagcca gcaacaccaa ggtggacgag	1200
aaggtggaac ccaagtcctg c	1221

<210> 148

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-254) - FAP (VHCL*) Fc knob chain

eolf-seql

<400> 148

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly

eolf-seql

180

185

190

Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu
 195 200 205

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
 210 215 220

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
 225 230 235 240

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
 245 250 255

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
 260 265 270

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
 275 280 285

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
 290 295 300

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
 305 310 315 320

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
 325 330 335

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
 340 345 350

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
 355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly

eolf-seql

370

375

380

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
 385 390 395 400

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 405 410 415

Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
 420 425 430

Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala
 435 440 445

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 450 455 460

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 465 470 475 480

Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln
 485 490 495

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val
 500 505 510

Phe Ile Phe Pro Pro Ser Asp Arg Lys Leu Lys Ser Gly Thr Ala Ser
 515 520 525

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
 530 535 540

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
 545 550 555 560

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu

eolf-seql

565

570

575

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
580 585 590

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
595 600 605

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
610 615 620

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
625 630 635 640

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
645 650 655

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
660 665 670

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
675 680 685

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
690 695 700

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
705 710 715 720

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
725 730 735

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
740 745 750

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

eolf-seql

755

760

765

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 770 775 780

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 785 790 795 800

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 805 810 815

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 820 825 830

Ser Leu Ser Pro Gly Lys
 835

<210> 149

<211> 407

<212> PRT

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (71-254) -FAP (VLCH1*)

<400> 149

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
 1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
 20 25 30

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

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

eolf-seql

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly
180 185 190

Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
195 200 205

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
210 215 220

Arg Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
225 230 235 240

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

eolf-seql

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
260 265 270

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Gln Val
275 280 285

Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser
290 295 300

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
305 310 315 320

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Glu Asp Tyr
325 330 335

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
340 345 350

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
370 375 380

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Glu
385 390 395 400

Lys Val Glu Pro Lys Ser Cys
405

<210> 150

<211> 2268

<212> DNA

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (52-254) - CH1* Fc knob chain

eolf-seql

<400> 150

ccttgggctg tgtctggcgc tagagcctct cctggatctg ccgccagccc cagactgaga	60
gagggacctg agctgagccc cgatgatcct gccggactgc tggatctgag acagggcatg	120
ttcggccagc tgggtggcca gaacgtgctg ctgatcgatg gccccctgtc ctggtacagc	180
gatcctggac tggctggcgt gtcactgaca ggcggcctga gctacaaaga ggacacaaaa	240
gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga	300
gtggtggccg gcgagggatc tggatctgtg tctctggccc tgcattctgca gccccctgaga	360
agcgctgctg gcgctgcagc tctggcactg acagtggatc tgccctctgc cagctccgag	420
gcccgggaata gcgcatttgg gtttcaaggc agactgctgc acctgtctgc cggccagagg	480
ctgggagtgatc atctgcacac agaggccagg gctagacacg cctggcagct gacacagggc	540
gctacagtgc tgggcctgtt cagagtgacc cccgagattc cagccggact gcccagccct	600
agatctgaag gcggcggagg aagcggaggc ggaggatccc cttgggctgt gtctggcgct	660
agagcctctc ctggatctgc cgccagcccc agactgagag agggacctga gctgagcccc	720
gatgatcctg ccggactgct ggacctgcgg cagggaatgt tcgctcagct ggtggctcag	780
aatgtgctgc tgattgacgg acctctgtcc tgggtactccg accctggcct ggagggggtg	840
tccctgactg ggggactgtc ctacaaagaa gatacaaaag aactggtggt ggctaaagct	900
ggggtgtact atgtgttttt tcagctggaa ctgaggcggg tgggtggctgg ggagggtca	960
ggatctgtgt ccctggctct gcatctgcag cctctgcgct ctgctgctgg cgcagctgca	1020
ctggctctga ctgtggacct gccaccagcc tctagcgagg ccagaaacag cgccttcggg	1080
ttccaaggac ggctgctgca tctgagcgcc ggacagcgcc tgggagtgca tctgcatact	1140
gaagccagag cccggcatgc ttggcagctg acccaggggg caactgtgct gggactgttt	1200
cgcgtgacac ctgagatccc cgctggcctg cctagcccaa gaagtgaagg gggaggcgga	1260
tctggcggag ggggatctgc tagcaccaag ggccccctcg tgttccccct ggccccagc	1320
agcaagagca ccagcggcgg cacagccgct ctgggctgcc tggtcgagga ctacttcccc	1380

eolf-seql

gagcccgtga ccggtgtcctg gaacagcgga gccctgacct ccggcgtgca caccttcccc	1440
gccgtgtctgc agagttcttg cctgtatagc ctgagcagcg tggtcaccgt gccttctagc	1500
agcctgggca cccagaccta catctgcaac gtgaaccaca agcccagcaa caccaagggtg	1560
gacgagaagg tggagcccaa gagctgcgac aaaactcaca catgcccacc gtgcccagca	1620
cctgaagctg caggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc	1680
atgatctccc ggacccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct	1740
gagggtcaagt tcaactggta cgtggacggc gtggagggtgc ataatgcca gacaaagccg	1800
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag	1860
gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cggcgcccc	1920
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg	1980
cccccatgcc gggatgagct gaccaagaac caggtcagcc tgtgggtgcct ggtcaaaggc	2040
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac	2100
aagaccacgc ctcccgctg ggactccgac ggctccttct tcctctacag caagctcacc	2160
gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	2220
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa	2268

<210> 151

<211> 960

<212> DNA

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (52-254) -CL*

<400> 151

ccttgggctg tgtctggcgc tagagcctct cctggatctg ccgccagccc cagactgaga	60
gagggacctg agctgagccc cgatgatcct gccggactgc tggatctgag acagggcatg	120
ttcgcccagc tgggtggcca gaacgtgctg ctgatcgatg gccccctgtc ctggtacagc	180
gatcctggac tggctggcgt gtcactgaca ggcggcctga gctacaaaga ggacacaaaa	240

eolf-seql

gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga	300
gtggtggccg gcgagggatc tggatctgtg tctctggccc tgcattctgca gcccctgaga	360
agcgctgctg gcgctgcagc tctggcactg acagtggatc tgcctcctgc cagctccgag	420
gcccggaata gcgcatttgg gtttcaaggc aggctgctgc acctgtctgc cggccagagg	480
ctgggagtgc atctgcacac agaggccagg gctagacacg cctggcagct gacacagggc	540
gctacagtgc tgggcctgtt cagagtgacc cccgagattc cagccggcct gccttctcca	600
agaagcgaag gcggaggcgg atctggcggc ggaggatctc gtacggtggc tgcaccatct	660
gtcttcatct tcccgccatc tgatcggaag ttgaaatctg gaactgcctc tgttgtgtgc	720
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc	780
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc	840
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaaagt ctacgcctgc	900
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt	960

<210> 152

<211> 2100

<212> DNA

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (80-254) - CH1* Fc knob chain

<400> 152

gacctgccg gcctgctgga tctgcggcag ggaatgtttg cccagctggt ggcccagaac	60
gtgctgctga tcgatggccc cctgagctgg tacagcgatc ctggactggc tggcgtgtca	120
ctgacaggcg gcctgagcta caaagaggac accaaagaac tggtggtggc caaggccggc	180
gtgtactacg tgttctttca gctggaactg cggagagtgg tggccggcga aggatctggc	240
tctgtgtctc tggccctgca tctgcagccc ctgagaagcg ctgctggcgc tgcagctctg	300
gcactgacag tggatctgcc tcctgccagc tccgaggccc ggaatagcgc atttgggttt	360
caaggcagac tgctgcacct gtctgccggc cagaggctgg gagtgcattc gcacacagag	420

eolf-seql

gccagggcta gacacgcctg gcagctgaca cagggcgcta cagtgcctggg cctgttcaga	480
gtgacccccg agattccagc cggactgccc agccctagat ctgaaggcgg cggaggaagc	540
ggaggcggag gatccgaccc agctggactg ctggacctgc ggcagggaat gttcgctcag	600
ctggtggctc agaattgtgt gctgattgac ggacctctgt cctgggtactc cgacctggc	660
ctggcagggg tgtccctgac tgggggactg tcctacaaag aagatacaaa agaactgggtg	720
gtggctaaag ctgggggtgta ctatgtgttt tttcagctgg aactgaggcg ggtgggtggct	780
ggggaggggct caggatctgt gtccctggct ctgcatctgc agcctctgcg ctctgctgct	840
ggcgcagctg cactggctct gactgtggac ctgccaccag cctctagcga ggccagaaac	900
agcgccttcg gggtccaagg acggctgctg catctgagcg ccggacagcg cctgggagtg	960
catctgcata ctgaagccag agcccggcat gcttggcagc tgacccaggg ggcaactgtg	1020
ctgggactgt ttcgcgtgac acctgagatc cccgctggcc tgcctagccc aagaagtga	1080
gggggaggcg gatctggcgg agggggatct gctagcacca agggcccctc cgtgttcccc	1140
ctggccccca gcagcaagag caccagcggc ggcacagccg ctctgggctg cctggctcag	1200
gactacttcc ccgagcccgt gaccgtgtcc tggaacagcg gagccctgac ctccggcgtg	1260
cacaccttcc ccgccgtgct gcagagttct ggctgtata gcctgagcag cgtggtcacc	1320
gtgccttcta gcagcctggg caccagacc tacatctgca acgtgaacca caagcccagc	1380
aacaccaagg tggacgagaa ggtggagccc aagagctgcg acaaaaactca cacatgcca	1440
ccgtgcccag cacctgaagc tgcaggggga ccgtcagtct tcctcttccc cccaaaaccc	1500
aaggacaccc tcatgatctc ccggaccctt gaggtcacat gcgtgggtggg ggacgtgagc	1560
cacgaagacc ctgagggtcaa gttcaactgg tacgtggacg gcgtggagggt gcataatgcc	1620
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtgggtcag cgtcctcacc	1680
gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaagggtctc caacaaagcc	1740
ctcggcgccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag	1800
gtgtacaccc tgcccccatg ccgggatgag ctgaccaaga accagggtcag cctgtgggtgc	1860

eolf-seql

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg	1920
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac	1980
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg	2040
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa	2100

<210> 153

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (80-254) -CL*

<400> 153

gatcctgccg gcctgctgga tctgcggcag ggaatgtttg cccagctggg gggccagaac	60
gtgctgctga tcgatggccc cctgagctgg tacagcgatc ctggactggc tggcgtgtca	120
ctgacaggcg gcctgagcta caaagaggac accaaagaac tggtggtggc caaggccggc	180
gtgtactacg tgttctttca gctggaactg cggagagtgg tggccggcga aggatctggc	240
tctgtgtctc tggccctgca tctgcagccc ctgagaagcg ctgctggcgc tgcagctctg	300
gcactgacag tggatctgcc tcctgccagc tccgaggccc ggaatagcgc atttgggttt	360
caaggcaggc tgctgcacct gtctgccggc cagaggctgg gaggatctct gcacacagag	420
gccaggggcta gacacgcctg gcagctgaca cagggcgcta cagtgcctggg cctgttcaga	480
gtgacccccg agattccagc cggcctgcct tctccaagaa gcgaaggcgg aggcggatct	540
ggcggcggag gatctcgtac ggtggctgca ccatctgtct tcatcttccc gccatctgat	600
cggaagtga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga	660
gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt	720
gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc	780
aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc	840
tcgcccgtca caaagagctt caacagggga gagggt	876

eolf-seql

<210> 154
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47 Fc KK chain DNA

<400> 154
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300
 ggatttgact actggggcca aggaaccctg gtcaccgtct cgagcgctaa gaccaccccc 360
 cctagcgtgt accctctggc ccctggatct gccgcccaga ccaacagcat ggtgaccctg 420
 ggctgcctgg tgaagggcta cttccccgag cctgtgaccg tgacctggaa cagcggcagc 480
 ctgagcagcg gcgtgcacac ctttccagcc gtgctgcaga gcgacctgta caccctgagc 540
 agctccgtga ccgtgcctag cagcacctgg cccagccaga cagtgacctg caacgtggcc 600
 caccctgcca gcagcaccaa ggtggacaag aaaatcgtgc cccgggactg cggctgcaag 660
 ccctgcatct gcaccgtgcc cgagggtgtcc agcgtgttca tcttcccacc caagcccaag 720
 gacgtgctga ccatcacctt gacccccaaa gtgacctgcg tgggtggtggc catcagcaag 780
 gacgaccccc aggtgcagtt ctcttggttt gtggacgacg tggaggtgca cacagcccag 840
 acaaagcccc gggaggaaca gatcaacagc accttcagaa gcgtgtccga gctgccccatc 900
 atgcaccagg actggctgaa cggcaaagaa ttcaagtgca gagtgaacag cgccgccttc 960
 ggcgccccca tcgagaaaac catcagcaag accaagggca gacccaaggc cccccagggtg 1020
 tacaccatcc cccaccccaa aaaacagatg gccaaaggaca aggtgtccct gacctgcatg 1080
 atcaccaact ttttccccga ggacatcacc gtggagtggc agtggaatgg ccagcccgcc 1140

eolf-seql

gagaactaca agaacaccca gcccatcatg aagaccgacg gcagctactt cgtgtacagc	1200
aagctgaacg tgcagaagtc caactgggag gccgggaaca cttcacctg tagcgtgctg	1260
cacgagggcc tgcacaacca ccacaccgag aagtcctga gccactcccc cggcaag	1317

<210> 155
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47 light chain DNA

<400> 155	
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgct gacgttcggc	300
caggggacca aagtggaaat caaacgtgcc gatgctgcac caactgtatc gattttccca	360
ccatccagtg agcagttaac atctggaggt gcctcagtcg tgtgcttctt gaacaacttc	420
taccccaaag acatcaatgt caagtggaaag attgatggca gtgaacgaca aaatggcgtc	480
ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc	540
acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag	600
acatcaactt caccattgt caagagcttc aacaggaatg agtgt	645

<210> 156
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47 Fc KK chain

<400> 156

eolf-seql

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

eolf-seql

Gln Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val
195 200 205

Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys
210 215 220

Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
225 230 235 240

Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val
245 250 255

Ala Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp
260 265 270

Asp Val Glu Val His Thr Ala Gln Thr Lys Pro Arg Glu Glu Gln Ile
275 280 285

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

Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe
305 310 315 320

Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys
325 330 335

Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Lys Gln Met Ala Lys
340 345 350

Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asn Phe Phe Pro Glu Asp
355 360 365

Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys
370 375 380

eolf-seql

Asn Thr Gln Pro Ile Met Lys Thr Asp Gly Ser Tyr Phe Val Tyr Ser
385 390 395 400

Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr
405 410 415

Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser
420 425 430

Leu Ser His Ser Pro Gly Lys
435

<210> 157

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> DP47 light chain

<400> 157

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

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

eolf-seql

85

90

95

Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala
100 105 110

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

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
130 135 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
145 150 155 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
165 170 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
180 185 190

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

Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 158

<211> 2298

<212> DNA

<213> Artificial Sequence

<220>

<223> Dimeric murine 4-1BBL (104-309, C160S) - CL Fc DD chain DNA

<400> 158

agaaccgagc ccagacccgc cctgaccatc accaccagcc ctaacctggg caccagagag 60

aacaacgccg accaagtgc ccccggtgcc cacatcggct gcccgaatac cacacagcag 120

eolf-seql

ggcagccctg tgttcgccaa gctgctggcc aagaaccagg ccagcctgag caacaccacc	180
ctgaactggc acagccagga tggcgccgga agcagctatc tgagccaggg cctgagatac	240
gaagaggaca agaaagaact ggtggtggac agccctggcc tgtactacgt gttcctggaa	300
ctgaagctga gccccacctt caccaacacc ggccacaagg tgcagggctg ggtgtcactg	360
gtgctgcagg ccaaacccca ggtggacgac ttcgacaacc tggccctgac cgtggaactg	420
ttccccctgca gcatggaaaa caagctgggtg gatcggagct ggtcccagct tctgctgctg	480
aaggccggac acagactgag cgtgggcctg agggcttatc tgcacggcgc ccaggacgcc	540
tacagagact gggagctgag ctaccccaac acaaccagct tcggcctgtt cctcgtgaag	600
cccgacaacc cttgggaagg cggcggaggc tccggaggag gcggatctag aacagagcct	660
cggcctgccc tgacaattac cacatcccc aatctgggca cccgggaaaa caatgcagat	720
caagtgcac ctgtgtctca tattgggtgc cccaacacta ccagcaggg gtccccagtg	780
tttgctaaac tgctggctaa aaatcaggcc tccctgtcta acacaacact gaattggcat	840
agtcaggacg gggctggcag cagctacctg tctcaggac tgcgctatga ggaagataag	900
aaagaactgg tgggtggattc ccccgactg tactatgtgt ttctggaact gaaactgtcc	960
cctaccttta caaataccgg gcacaaagtg cagggatggg tgtccctggg gctgcaggct	1020
aagcctcagg tggacgattt tgataatctg gctctgacag tggaactgtt tccttgctct	1080
atggaaaaca aactggtgga ccgctcttgg agccagttgc tgctgctgaa agctggccac	1140
cggctgtctg tgggactgag agcatacctg catggggcac aggatgccta ccgggattgg	1200
gaactgtcct accctaacac tacttccttc ggactgttcc tcgtgaaacc tgataatccc	1260
tgggagggcg gaggcggaag tggcggaggg ggatccagag ctgatgctgc ccctaccgtg	1320
tccatcttcc caccagcag cgagcagctg acatctgggg gagctagcgt cgtgtgcttc	1380
ctgaacaact tctaccccaa ggacatcaac gtgaagtgga agatcgacgg cagcgagcgg	1440
cagaacggcg tgctgaatag ctggaccgac caggacagca aggactccac ctacagcatg	1500
agcagcacc tgaccctgac caaggacgag tacgagcggc acaacagcta cacatgcgag	1560

eolf-seql

gccacccaca agaccagcac cagccccatc gtgaagtcct tcaaccggaa cgagtgcgtg	1620
cccagagact gcggtgcaa gccttgcac tgcaccgtgc ctgaggtgtc cagcgtgttc	1680
atcttccac ccaagcccaa ggacgtgctg accatcacc tgacacccaa agtgacctgc	1740
gtggtggtgg ccatcagcaa ggatgacccc gaggtgcagt tcagttggtt cgtggacgac	1800
gtggaagtgc acaccgctca gaccaagccc agagaggaac agatcaacag caccttcaga	1860
agcgtgtccg agctgcccac catgcaccag gactggctga acggcaaaga attcaagtgc	1920
agagtgaaca gcgccgcctt tggcgcccct atcgagaaaa ccatctccaa gaccaagggc	1980
agaccaagg ccccccaggt gtacacaatc cccccacca aagaacagat ggccaaggac	2040
aaggtgtccc tgacctgcat gatcaccaat ttcttcccag aggatatcac cgtggaatgg	2100
cagtggaacg gccagccgc cgagaactac gacaacaccc agcctatcat ggacaccgac	2160
ggctcctact tcgtgtacag cgacctgaac gtgcagaagt ccaactggga ggccggcaac	2220
accttcacct gtagcgtgct gcacgagggc ctgcacaacc accacaccga gaagtccctg	2280
tcccacagcc ctggcaag	2298

<210> 159
 <211> 954
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Monomeric murine 4-1BBL (104-309, C160S) - CH1 DNA

<400> 159	
agaaccgagc ccagaccgc cctgaccatc accaccagcc ctaacctggg caccagagag	60
aacaacgccg accaagtgac ccccggtgcc cacatcggct gcccgaatac cacacagcag	120
ggcagccctg tgttcgcaa gctgctggcc aagaaccagg ccagcctgag caacaccacc	180
ctgaactggc acagccagga tggcgccgga agcagctatc tgagccaggg cctgagatac	240
gaagaggaca agaaagaact ggtggtggac agccctggcc tgtactacgt gttcctggaa	300
ctgaagctga gcccacctt caccaacacc ggccacaagg tgcagggctg ggtgtcactg	360

eolf-seql

```

gtgctgcagg ccaaacccca ggtggacgac ttcgacaacc tggccctgac cgtggaactg      420
ttcccctgca gcatggaaaa caagctgggtg gatcggagct ggtcccagct tctgctgctg      480
aaggccggac acagactgag cgtgggcctg agggcttatc tgcacggcgc ccaggacgcc      540
tacagagact gggagctgag ctacccaac acaaccagct tcggcctgtt cctcgtgaag      600
cccgacaacc cttgggaagg cggcggaggc tccggaggag gcggaagcgc taagaccacc      660
ccccccagcg tgtaccctct ggcccctgga tctgccgcc agaccaacag catggtgacc      720
ctgggctgcc tgggtgaaggg ctacttcccc gagcctgtga ccgtgacctg gaacagcggc      780
agcctgagca gcggcgtgca cacctttcca gccgtgctgc agagcgacct gtacaccctg      840
agcagctccg tgaccgtgcc tagcagcacc tggcccagcc agacagtgc ctgcaacgtg      900
gcccaccctg ccagcagcac caaggtggac aagaaaatcg tgccccggga ctgc          954

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<210> 160

<211> 766

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric murine 4-1BBL (104-309, C160S) - CL Fc DD chain

<400> 160

```

Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile Thr Thr Ser Pro Asn Leu
1           5           10           15

```

```

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

```

```

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

```

```

Leu Ala Lys Asn Gln Ala Ser Leu Ser Asn Thr Thr Leu Asn Trp His
          50           55           60

```

```

Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser Gln Gly Leu Arg Tyr

```

eolf-seql

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

eolf-seql

260

265

270

Ser Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser
 275 280 285

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

Val Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser
 305 310 315 320

Pro Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu
 325 330 335

Val Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu
 340 345 350

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

Ser Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val
 370 375 380

Gly Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp
 385 390 395 400

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

Pro Asp Asn Pro Trp Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 420 425 430

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 435 440 445

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe

eolf-seql

450

455

460

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 465 470 475 480

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 485 490 495

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 500 505 510

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 515 520 525

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Val Pro Arg Asp Cys
 530 535 540

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
 545 550 555 560

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
 565 570 575

Lys Val Thr Cys Val Val Val Ala Ile Ser Lys Asp Asp Pro Glu Val
 580 585 590

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
 595 600 605

Lys Pro Arg Glu Glu Gln Ile Asn Ser Thr Phe Arg Ser Val Ser Glu
 610 615 620

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
 625 630 635 640

Arg Val Asn Ser Ala Ala Phe Gly Ala Pro Ile Glu Lys Thr Ile Ser

eolf-seql

645

650

655

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
660 665 670

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
675 680 685

Thr Asn Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
690 695 700

Gln Pro Ala Glu Asn Tyr Asp Asn Thr Gln Pro Ile Met Asp Thr Asp
705 710 715 720

Gly Ser Tyr Phe Val Tyr Ser Asp Leu Asn Val Gln Lys Ser Asn Trp
725 730 735

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
740 745 750

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
755 760 765

<210> 161

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> Monomeric murine 4-1BBL (104-309, C160S) - CH1

<400> 161

Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile Thr Thr Ser Pro Asn Leu
1 5 10 15

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

eolf-seql

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

Leu Ala Lys Asn Gln Ala Ser Leu Ser Asn Thr Thr Leu Asn Trp His
50 55 60

Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser Gln Gly Leu Arg Tyr
65 70 75 80

Glu Glu Asp Lys Lys Glu Leu Val Val Asp Ser Pro Gly Leu Tyr Tyr
85 90 95

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

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

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

Met Glu Asn Lys Leu Val Asp Arg Ser Trp Ser Gln Leu Leu Leu Leu
145 150 155 160

Lys Ala Gly His Arg Leu Ser Val Gly Leu Arg Ala Tyr Leu His Gly
165 170 175

Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu Ser Tyr Pro Asn Thr Thr
180 185 190

Ser Phe Gly Leu Phe Leu Val Lys Pro Asp Asn Pro Trp Glu Gly Gly
195 200 205

Gly Gly Ser Gly Gly Gly Gly Ser Ala Lys Thr Thr Pro Pro Ser Val
210 215 220

eolf-seql

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
225 230 235 240

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
245 250 255

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
260 265 270

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
275 280 285

Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Asn Val Ala His Pro Ala
290 295 300

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
305 310 315

<210> 162
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-FAP (4B9) Fc hole chain DNA

<400> 162
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120
cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac 180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc 360
aagggccccct ccgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcacagcc 420

eolf-seql

gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgaccgtgtc ctggaacagc	480
ggagccctga cctccggcgt gcacaccttc cccgccgtgc tgcagagttc tggcctgtat	540
agcctgagca gcgtgggtcac cgtgccttct agcagcctgg gcacccagac ctacatctgc	600
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc	660
gacaaaactc acacatgccc accgtgcccga gcacctgaag ctgcaggggg accgtcagtc	720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	780
tgcgtgggtg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac	840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	960
tgcaaggctc ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	1020
gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag	1080
aaccagggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag	1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1200
gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcagggtg gcagcagggg	1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1320
ctctccctgt ctccgggtaa a	1341

<210> 163

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-FAP (4B9) light chain DNA

<400> 163

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cccgccagg cccctcggct gctgatcaac gtgggcagtc ggagagccac cggcatccct	180

eolf-seql

gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240
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 cagggcacca aggtggaaat caagcgtacg gtggctgcac catctgtctt catcttccc 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
 ggcttgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 164
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-FAP (4B9) Fc hole chain

<400> 164

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

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

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

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

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

eolf-seql

85

90

95

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

eolf-seql

275

280

285

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

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

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

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

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

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

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

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

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

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

<210> 165

<211> 2166

<212> DNA

<213> Artificial Sequence

eolf-seq1

<220>

<223> Dimeric hu 4-1BBL (71-254) - CL Fc knob chain DNA

<400> 165

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atgtttgctc	agctgggtggc	ccagaacgtg	ctgctgatcg	atggccccct	gtcctggtac	120
agcgatcctg	gactggctgg	cgtgtcactg	acaggcggcc	tgagctacaa	agaggacacc	180
aaagaactgg	tggtggccaa	ggccggcgtg	tactacgtgt	tctttcagct	ggaactgcgg	240
agagtgggtg	ccggcgaagg	atctggctct	gtgtctctgg	ccctgcatct	gcagcctctg	300
agaagcgctg	ctggcgctgc	agctctggca	ctgacagtgg	atctgcctcc	tgccagctcc	360
gaggccccga	atagcgcatt	tgggtttcaa	ggcaggctgc	tgcacctgtc	tgccggccag	420
aggctggggag	tgcatctgca	cacagaggcc	agggctagac	acgcctggca	gctgacacag	480
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gctcagaatg	tgctgctgat	tgacggacct	ctgagctggt	actccgaccc	agggctggca	720
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aaagctgggg	tgtactatgt	gttttttcag	ctggaactga	ggcgggtggt	ggctggggag	840
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gctgcactgg	ctctgactgt	ggacctgcca	ccagcctcta	gcgaggccag	aaacagcgcc	960
ttcgggttcc	aaggacgcct	gctgcatctg	agcgccggac	agcgctggg	agtgcattctg	1020
catactgaag	ccagagcccc	gcatgcttgg	cagctgactc	agggggcaac	tgtgctggga	1080
ctgttttcgcg	tgacacctga	gatccctgcc	ggactgccaa	gccctagatc	agaagggggc	1140
ggagggttccg	gagggggagg	atctcgtacg	gtggccgctc	cctccgtggt	tatctttccc	1200
ccatccgatg	aacagctgaa	aagcggcacc	gcctccgtcg	tgtgtctgct	gaacaatttt	1260
taccctaggg	aagctaaagt	gcagtggaaa	gtggataacg	cactgcagtc	cggcaactcc	1320

eolf-seq1

caggaatctg tgacagaaca ggactccaag gacagcacct actccctgtc ctccaccctg	1380
acactgtcta aggctgatta tgagaaacac aaagtctacg cctgcgaagt cacccatcag	1440
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtgacaa gaccacacc	1500
tgtccccctt gtcctgcccc tgaagctgct ggcgccctt ctgtgttcct gttccccca	1560
aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt ggtggtggat	1620
gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac	1680
aatgccaaga ccaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc	1740
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aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa	1860
ccacaggtgt acaccctgcc cccatgccgg gatgagctga ccaagaacca ggtcagcctg	1920
tgggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg	1980
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttcttc	2040
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ggtaaa	2166

<210> 166
 <211> 891
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Monomeric hu 4-1BBL (71-254) - CH1 DNA

<400> 166	
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atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240

eolf-seql

agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
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gaggccccgga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag	420
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agcgtgggtga cagtgcctcag cagcagcctg ggcccccaga cctacatctg caacgtgaac	840
cacaagccca gcaacaccaa ggtggacaag aaggtggaac ccaagtcttg t	891

<210> 167

<211> 2502

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-FAP (4B9) Fc hole chain fused to dimeric hu 4-1BBL (71-254)
DNA

<400> 167

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cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac	180
gccgacagcg tgaaggggccg gttcaccatc agccggggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc	360
aagggccccct ccgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcacagcc	420
gctctgggct gcctgggtcaa ggactacttc cccgagcccc tgaccgtgtc ctggaacagc	480

eolf-seq1

ggagccctga cctccggcgt gcacaccttc cccgccgtgc tgcagagttc tggcctgtat	540
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aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc	660
gacaaaactc acacatgccc accgtgcccga gcacctgaag ctgcaggggg accgtcagtc	720
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catctgcaca cagaggccag ggctagacac gcctggcagc tgacacaggg cgctacagtg	1860
ctgggcctgt tcagagtgac ccccgagatt ccagccggcc tgccttctcc aagaagcgaa	1920

eolf-seql

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ccagccgggc tgctggatct gagacaggga atgttcgccc agctgggtggc tcagaatgtg	2040
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ctgactgtgg acctgccacc agcctctagc gaggccagaa acagcgcctt cgggttccaa	2340
ggacgcctgc tgcactgag cgccggacag cgctgggag tgcactgca tactgaagcc	2400
agagcccggc atgcttggca gctgactcag ggggcaactg tgctgggact gtttcgcgtg	2460
acacctgaga tccctgccgg actgccaagc cctagatcag aa	2502

<210> 168
 <211> 1920
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-FAP (4B9) Fc knob chain fused to monomeric hu 4-1BBL
 (71-254) DNA

<400> 168	
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cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac	180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc	360
aagggcccat cggcttcccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480

eolf-seql

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aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	660
gacaaaactc acacatgccc accgtgcccga gcacctgaag ctgcagggggg accgtcagtc	720
ttcctcttcc ccccaaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	780
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tgcaagggtct ccaacaaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	1020
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catctgcaca cagaggccag ggctagacac gcctggcagc tgacacaggg cgctacagtg	1860
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eolf-seql

<210> 169
 <211> 2130
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Dimeric hu 4-1BBL (71-248) - CL* Fc knob chain DNA

<400> 169
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 agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180
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 gtggacctgc cccagcttc ttccgaggcc agaaacagcg ccttcgggtt ccaaggacgc 960
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 cggcatgctt ggcagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct 1080
 gagatccccg ctggactggg cggaggcgggt tccggagggg gaggatctcg tacggtggct 1140

eolf-seql

gcaccatctg tctttatctt cccacccagc gaccggaagc tgaagtctgg cacagccagc	1200
gtcgtgtgcc tgctgaataa cttctacccc cgcgaggcca aggtgcagtg gaaggtggac	1260
aatgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggacag caaggactcc	1320
acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaagggtg	1380
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cctagcgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccctt	1560
gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtga gttcaattgg	1620
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ctgaccaaga accaggctcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc	1920
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cagaagagcc tctccctgtc tccgggtaaa	2130

<210> 170

<211> 873

<212> DNA

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (71-248) - CH1* DNA

<400> 170

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atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
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eolf-seql

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aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300
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gaggccccga atagcgcat tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420
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cctagcagca agagcacatc tggcggaaca gccgccctgg gctgcctggg ggaagattac 660
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tttccagccg tgctgcagag cagcggcctg tactctctga gcagcgtcgt gacagtgtcc 780
agcagctctc tgggcaccca gacctacatc tgcaacgtga accacaagcc cagcaacacc 840
aaggtggacg agaaggtgga acccaagtcc tgc 873

<210> 171
<211> 2130
<212> DNA
<213> Artificial Sequence

<220>
<223> dimeric hu 4-1BBL (71-248) - CL Fc knob chain DNA

<400> 171
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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300
agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 360

eolf-seql

gaggccccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag	480
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg actgggaggc	540
ggcggatctg gcggcggagg atctagagaa ggacccgagc tgtcccctga cgatccagcc	600
gggctgctgg atctgagaca gggaatgttc gcccagctgg tggctcagaa tgtgctgctg	660
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gtggacctgc ccccagcttc ttccgaggcc agaaacagcg ccttcggggtt ccaaggacgc	960
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cggcatgctt ggcagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct	1080
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gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc	1800

eolf-seql

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccattg ccgggatgag	1860
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gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1980
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cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	2100
cagaagagcc tctccctgtc tccgggtaaa	2130

<210> 172

<211> 873

<212> DNA

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (71-248) - CH1 DNA

<400> 172

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	60
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	120
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	180
aaagaactgg tgggtggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	240
agagtgggtg ccggcgaaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	300
agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc	360
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	420
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ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg actgggaggc	540
ggaggttccg gaggcggagg atctgctagc accaaaggcc cttccgtgtt tcctctggct	600
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tttctgagc ctgtgacagt gtcctggaat agcggagcac tgacctctgg agtgcatact	720
ttccccgctg tgctgcagtc ctctggactg tacagcctga gcagcgtggt gacagtgccc	780

eolf-seql

agcagcagcc tgggcaccca gacctacatc tgcaacgtga accacaagcc cagcaacacc 840

aaggtggaca agaaggtgga acccaagtct tgt 873

<210> 173

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu 4-1BBL (71-248) - CL Fc knob chain

<400> 173

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val

eolf-seql

130

135

140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
 145 150 155 160

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

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
 180 185 190

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
 195 200 205

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
 210 215 220

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 225 230 235 240

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
 245 250 255

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

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
 275 280 285

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
 290 295 300

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
 305 310 315 320

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr

eolf-seql

325

330

335

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
340 345 350

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val
370 375 380

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
385 390 395 400

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
405 410 415

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
435 440 445

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
450 455 460

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
465 470 475 480

Gly Glu Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
485 490 495

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
500 505 510

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

eolf-seql

515

520

525

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 530 535 540

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 545 550 555 560

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 565 570 575

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
 580 585 590

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 595 600 605

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
 610 615 620

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 625 630 635 640

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 645 650 655

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 660 665 670

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 675 680 685

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 690 695 700

Ser Leu Ser Pro Gly Lys

eolf-seql

705

710

<210> 174

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> Monomeric hu 4-1BBL (71-248) - CH1

<400> 174

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
 1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
 20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
 65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
 85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
 100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
 115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
 130 135 140

eolf-seql

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Thr Lys
180 185 190

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
195 200 205

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
210 215 220

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
225 230 235 240

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
245 250 255

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
260 265 270

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
275 280 285

Lys Ser Cys
290

<210> 175
<211> 2466
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-FAP (4B9) Fc hole chain fused to dimeric hu 4-1BBL (71-248)

eolf-seql

DNA

<400> 175

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cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac	180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc	360
aagggccccct ccgtgttccc cctggcccc agcagcaaga gcaccagcgg cggcacagcc	420
gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgaccgtgtc ctggaacagc	480
ggagccctga cctccggcgt gcacaccttc cccgccgtgc tgcagagttc tggcctgtat	540
agcctgagca gcgtgggtcac cgtgccttct agcagcctgg gcacccagac ctacatctgc	600
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc	660
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tgctgtgtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	900
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tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	1020
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aaccagggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag	1140
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gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcagggtg gcagcagggg	1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1320
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eolf-seql

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ggcgaaggat ctggctctgt gtctctggcc ctgcatctgc agcctctgag aagcgctgct      1680
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ggactg                                                                    2466

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<210> 176
 <211> 1902
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-FAP (4B9) Fc knob chain fused to monomeric hu 4-1BBL
 (71-248) DNA

eolf-seql

<400> 176
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cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac 180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
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gacggcagct tcttctgtga ctccaaactg accgtggaca agagccgggtg gcagcagggc 1260
aacgtgttca gctgcagcgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
ctgagcctga gccccggcgg aggcggcgga agcggaggag gaggatccag agagggccct 1380

eolf-seql

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ctggctggcg tgctactgac aggcggcctg agctacaaag aggacaccaa agaactgggtg	1560
gtggccaagg ccggcgtgta ctacgtgttc tttcagctgg aactgcggag agtgggtggcc	1620
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<210> 177
 <211> 2496
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47 Fc hole chain fused to dimeric hu 4-1BBL (71-254) DNA

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agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg	600

eolf-seql

aaccacaagc ccagcaacac caaggtggac aagaaggtgg agcccaagag ctgcgacaaa	660
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gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1140
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gcagctctgg cactgacagt ggatctgcct cctgccagct ccgaggcccc gaatagcgca	1740
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ggcggatctg gcggcgagg atctagagag ggacccgaac tgtccccctga cgatccagcc	1980
gggctgctgg atctgagaca gggaatgttc gcccagctgg tggctcagaa tgtgctgctg	2040

eolf-seql

attgacggac ctctgagctg gtactccgac ccagggctgg caggggtgtc cctgactggg	2100
ggactgtcct acaaagaaga tacaaaagaa ctggtggtgg ctaaagctgg ggtgtactat	2160
gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc	2220
ctggctctgc atctgcagcc actgcgctct gctgctggcg cagctgcact ggctctgact	2280
gtggacctgc caccagcctc tagcgaggcc agaaacagcg ctttcgggtt ccaaggacgc	2340
ctgctgcatc tgagcgccgg acagcgcttg ggagtgcac tgcataactga agccagagcc	2400
cggcatgctt ggagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct	2460
gagatccctg ccggactgcc aagccctaga tcagaa	2496

<210> 178
 <211> 1914
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47 Fc knob chain fused to monomeric hu 4-1BBL (71-254) DNA

<400> 178	
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccatcggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg	420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc	480
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc	540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	600
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatac ttgtgacaaa	660

eolf-seql

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcag	960
gtctccaaca aagccctcgg cgccccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagaac cacaggtgta caccctgccc ccctgcagag atgagctgac caagaaccag	1080
gtgtcccctgt ggtgtctggt caagggttc taccacagcg atatcgccgt ggagtgggag	1140
agcaacggcc agcctgagaa caactacaag accaccccc ctgtgctgga cagcgacggc	1200
agcttcttcc tgtactcaa actgaccgtg gacaagagcc ggtggcagca gggcaacgtg	1260
ttcagctgca gcgtgatgca cgaggccctg cacaaccact acaccagaa gtccctgagc	1320
ctgagccccg gcggaggcgg cggaagcgga ggaggaggat ccagagaggg ccctgagctg	1380
agccccgatg atcctgctgg actgctggac ctgcggcagg gcatgtttgc tcagctggtg	1440
gcccagaacg tgctgctgat cgatggcccc ctgtcctggt acagcgatcc tggactggct	1500
ggcgtgtcac tgacaggcgg cctgagctac aaagaggaca ccaaagaact ggtggtggcc	1560
aaggccggcg tgtactacgt gttctttcag ctggaactgc ggagagtggg ggccggcgaa	1620
ggatctggct ctgtgtctct ggccctgcat ctgcagcctc tgagaagcgc tgctggcgct	1680
gcagctctgg cactgacagt ggatctgcct cctgccagct ccgaggcccc gaatagcgca	1740
tttgggtttc aaggcaggct gctgcacctg tctgccggcc agaggctggg agtgcactg	1800
cacacagagg ccagggctag acacgcctgg cagctgacac agggcgctac agtgctgggc	1860
ctgttcagag tgacccccga gattccagcc ggcctgcctt ctccaagaag cgaa	1914

<210> 179

<211> 834

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> DP47 Fc hole chain fused to dimeric hu 4-1BBL (71-254)

<400> 179

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

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

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

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

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

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

eolf-seql

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
450 455 460

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
465 470 475 480

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
485 490 495

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
500 505 510

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
515 520 525

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
530 535 540

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
545 550 555 560

eolf-seql

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
565 570 575

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
580 585 590

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
595 600 605

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
610 615 620

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu
645 650 655

Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe
660 665 670

Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser
675 680 685

Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu
690 695 700

Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val
705 710 715 720

Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu
725 730 735

Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser
740 745 750

eolf-seql

Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala
755 760 765

Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu
770 775 780

His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala
785 790 795 800

Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly
805 810 815

Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg
820 825 830

Ser Glu

<210> 180
<211> 640
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47 Fc knob chain fused to monomeric hu 4-1BBL (71-254)
<400> 180

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

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

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

Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val

eolf-seql

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 Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr

eolf-seql

245

250

255

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

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

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

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

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

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

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

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

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

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

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

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly

eolf-seql

435

440

445

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
 450 455 460

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
 465 470 475 480

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
 485 490 495

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
 500 505 510

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
 515 520 525

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
 530 535 540

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
 545 550 555 560

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
 565 570 575

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
 580 585 590

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
 595 600 605

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
 610 615 620

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu

625	630	eolf-seql 635	640
<210>	181		
<211>	1335		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	DP47 heavy chain (hu IgG1 PGLALA) DNA		
<400>	181		
gagggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc			60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct			120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac			180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat			240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc			300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc			360
ccatcggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg			420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc			480
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc			540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg			600
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaadc ttgtgacaaa			660
actcacacat gccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc			720
ttccccccaa aacccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg			780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg			840
gagggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg			900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag			960
gtctccaaca aagccctcgg cgccccatc gagaaaacca tctccaaagc caaagggcag			1020
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag			1080

eolf-seql

gtcagcctga cctgcctggc caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140
 agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200
 tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260
 ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320
 ctgtctccgg gtaaa 1335

<210> 182

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> DP47 heavy chain (hu IgG1 PGLALA)

<400> 182

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

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

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

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

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

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

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

eolf-seql

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

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

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

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

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

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

eolf-seql

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

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

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

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

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

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

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 183

<211> 189

<212> PRT

<213> Artificial Sequence

<220>

<223> monomeric hu 4-1BBL (71-254) plus (G4S)₁ linker

<400> 183

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp

eolf-seql

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1           5           10           15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
      20           25           30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
      65           70           75           80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
      85           90           95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
      100          105          110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
      115          120          125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
      130          135          140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
      145          150          155          160

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

Gly Leu Pro Ser Pro Arg Ser Glu Gly Gly Gly Gly Ser
      180          185

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<210> 184

eolf-seql

<211> 188

<212> PRT

<213> Artificial Sequence

<220>

<223> monomeric hu 4-1BBL (71-248) plus (G4S)₂ linker

<400> 184

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
115 120 125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

eolf-seql

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

Gly Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
180 185

<210> 185
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> monomeric hu 4-1BBL (71-248) plus (G4S)₁ linker

<400> 185

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
1 5 10 15

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
20 25 30

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

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

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
65 70 75 80

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
85 90 95

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
100 105 110

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

eolf-seql

115

120

125

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val
130 135 140

His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln
145 150 155 160

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

Gly Leu Gly Gly Gly Gly Ser
180

<210> 186
<211> 1602
<212> DNA
<213> Artificial Sequence

<220>
<223> human CD19 antigen Fc knob chain avi tag DNA

<400> 186
cccgaggaac ccctggtcgt gaagggtggaa gagggcgaca atgccgtgct gcagtcctg 60
aagggcacct ccgatggccc taccagcag ctgacctggc ccagagagag cccctgaag 120
cccttcctga agctgtctct gggcctgcct ggctgggca tccatatgag gcctctggcc 180
atctggctgt tcatcttcaa cgtgtcccag cagatgggcg gcttctacct gtgtcagcct 240
ggccccccat ctgagaaggc ttggcagcct ggctggaccg tgaacgtgga aggatccggc 300
gagctgttcc ggtggaacgt gtccgatctg ggcggcctgg gatgcggcct gaagaacaga 360
tctagcgagg gcccagcag cccagcggc aaactgatga gcccgaagct gtacgtgtgg 420
gccaaggaca gaccgagat ctgggagggc gagcctcctt gcctgcccc tagagacagc 480
ctgaaccaga gcctgagcca ggacctgaca atggcccctg gcagcacact gtggctgagc 540
tgtggcgtgc caccgactc tgtgtctaga ggccctctga gctggacca cgtgcaccct 600

eolf-seql

aagggcccta agagcctgct gagcctggaa ctgaaggacg acaggcccg cagagatatg 660
 tgggtcatgg aaaccggcct gctgctgcct agagccacag cccaggatgc cggcaagtac 720
 tactgccaca gaggcaacct gaccatgagc ttccacctgg aaatcaccgc cagacccgtg 780
 ctgtggcact ggctgctgag aacaggcggc tggaaggctc acgctagcgg tggtagtccg 840
 acacctccga cccccggggg tggttctgca gacaaaactc acacatgccc accgtgccc 900
 gcacctgaag ccgcaggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc 960
 ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1020
 cctgagggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1080
 ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1140
 caggactggc tgaatggcaa ggagtacaag tgcaaggctc ccaacaaagc cctcggagcc 1200
 cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1260
 ctgcccccat gccgggatga gctgaccaag aaccagggtc gcctgtggtg cctggtcaaa 1320
 ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1380
 tacaagacca cgcctcccgt gctggactcc gacggctcct tcttctctta cagcaagctc 1440
 accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1500
 gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atccggaggc 1560
 ctgaacgaca tcttcgaggc ccagaagatt gaatggcacg ag 1602

<210> 187

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<223> human CD19 antigen Fc knob chain avi tag

<400> 187

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

eolf-seql

Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
20 25 30

Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
35 40 45

Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
50 55 60

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

Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
85 90 95

Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly
100 105 110

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
115 120 125

Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg
130 135 140

Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser
145 150 155 160

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
165 170 175

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
180 185 190

Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser
195 200 205

eolf-seql

Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu
210 215 220

Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr
225 230 235 240

Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr
245 250 255

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

Val Asp Ala Ser Gly Gly Ser Pro Thr Pro Pro Thr Pro Gly Gly Gly
275 280 285

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
290 295 300

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
305 310 315 320

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
325 330 335

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
340 345 350

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
355 360 365

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
370 375 380

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala
385 390 395 400

eolf-seql

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
405 410 415

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
420 425 430

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
435 440 445

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
450 455 460

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
465 470 475 480

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
485 490 495

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
500 505 510

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
515 520 525

Lys Ile Glu Trp His Glu
530

<210> 188

<211> 1605

<212> DNA

<213> Artificial Sequence

<220>

<223> cynomolgus CD19 antigen Fc knob chain avi tag DNA

<400> 188

ccccaggaac ccctggtcgt gaaggtggaa gagggcgaca atgccgtgct ccagtcctg

60

eolf-seql

gaaggcacct ccgatggccc tacacagcag ctcgtgtggt gcagagacag ccccttcgag	120
cccttcctga acctgtctct gggcctgcct ggcatgggca tcagaatggg ccctctgggc	180
atctggctgc tgatcttcaa cgtgtccaac cagaccggcg gcttctacct gtgtcagcct	240
ggcctgccaa gcgagaaggc ttggcagcct ggatggaccg tgtccgtgga aggatctggc	300
gagctgttcc ggtggaacgt gtccgatctg ggcggcctgg gatgcggcct gaagaacaga	360
agcagcgagg gccctagcag ccccgacggc aagctgaata gcagccagct gtacgtgtgg	420
gccaaggaca gacccgagat gtgggagggc gagcctgtgt gtggcccccc tagagatagc	480
ctgaaccaga gcctgagcca ggacctgaca atggcccctg gcagcacact gtggctgagc	540
tgtggcgtgc caccgactc tgtgtccaga ggccctctga gctggacaca cgtgcggcca	600
aagggcccta agagcagcct gctgagcctg gaactgaagg acgaccggcc cgaccgggat	660
atgtgggtgg tggatacagg cctgctgctg accagagcca cagcccagga tgccggcaag	720
tactactgcc acagaggcaa ctggaccaag agcttttacc tggaaatcac cgccagaccc	780
gccctgtggc actggctgct gagaatcgga ggctggaagg tcgacgctag cgggtggtagt	840
ccgacacctc cgacacccgg ggggtggttct gcagacaaaa ctcacacatg cccaccgtgc	900
ccagcacctg aagccgcagg gggaccgtca gtcttcctct tcccccaaa acccaaggac	960
accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtaggacgt gagccacgaa	1020
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	1080
aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg	1140
caccaggact ggctgaatgg caaggagtac aagtgaagg tctccaacaa agccctcgga	1200
gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	1260
accctgcccc catgccggga tgagctgacc aagaaccagg tcagcctgtg gtgcctggtc	1320
aaaggcttct atcccagcga catcgccgtg gagggggaga gcaatgggca gccggagaac	1380
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct ctacagcaag	1440
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	1500

eolf-seql

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatccgga 1560

ggcctgaacg acatcttcga ggcccagaag attgaatggc acgag 1605

<210> 189

<211> 535

<212> PRT

<213> Artificial Sequence

<220>

<223> cynomolgus CD19 antigen Fc knob chain avi tag

<400> 189

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

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

Trp Cys Arg Asp Ser Pro Phe Glu Pro Phe Leu Asn Leu Ser Leu Gly
35 40 45

Leu Pro Gly Met Gly Ile Arg Met Gly Pro Leu Gly Ile Trp Leu Leu
50 55 60

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

Gly Leu Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Ser Val
85 90 95

Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly
100 105 110

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
115 120 125

Ser Gly Lys Leu Asn Ser Ser Gln Leu Tyr Val Trp Ala Lys Asp Arg

eolf-seql

130

135

140

Pro Glu Met Trp Glu Gly Glu Pro Val Cys Gly Pro Pro Arg Asp Ser
145 150 155 160

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
165 170 175

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
180 185 190

Leu Ser Trp Thr His Val Arg Pro Lys Gly Pro Lys Ser Ser Leu Leu
195 200 205

Ser Leu Glu Leu Lys Asp Asp Arg Pro Asp Arg Asp Met Trp Val Val
210 215 220

Asp Thr Gly Leu Leu Leu Thr Arg Ala Thr Ala Gln Asp Ala Gly Lys
225 230 235 240

Tyr Tyr Cys His Arg Gly Asn Trp Thr Lys Ser Phe Tyr Leu Glu Ile
245 250 255

Thr Ala Arg Pro Ala Leu Trp His Trp Leu Leu Arg Ile Gly Gly Trp
260 265 270

Lys Val Asp Ala Ser Gly Gly Ser Pro Thr Pro Pro Thr Pro Gly Gly
275 280 285

Gly Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
290 295 300

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
305 310 315 320

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp

eolf-seql

325

330

335

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
340 345 350

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
355 360 365

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
370 375 380

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
385 390 395 400

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
405 410 415

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
420 425 430

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
435 440 445

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
450 455 460

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
465 470 475 480

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
485 490 495

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
500 505 510

Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala

eolf-seql

515

520

525

Gln Lys Ile Glu Trp His Glu
 530 535

<210> 190

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized CD19 (8B8) HVR-L1

<400> 190

Asn Ser Asn Gly Asn Thr
 1 5

<210> 191

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized CD19 (8B8) HVR-H2

<400> 191

Lys Phe Asn Gly
 1

<210> 192

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> humanized CD19 (8B8) var.1 to 9 HVR-H2

<400> 192

Thr Glu Lys Phe Gln Gly Arg Val Thr Met
 1 5 10

eolf-seql

<210> 193
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CD19 (8B8) var.5 HVR-L1

<400> 193

Leu Glu Asn Pro Asn Gly Asn Thr
1 5

<210> 194
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized CD19 (8B8) var.9 HVR-L1

<400> 194

Leu Glu Asn Pro Ser Gly Asn Thr
1 5

<210> 195
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-018) CDR-H1

<400> 195

Asp Tyr Ile Met His
1 5

<210> 196
<211> 17
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> CD19 (8B8-018) CDR-H2

<400> 196

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

Gly

<210> 197

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-018) CDR-H3

<400> 197

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

<210> 198

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-018) CDR-L1

<400> 198

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

<210> 199

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-018) CDR-L2

eolf-seql

<400> 199

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 200

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-018) CDR-L3

<400> 200

Leu Gln Leu Thr His Val Pro Tyr Thr
1 5

<210> 201

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-018) VH

<400> 201

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr

															eolf-seql										
65											70						75						80		
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys										
				85					90					95											
Ala	Arg	Gly	Thr	Tyr	Tyr	Tyr	Gly	Ser	Ala	Leu	Phe	Asp	Tyr	Trp	Gly										
				100					105					110											
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser																	
				115					120																
<210> 202																									
<211> 112																									
<212> PRT																									
<213> Artificial Sequence																									
<220>																									
<223> CD19 (8B8-018) VL																									
<400> 202																									
Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Thr	Pro	Gly										
1					5					10					15										
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Glu	Asn	Pro										
				20					25					30											
Asn	Gly	Asn	Thr	Tyr	Leu	Asn	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser										
				35					40					45											
Pro	Gln	Leu	Leu	Ile	Tyr	Arg	Val	Ser	Lys	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	Val	Gly	Val	Tyr	Tyr	Cys	Leu	Gln	Leu										
				85					90					95											

eolf-seql

Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 203
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-CD19(8B8-018) Fc hole chain DNA

<400> 203
 cagggtccagc tgggtgcagtc cggcgccgag gtcaagaaac ccggggcttc tgtgaaggtt 60
 tcatgcaagg caagcggata caccttcacc gactatatca tgcattgggt caggcaggcc 120
 cctggccaag gtctcgaatg gatgggctac attaacccat ataatgatgg ctccaaatac 180
 accgagaagt ttcagggaag agtcactatg acatctgaca ccagtatcag cactgcttac 240
 atggagctgt cccgccttcg gtctgatgac accgcagtgt attactgtgc caggggcaca 300
 tattactacg gctcagctct gtctgactat tgggggcagg gaaccacagt aaccgtgagc 360
 tccgctagca ccaaggggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc 420
 ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480
 tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540
 tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcaccacag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
 cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccgacc 780
 cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020

eolf-seql

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

<210> 204
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-CD19(8B8-018) light chain DNA

<400> 204	
gacatcgta tgaccagac acccctgtcc ctctctgtga cccctggcca gccagcctca	60
attagctgca agtcctctca aagtctggag aacccaatg ggaacactta ccttaattgg	120
tatctgcaga aacccggaca atccccctcaa ctctgatct acagggtctc taagagattc	180
tcaggcgtgc cagatcgctt tagcggttcc gggctctggca cagacttcac cttgaagatt	240
agtcgggttg aagctgagga tgtgggagtc tattactgtc tgcagctcac tcatgtgccc	300
tacacctttg gtcagggcac aaaactggag atcaagcgga ccgtggccgc tccctccgtg	360
ttcatcttcc caccctccga cgagcagctg aagtccggca ccgccagcgt ggtgtgcctg	420
ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa cgccctgcag	480
tccggcaact cccaggaatc cgtgaccgag caggactcca aggacagcac ctactccctg	540
tcctccaccc tgaccctgtc caaggccgac tacgagaagc acaagggtgta cgcctgcgaa	600
gtgaccacc aggccctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc	657

<210> 205
 <211> 451
 <212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<223> anti-CD19(8B8-018) Fc hole chain

<400> 205

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

eolf-seq1

165

170

175

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

355

360

365

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

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

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

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

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

Pro Gly Lys
450

<210> 206

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-CD19(8B8-018) light chain

<400> 206

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Asn Pro
20 25 30

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

eolf-seql

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gln 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> 207
<211> 2514
<212> DNA

eolf-seql

<213> Artificial Sequence

<220>

<223> anti-CD19(8B8-018) Fc hole dimeric ligand chain DNA

<400> 207

cagggtccagc tgggtgcagtc cggcgccgag gtcaagaaac ccggggccttc tgtgaagggt	60
tcatgcaagg caagcggata caccttcacc gactatatca tgcattgggt caggcaggcc	120
cctggccaag gtctcgaatg gatgggctac attaacccat ataatgatgg ctccaaatac	180
accgagaagt ttcagggaag agtcactatg acatctgaca ccagtatcag cactgcttac	240
atggagctgt cccgccttcg gtctgatgac accgcagtgt attactgtgc caggggcaca	300
tattactacg gctcagctct gttcgactat tgggggcagg gaaccacagt aaccgtgagc	360
tccgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg	480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt	540
tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcaccagg	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag	660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
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aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtgca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260

eolf-seql

tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	1440
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aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
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aaagctgggg tgtactatgt gttttttcag ctggaactga ggccgggtgg ggctggggag	2220
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catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga	2460
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<210> 208

<211> 1932

<212> DNA

<213> Artificial Sequence

eolf-seql

<220>

<223> anti-CD19(8B8-018) Fc knob monomeric ligand DNA

<400> 208

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cctggccaag	gtctcgaatg	gatgggctac	attaacccat	ataatgatgg	ctccaaatac	180
accgagaagt	ttcagggaag	agtcactatg	acatctgaca	ccagtatcag	cactgcttac	240
atggagctgt	ccgccttcg	gtctgatgac	accgcagtgt	attactgtgc	caggggcaca	300
tattactacg	gctcagctct	gttcgactat	tgggggcagg	gaaccacagt	aaccgtgagc	360
tccgctagca	ccaagggccc	atcgggtcttc	cccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacgggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggtg	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggacaa	gaaagttgag	660
cccaaattctt	gtgacaaaac	tcacacatgc	ccaccgtgcc	cagcacctga	agctgcaggg	720
ggaccgtcag	tcttcctctt	cccccaaaa	ccaaggaca	ccctcatgat	ctcccgacc	780
cctgaggtca	catgcgtggg	ggtggacgtg	agccacgaag	accctgaggt	caagttcaac	840
tgggtacgtgg	acggcgtgga	ggtgcataat	gccaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggg	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
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gagctgacca	agaaccaggt	gtccctgtgg	tgtctgggtca	agggtttcta	ccccagcgat	1140
atgccgtgg	agtgggagag	caacggccag	cctgagaaca	actacaagac	cacccccct	1200
gtgctggaca	gcgacggcag	cttcttcctg	tactccaaac	tgaccgtgga	caagagccgg	1260
tggcagcagg	gcaacgtgtt	cagctgcagc	gtgatgcacg	aggccctgca	caaccactac	1320

eolf-seql

acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc 1380
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 atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac 1500
 agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 1560
 aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620
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 aggctggggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860
 ggcgctacag tgctgggcct gttcagagtg accccccgaga ttccagccgg cctgccttct 1920
 ccaagaagcg aa 1932

<210> 209
 <211> 838
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-CD19(8B8-018) Fc hole dimeric ligand chain

<400> 209

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

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

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

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

eolf-seql

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

eolf-seql

Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu
645 650 655

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
660 665 670

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
675 680 685

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
690 695 700

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
705 710 715 720

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
725 730 735

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
740 745 750

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
755 760 765

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
770 775 780

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
785 790 795 800

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
805 810 815

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825 830

eolf-seql

Pro Ser Pro Arg Ser Glu
835

<210> 210
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD19(8B8-018) Fc knob monomeric ligand

<400> 210

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

eolf-seql

130

135

140

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

325

330

335

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

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

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

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

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

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

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

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
 450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
 465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
 485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 500 505 510

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

eolf-seql

515

520

525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

Pro Arg Ser Glu

<210> 211

<211> 2478

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-CD19(8B8-018) Fc hole dimeric ligand (71-248) chain DNA

<400> 211

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tcatgcaagg caagcggata caccttcacc gactatatca tgcattgggt caggcaggcc 120

eolf-seql

cctggccaag gtctcgaatg gatgggctac attaacccat ataatgatgg ctccaaatac	180
accgagaagt ttccagggaag agtcactatg acatctgaca ccagtatcag cactgcttac	240
atggagctgt cccgccttcg gtctgatgac accgcagtgt attactgtgc caggggcaca	300
tattactacg gctcagctct gttcgactat tgggggcagg gaaccacagt aaccgtgagc	360
tccgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc	420
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acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag	660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
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eolf-seq1

aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
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cggcatgctt ggcagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct	2460
gagatcccag ccgggctc	2478

<210> 212
 <211> 1914
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-CD19(8B8-018) Fc knob monomeric (71-248) ligand DNA

<400> 212	
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tcatgcaagg caagcggata caccttcacc gactatatca tgcatgggt caggcaggcc	120
cctggccaag gtctcgaatg gatgggctac attaaccat ataatgatgg ctccaaatac	180

eolf-seq1

accgagaagt ttcaggggaag agtcactatg acatctgaca ccagtatcag cactgcttac	240
atggagctgt cccgccttcg gtctgatgac accgcagtgt attactgtgc caggggcaca	300
tattactacg gctcagctct gttcgactat tgggggcagg gaaccacagt aaccgtgagc	360
tccgctagca ccaagggccc atcggctctt cccctggcac cctcctcaa gagcacctct	420
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tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
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aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
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gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat	1140
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accagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccctgatgat cctgccggac tgctggacct gcggcaggga	1440
atgtttgccc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620

eolf-seql

agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680
 agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 1740
 gaggccccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 1800
 aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860
 ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg gctc 1914

<210> 213

<211> 826

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-CD19(8B8-018) Fc hole dimeric ligand (71-248) chain

<400> 213

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

eolf-seql

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
645 650 655

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
660 665 670

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
675 680 685

eolf-seql

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
690 695 700

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
705 710 715 720

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
725 730 735

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
740 745 750

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
755 760 765

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
770 775 780

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
785 790 795 800

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
805 810 815

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825

<210> 214

<211> 638

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-CD19(8B8-018) Fc knob monomeric (71-248) ligand

<400> 214

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

eolf-seql

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

eolf-seql

195

200

205

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

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385              390              395              400

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

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

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

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
      450              455              460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465              470              475              480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
      485              490              495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
      500              505              510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
      515              520              525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
      530              535              540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545              550              555              560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
      565              570              575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg

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eolf-seql

580

585

590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
625 630 635

<210> 215
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence CD19 (8B8) VH Parental clone DNA

<400> 215
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagatg 60
gcctgcaagg cttctggata cacattcact gactatatta tgcactgggt gaagcagaag 120
actgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg ttctaagtac 180
actgagaagt tcaacggcaa ggccacactg acttcagaca aatcttccat cacagcctac 240
atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagagggacc 300
tattattatg gtagcgccct ctttgactac tggggccaag gcaccactct cacagtctcc 360
tcg 363

<210> 216
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence CD19 (8B8) VL Parental clone DNA

<400> 216

eolf-seql

gatgctgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc	60
atctcttgca ggtctagtca gagccttgaa aacagtaatg gaaacaccta tttgaactgg	120
tacctccaga aaccaggcca gtctccacaa ctctgatct acagggtttc caaacgattt	180
tctgggggtcc tagacagggt cagtggtagt ggatcaggga cagatttcac actgaaaatc	240
agcagagtgg aggctgagga tttgggagtt tatttctgcc tacaacttac acatgtcccg	300
tacacgttcg gaggggggac caagctggaa ataaaa	336

<210> 217
 <211> 94
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 43-45: 40% Y, 6% A/S/T/G/P/D/N/E/Q/V, 49-51: 40% N, 6%
 A/S/T/Y/G/P/D/E/Q/V, 55-57: 25% S/T/Q/E, 61-63: 25% S/T/Q/E

<220>
 <221> misc_feature
 <222> (43)..(45)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (49)..(51)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (55)..(57)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (61)..(63)
 <223> n is a, c, g or t

<400> 217	
cagctgcggg ctctgacccg gtttctggag ataccagttc agnnncgtnn ngccnnngga	60
nnnttccaga gattggctgg atttgcaaga aatg	94

eolf-seql

<210> 218
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 40-42: 30% R, 20% E, 5% A/S/T/Y/G/P/D/N/Q/V. 49-51: 30% K, 20% S,
 5% A/N/T/Y/G/P/D/E/Q/V, 55-57: 40% F, 5% A/S/T/Y/G/P/D/E/Q/V/I/L,
 58-60: 40% S, 6.6% A/T/Y/G/P/D/E/Q/V, 67-69: 50% P, 50% L

<220>
 <221> misc_feature
 <222> (40)..(42)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (49)..(51)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (55)..(57)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (58)..(60)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (67)..(69)
 <223> n is a, c, g or t

<400> 218
 ctccagaaac cgggtcagag cccgcagctg ctgatctacn nngtatctnn ncgcnnnnnn 60
 ggcgttnnng atcgtttcag cggttctgga tccggcacc 99

<210> 219
 <211> 99
 <212> DNA
 <213> Artificial Sequence

eolf-seql

<220>

<223> 40-42: 52% H, 4% G/A/S/P/T/N/Y/D/E/Q/V/I, 46-48: 30% I, 15% Y, 5% G/A/S/T/P/N/H/D/E/Q/V, 49-51: 52% Y, 4% G/A/S/P/T/N/H/D/E/Q/V/I, 52-54: 30% D, 15% G, 5% A/S/P/Y/N/H/D/E/Q/V/I, 55-57: 52% T, 4% G/A/S/P/Y/N/H/D/E/Q/V/I, 61-63: 52% T, 4% G/A/S/P/Y/N/H/D/E/Q/V/I

<220>

<221> misc_feature

<222> (40)..(42)

<223> n is a, c, g or t

<220>

<221> misc_feature

<222> (46)..(48)

<223> n is a, c, g or t

<220>

<221> misc_feature

<222> (49)..(51)

<223> n is a, c, g or t

<220>

<221> misc_feature

<222> (52)..(54)

<223> n is a, c, g or t

<220>

<221> misc_feature

<222> (55)..(57)

<223> n is a, c, g or t

<220>

<221> misc_feature

<222> (61)..(63)

<223> n is a, c, g or t

<400> 219

catccactcc agaccctggc ccggggcctg acgaacccan nncatnnnnn nnnnnnngaa 60

nnngtaacca gatgctttgc agctcacttt aacggaagc 99

<210> 220

<211> 99

<212> DNA

<213> Artificial Sequence

eolf-seql

<220>
<223> 34-36: 45% Y, 5% others, 40-42: 52% N, 4% others, 46-48: 40% Y,
5% others, 49-51: 30% N, 15% S, 5% others, 52-54: 30% D, 15% G,
5% others, 55-57: 52% G, 4% others, 61-63: 30% K, 15% N, 4%
others, 70-72: 30% E, 15% Q, 5% others

<220>
<221> misc_feature
<222> (34)..(36)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (40)..(42)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (46)..(48)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (49)..(51)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (52)..(54)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (55)..(57)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (61)..(63)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (70)..(72)
<223> n is a, c, g or t

<400> 220

eolf-seql
caggccccgg gccagggctt ggagtggatg ggcnnnattn nnccannnnn nnnnnntcc 60
nnntataccn nnaaattcca gggccgcgtc acgatgacc 99

<210> 221
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 H3 reverse constant

<400> 221
cgtcaccggt tcggggaagt agtccttgac cag 33

<210> 222
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> LMB3

<400> 222
caggaaacag ctatgaccat gattac 26

<210> 223
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 L1 forward constant

<400> 223
tggtatctcc agaaaccggg tcagagcccg cag 33

<210> 224
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> 34-36: 52% Y, 4% others, 37-39: 52% P, 4% others, 40-42: 42% V,

eolf-seq1

10% L, 4% others, 43-45: 52% H, 4% others, 46-48: 42% T, 10% I,
4% others, 49-51: 45% L, 11% G, 4% others

<220>
<221> misc_feature
<222> (34)..(36)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (37)..(39)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (40)..(42)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (43)..(45)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (46)..(48)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (49)..(51)
<223> n is a, c, g or t

<400> 224
tttaatttcc agtttagttc cttgaccgaa ggtnnnnnnn nnnnnnnnnn nctgcagaca 60

atagtagacg ccaacgtctt cagc 84

<210> 225
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 L3 forward constant

eolf-seq1

<400> 225
accttcggtc aaggaactaa actggaaatt aaacg

35

<210> 226
<211> 107
<212> DNA
<213> Artificial Sequence

<220>
<223> pos. 59-61: 50% L, 3.8% others, 62-64: 50% A, 4.2% others, 65-67:
50% S, 4.2% others, 68-70: 50% G, 4.2% others, 71-73: 50% Y, 4.2%
others, 74-76: 50% Y, 4.2% others, 77-79: 50% Y, 4.2% others,
80-82: 50% T, 4.2% others, 83-85: 50% G, 4.2% others.

<220>
<221> misc_feature
<222> (54)..(58)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (59)..(61)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (62)..(64)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (65)..(67)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (68)..(70)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (71)..(73)
<223> n is a, c, g or t

<220>
<221> misc_feature

eolf-seql

<222> (74)..(76)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (77)..(79)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (80)..(82)
 <223> n is a, c, g or t

<220>
 <221> misc_feature
 <222> (83)..(85)
 <223> n is a, c, g or t

<400> 226
 ttggtgctag cagagcttac ggtcaccgtg gtaccttggc cccagtaatc aaannnnnnn 60
 nnnnnnnnnn nnnnnnnnnn gcgtgcacaa tagtaaacag cggtgtc 107

<210> 227
 <211> 1615
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> SNAP tag human CD19 ECD- PDGFR DNA

<400> 227
 ggccgccgct agcggcatcg actacaagga cgacgatgac aaggccggca tcgatgccat 60
 catggacaaa gactgcgaaa tgaagcgac caccctggat agccctctgg gcaagctgga 120
 actgtctggg tgcgaacagg gcctgcacga gatcaagctg ctgggcaaag gaacatctgc 180
 cgccgacgcc gtggaagtgc ctgccccagc cgccgtgctg ggccggaccag agccactgat 240
 gcaggccacc gcctggctca acgcctactt tcaccagcct gaggccatcg aggagtcccc 300
 tgtgccagcc ctgcaccacc cagtgttcca gcaggagagc tttacccgcc aggtgtgtg 360
 gaaactgctg aaagtgggtga agttcggaga ggcatcagc taccagcagc tggccgccct 420
 ggccggcaat cccgccgcca ccgccgccgt gaaaaccgcc ctgagcggaa atcccgtgcc 480

eolf-seql

cattctgatc ccctgccacc ggggtggtgtc tagctctggc gccgtggggg gctacgaggg	540
cgggctcgcc gtgaaagagt ggctgctggc ccacgagggc cacagactgg gcaagcctgg	600
gctgggtgat atccccgagg aacccttggc cgtgaagggtg gaagagggcg acaatgccgt	660
gctgcagtgc ctgaaggga cctccgatgg ccctaccag cagctgacct ggtccagaga	720
gagccccctg aagcccttcc tgaagctgtc tctgggcctg cctggcctgg gcatccatat	780
gaggcctctg gccatctggc tgttcatctt caacgtgtcc cagcagatgg gcggcttcta	840
cctgtgtcag cctggcccc catctgagaa ggcttggcag cctggctgga cctgaacgt	900
ggaaggatcc ggcgagctgt tccggtggaa cgtgtccgat ctgggcggcc tgggatgcgg	960
cctgaagaac agatctagcg agggccccag cagccccagc ggcaaactga tgagcccaa	1020
gctgtacgtg tgggccaagg acagaccga gatctgggag ggcgagcctc cttgcctgcc	1080
ccctagagac agcctgaacc agagcctgag ccaggacctg acaatggccc ctggcagcac	1140
actgtggctg agctgtggcg tgccaccga ctctgtgtct agaggccctc tgagctggac	1200
ccacgtgcac cctaagggcc ctaagagcct gctgagcctg gaactgaagg acgacaggcc	1260
cgccagagat atgtgggtca tggaaaccgg cctgctgctg cctagagcca cagcccagga	1320
tgccggcaag tactactgcc acagaggcaa cctgaccatg agcttccacc tggaaatcac	1380
cgccagaccc gtgctgtggc actggctgct gagaacaggc ggctggaagg tcgacgaaca	1440
aaaactcatc tcagaagagg atctgaatgc tgtgggccag gacacgcagg aggtcatcgt	1500
ggtgccacac tccttgccct ttaagggtgt ggtgatctca gccatcctgg ccctggtggt	1560
gctcaccatc atctccctta tcatcctcat catgcttttg cagaagaagc cacgt	1615

<210> 228

<211> 1620

<212> DNA

<213> Artificial Sequence

<220>

<223> SNAP tag cynomolgus CD19 ECD- PDGFR DNA

eolf-seq1

<400> 228

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ccggccgccc ctagcggcat cgactacaag gacgacgatg acaaggccgg catcgatgcc      60
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gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct      180
gccgccgacg ccgtggaagt gcctgcccca gccgccgtgc tgggcggacc agagccactg      240
atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagtgc      300
cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccagggtgctg      360
tggaaactgc tgaaagtggg gaagttcgga gaggtcatca gctaccagca gctggccgcc      420
ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg      480
cccattctga tcccctgcc a cgggtgggtg tctagctctg gcgccgtggg gggctacgag      540
ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct      600
gggctgggtg atatcccca ggaaccctg gtcgtgaagg tggaagaggg cgacaatgcc      660
gtgctccagt gtctcgaggg cacctccgat ggccctacac agcagctcgt gtggtgcaga      720
gacagcccct tcgagccctt cctgaacctg tctctgggcc tgcctggcat gggcatcaga      780
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ggcctgaaga acagaagcag cgagggccct agcagcccca gcggcaagct gaatagcagc     1020
cagctgtacg tgtgggcaa ggacagaccc gagatgtggg agggcgagcc tgtgtgtggc     1080
ccccctagag atagcctgaa ccagagcctg agccaggacc tgacaatggc ccctggcagc     1140
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acacacgtgc ggcctaaggg ccctaagagc agcctgctga gcctggaact gaaggacgac     1260
cggcccgacc gggatatgtg ggtggtggat acaggcctgc tgctgaccag agccacagcc     1320
caggatgccg gcaagtacta ctgccacaga ggcaactgga ccaagagctt ttacctggaa     1380
atcaccgcca gacccgccct gtggcactgg ctgctgagaa tcggaggctg gaaggctcac     1440

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eolf-seql

gagcagaagc tgatctccga agaggacctg aacgccgtgg gccaggatac ccaggaagtg 1500
 atcgtggtgc cccacagcct gcccttcaag gtggtcgtga tcagcgccat tctggccctg 1560
 gtggtgctga ccatcatcag cctgatcatc ctgattatgc tgtggcagaa aaagccccgc 1620

<210> 229
 <211> 539
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SNAP tag human CD19 ECD- PDGFR

<400> 229

Pro Ala Ala Ala Ser Gly Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ala
 1 5 10 15

Gly Ile Asp Ala Ile Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr
 20 25 30

Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly
 35 40 45

Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala
 50 55 60

Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu
 65 70 75 80

Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala
 85 90 95

Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln
 100 105 110

Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys
 115 120 125

eolf-seql

Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn
130 135 140

Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val
145 150 155 160

Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val
165 170 175

Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His
180 185 190

Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Asp Ile Pro Glu Glu
195 200 205

Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val Leu Gln Cys
210 215 220

Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr Trp Ser Arg
225 230 235 240

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

Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe Ile Phe Asn
260 265 270

Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro Gly Pro Pro
275 280 285

Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val Glu Gly Ser
290 295 300

Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly Leu Gly Cys
305 310 315 320

eolf-seql

Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro Ser Gly Lys
 325 330 335

Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg Pro Glu Ile
 340 345 350

Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser Leu Asn Gln
 355 360 365

Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr Leu Trp Leu
 370 375 380

Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro Leu Ser Trp
 385 390 395 400

Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser Leu Glu Leu
 405 410 415

Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu Thr Gly Leu
 420 425 430

Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr Tyr Cys His
 435 440 445

Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr Ala Arg Pro
 450 455 460

Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys Val Asp Glu
 465 470 475 480

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr
 485 490 495

Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val
 500 505 510

eolf-seql

Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile
515 520 525

Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
530 535

<210> 230
<211> 540
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP tag cynomolgus CD19 ECD- PDGFR

<400> 230

Pro Ala Ala Ala Ser Gly Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ala
1 5 10 15

Gly Ile Asp Ala Ile Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr
20 25 30

Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly
35 40 45

Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala
50 55 60

Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu
65 70 75 80

Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala
85 90 95

Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln
100 105 110

eolf-seq1

Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys
 115 120 125

Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn
 130 135 140

Pro Ala Ala Thr Ala Ala Val Lys Thr Ala Leu Ser Gly Asn Pro Val
 145 150 155 160

Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val
 165 170 175

Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His
 180 185 190

Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Asp Ile Pro Gln Glu
 195 200 205

Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val Leu Gln Cys
 210 215 220

Leu Glu Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Val Trp Cys Arg
 225 230 235 240

Asp Ser Pro Phe Glu Pro Phe Leu Asn Leu Ser Leu Gly Leu Pro Gly
 245 250 255

Met Gly Ile Arg Met Gly Pro Leu Gly Ile Trp Leu Leu Ile Phe Asn
 260 265 270

Val Ser Asn Gln Thr Gly Gly Phe Tyr Leu Cys Gln Pro Gly Leu Pro
 275 280 285

Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Ser Val Glu Gly Ser
 290 295 300

eolf-seq1

Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly Leu Gly Cys
305 310 315 320

Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro Ser Gly Lys
325 330 335

Leu Asn Ser Ser Gln Leu Tyr Val Trp Ala Lys Asp Arg Pro Glu Met
340 345 350

Trp Glu Gly Glu Pro Val Cys Gly Pro Pro Arg Asp Ser Leu Asn Gln
355 360 365

Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr Leu Trp Leu
370 375 380

Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro Leu Ser Trp
385 390 395 400

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

Leu Lys Asp Asp Arg Pro Asp Arg Asp Met Trp Val Val Asp Thr Gly
420 425 430

Leu Leu Leu Thr Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr Tyr Cys
435 440 445

His Arg Gly Asn Trp Thr Lys Ser Phe Tyr Leu Glu Ile Thr Ala Arg
450 455 460

Pro Ala Leu Trp His Trp Leu Leu Arg Ile Gly Gly Trp Lys Val Asp
465 470 475 480

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp
485 490 495

eolf-seq1

Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val
500 505 510

Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu
515 520 525

Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
530 535 540

<210> 231
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5H09) CDR-L1

<400> 231

Lys Ser Ser Gln Ser Leu Glu Ser Ser Thr Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 232
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-5H09) CDR-L2

<400> 232

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 233
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-5H09) CDR-L3

eolf-seql

<400> 233

Leu Gln Leu Ile Asp Tyr Pro Val Thr
1 5

<210> 234

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19(8B8-5H09) CDR-H1

<400> 234

Asp Tyr Ile Met His
1 5

<210> 235

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19(8B8-5H09) CDR-H2

<400> 235

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

Gly

<210> 236

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR(8B8-5H09) CDR-H3

<400> 236

eolf-seql

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

<210> 237
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19(8B8-7H07) CDR-L1

<400> 237

Lys	Ser	Ser	Gln	Ser	Leu	Glu	Thr	Ser	Thr	Gly	Asn	Thr	Tyr	Leu	Asn
1				5					10					15	

<210> 238
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-7H07) CDR-L2

<400> 238

Arg	Val	Ser	Lys	Arg	Phe	Ser
1				5		

<210> 239
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-7H07) CDR-L3

<400> 239

Leu	Gln	Ala	Thr	His	Ile	Pro	Tyr	Thr
1				5				

<210> 240
 <211> 5

eolf-seql

<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) CDR-H1

<400> 240

Asp Tyr Ile Met His
1 5

<210> 241
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) CDR-H2

<400> 241

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

Gly

<210> 242
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) CDR-H3

<400> 242

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

<210> 243
<211> 16
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> CD19 (8B8-2B03) CDR-L1

<400> 243

Lys	Ser	Ser	Gln	Ser	Leu	Glu	Thr	Ser	Thr	Gly	Asn	Thr	Tyr	Leu	Asn
1				5					10					15	

<210> 244

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-2B03) CDR-L2

<400> 244

Arg	Val	Ser	Lys	Arg	Phe	Ser
1			5			

<210> 245

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-2B03) CDR-L3

<400> 245

Leu	Gln	Leu	Thr	His	Val	Pro	Tyr	Thr
1			5					

<210> 246

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-2B03) CDR-H1

<400> 246

eolf-seql

Asp Tyr Ile Thr His
1 5

<210> 247
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-H2

<400> 247

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

Gly

<210> 248
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-H3

<400> 248

Gly Thr Tyr Tyr Tyr Gly Pro Asp Leu Phe Asp Tyr
1 5 10

<210> 249
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L1

<400> 249

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Thr Thr Tyr Leu Asn
1 5 10 15

eolf-seql

<210> 250
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L2

<400> 250

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 251
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L3

<400> 251

Leu Gln Leu Leu Glu Asp Pro Tyr Thr
1 5

<210> 252
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-H1

<400> 252

Asp Tyr Ile Met His
1 5

<210> 253
<211> 17
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> CD19 (8B8-2B11) CDR-H2

<400> 253

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

Gly

<210> 254

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-2B11) CDR-H3

<400> 254

Gly	Thr	Tyr	Tyr	Tyr	Gly	Pro	Gln	Leu	Phe	Asp	Tyr
1				5					10		

<210> 255

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) CDR-L1

<400> 255

Lys	Ser	Ser	Gln	Ser	Leu	Glu	Thr	Ser	Thr	Gly	Asn	Thr	Tyr	Leu	Asn
1				5					10					15	

<210> 256

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

eolf-seql

<223> CD19 (8B8-5A07) CDR-L2

<400> 256

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 257

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) CDR-L3

<400> 257

Leu Gln Pro Gly His Tyr Pro Gly Thr
1 5

<210> 258

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) CDR-H1

<400> 258

Asp Tyr Ile Met His
1 5

<210> 259

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) CDR-H2

<400> 259

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

eolf-seql

Gly

<210> 260
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) CDR-H3

<400> 260

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

<210> 261
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-L1

<400> 261

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 262
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-L2

<400> 262

Arg Val Ser Lys Arg Phe Ser
1 5

eolf-seql

<210> 263
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) CDR-L3

<400> 263

Leu Gln Leu Asp Ser Tyr Pro Asn Thr
 1 5

<210> 264
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) CDR-H1

<400> 264

Asp Tyr Ile Met His
 1 5

<210> 265
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) CDR-H2

<400> 265

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

Gly

<210> 266
 <211> 12

eolf-seql

<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-H3

<400> 266

Gly	Thr	Tyr	Tyr	Tyr	Gly	Pro	Gln	Leu	Phe	Asp	Tyr
1				5					10		

<210> 267
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-L1

<400> 267

Lys	Ser	Ser	Gln	Ser	Leu	Glu	Thr	Ser	Thr	Gly	Asn	Thr	Tyr	Leu	Asn
1				5					10					15	

<210> 268
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-L2

<400> 268

Arg	Val	Ser	Lys	Arg	Phe	Ser
1				5		

<210> 269
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-L3

eolf-seql

<400> 269

Leu Gln Leu Thr His Glu Pro Tyr Thr
1 5

<210> 270

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5D08) CDR-H1

<400> 270

Asp Tyr Ile Met His
1 5

<210> 271

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5D08) CDR-H2

<400> 271

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

Gly

<210> 272

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5D08) CDR-H3

<400> 272

eolf-seql

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

<210> 273
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8) parental light chain DNA

<400> 273
 gatgctgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
 atctcttgca ggtctagtca gagccttgaa aacagtaatg gaaacaccta tttgaactgg 120
 tacctccaga aaccaggcca gtctccacaa ctctgatct acagggtttc caaacgattt 180
 tctgggggtcc tagacagggt cagtggtagt ggatcaggga cagatttcac actgaaaatc 240
 agcagagtgg aggctgagga tttgggagtt tatttctgcc tacaacttac acatgtcccg 300
 tacacgttcg gaggggggac caagctggaa ataaaacgta cggtggctgc accatctgtc 360
 ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
 ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480
 tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540
 agcagcaccc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
 gtcacccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 274
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8) parental heavy chain DNA

<400> 274
 gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagatg 60
 gcctgcaagg cttctggata cacattcact gactatatta tgcactgggt gaagcagaag 120

eolf-seql

actgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg ttctaagtac	180
actgagaagt tcaacggcaa ggccacactg acttcagaca aatcttccat cacagcctac	240
atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagagggacc	300
tattattatg gtagcgccct ctttgactac tggggccaag gcaccactct cacagtctcc	360
tcggctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tgggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctgacc tgcttgggtc aaggcttcta tcccagcgac	1140
atgcccggtg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

<210> 275

<211> 219

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> CD19 (8B8) parental light chain

<400> 275

Asp Ala 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 Glu Asn Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val Leu
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 Leu Gln Leu
85 90 95

Thr His Val Pro Tyr 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

eolf-seql

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> 276
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8) parental heavy chain

<400> 276

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

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

Ile Met His Trp Val Lys Gln Lys Thr Gly Gln Gly Leu Glu Trp Ile
35 40 45

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

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

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

eolf-seq1

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 277
<211> 657
<212> DNA
<213> Artificial Sequence

eolf-seql

<220>

<223> CD19 (8B8-2B11) light chain DNA

<400> 277

gatattgtca tgactcaaac tccactgtct ctgtccgtga ccccggttca gccagcgagc	60
atttcttgca aatccagcca atctctggaa acctccaccg gcaccacgta cctgaactgg	120
tatctccaga aaccgggtca gagcccgag ctgctgatct accgtgtatc taagcgcttc	180
tccggcgcttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc	240
agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgct ggaagatcca	300
tacaccttcg gtcaaggaac gaaactggaa attaaacgta cggtggctgc accatctgtc	360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg	420
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa	480
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	540
agcagcagcc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	600
gtcaccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt	657

<210> 278

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> CD19 (8B8-2B11) heavy chain DNA

<400> 278

caggtgcaat tggttcaatc tgggtctgaa gtaaaaaaac cgggcgcttc cgttaaagt	60
agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc	120
ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc	300
tactactacg gtccacagct gtttgattac tggggccaag gtaccacggt gaccgtaagc	360

eolf-seql

tctgctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcaccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac	1140
atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

<210> 279

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-2B11) light chain

<400> 279

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

eolf-seql

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

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

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
85 90 95

Leu Glu Asp Pro Tyr Thr Phe Gly Gln 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

eolf-seql

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

<210> 280
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) heavy chain

<400> 280

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

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

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

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

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

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

eolf-seql

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

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

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

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

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

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

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

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

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

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

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

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

eolf-seql

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

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

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 281

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> CD19 (8B8-7H07) light chain DNA

<400> 281

gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccggtca gccagcgagc 60

atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

eolf-seql

tatctccaga aaccgggtca gagcccgag ctgctgatct accgtgtatc taagcgcttc	180
tccggcgcttc ctgatcggtt cagcggttct ggatccggca ccgactttac tctgaaaatc	240
agccgtgtgg aagctgaaga cggtggcgtc tactattgtc tgcaggcaac ccatatccca	300
tacaccttcg gtcaaggaac taaactggaa attaaacgta cgggtggctgc accatctgtc	360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg	420
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa	480
tcgggtaact ccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	540
agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	600
gtcaccatc agggcctgag ctgccccgtc acaaagagct tcaacagggg agagtgt	657

<210> 282

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> CD19 (8B8-7H07) heavy chain DNA

<400> 282

cagggtgcaat tggttcaatc tgggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagt	60
agctgcaaag catctgggtta caccttcaact gactatatca tgcaactgggt tcgtcaggcc	120
ccgggccagg gtctggagtg gatgggctac attaaccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgag ttctgacgac accgctgttt actattgtgc acgcggtacc	300
tactactacg gttctgaact gtttgattac tggggccaag gtaccacggt gaccgtaagc	360
tctgctagca ccaagggcc atcggctctc cccctggcac ctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag	600

eolf-seql

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtag 900
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat 1080
 gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
 gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 283
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-7H07) light chain

<400> 283

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
 20 25 30

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

eolf-seql

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Ala
85 90 95

Thr His Ile Pro Tyr Thr Phe Gly Gln 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> 284

<211> 451

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-7H07) heavy chain

<400> 284

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Glu Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

eolf-seq1

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

eolf-seql

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> 285
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-2B03) light chain DNA

<220>
 <221> misc_feature
 <222> (320)..(321)
 <223> n is a, c, g, or t

<400> 285
 gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccggtca gccagcgagc 60
 atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120
 tatctccaga aaccgggtca gagcccgag ctgctgatct accgtgtatc taagcgcttc 180

eolf-seql

tccggcggtc ctgatcggtt cagcgggttct ggatccggca ccgactttac tctgaaaatc	240
agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagttgac ccacgttccg	300
tacaccttcg gtcaaggaan naaactggaa attaaacgta cggtaggctgc accatctgtc	360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg	420
ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgccctccaa	480
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	540
agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	600
gtcaccatc agggcctgag ctgccccgtc acaaagagct tcaacagggg agagtgt	657

<210> 286
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-2B03) heavy chain DNA

<400> 286	
cagggtgcaat tgggttcaatc tgggtgctgaa gtaaaaaaac cgggcgcttc cggttaaagtg	60
agctgcaaag catctgggta caccttcact gactatatca cgactgggt tcgtcaggcc	120
ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgag ttctgacgac accgctgttt actattgtgc acgcggtacc	300
tactactacg gtccagatct gtttgattac tggggccaag gtaccacggg gaccgtaagc	360
tctgctagca ccaaggggcc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctgggc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccacg	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660

eolf-seql

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cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg      720
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc      780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac      900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc     1020
tcaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat     1080
gagctgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc     1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg     1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1320
acgcagaaga gcctctccct gtctccgggt aaa                                  1353

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<210> 287
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-2B03) light chain

<220>
 <221> misc_feature
 <222> (107)..(107)
 <223> Xaa can be any naturally occurring amino acid

<400> 287

```

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1           5           10           15

```

```

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
          20           25           30

```

eolf-seql

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gln Gly Xaa 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

eolf-seql

<210> 288
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-2B03) heavy chain

<400> 288

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ile Thr His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Asp Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

eolf-seq1

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

eolf-seq1

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> 289
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) light chain DNA

<400> 289
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccggtca gccagcgagc 60
atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120
tatctccaga aaccgggtca gagcccgag ctgctgatct accgtgtatc taagcgcttc 180
tccggcgcttc ctgatcggtt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

eolf-seq1

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagccagg tcattaccca	300
ggtaccttcg gtcaaggaac taaactggaa attaaacgta cggcggctgc accatctgtc	360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg	420
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa	480
tcgggtaact cccaggagag tgctcacagag caggacagca aggacagcac ctacagcctc	540
agcagcacc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	600
gtcacccatc agggcctgag ctgccccgtc acaaagagct tcaacagggg agagtgt	657

<210> 290

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) heavy chain DNA

<400> 290

caggtgcaat tggttcaatc tggctgtgaa gtaaaaaaac cgggcgcttc cgttaaagtg	60
agctgcaaag catctgggta caccttcact gactatatca tgcactgggt tcgtcaggcc	120
ccgggccagg gtctggagt gatgggtac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtact	300
tactactacg gttccgccct ctttgattac tggggccaag gtaccacggt gaccgtaagc	360
tctgctagca ccaagggtccc atcggctctc cccctggcac ctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720

eolf-seql

```

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc      780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac      900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc     1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat     1080
gagctgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc     1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg     1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1320
acgcagaaga gcctctccct gtctccgggt aaa                                  1353

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<210> 291

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) light chain

<400> 291

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1           5           10          15

```

```

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
          20          25          30

```

```

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
          35          40          45

```

```

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val Pro
          50          55          60

```


eolf-seql

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Pro
85 90 95

Gly His Tyr Pro Gly Thr Phe Gly Gln 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> 292

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

eolf-seql

<223> CD19 (8B8-5A07) heavy chain

<400> 292

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

eolf-seq1

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

eolf-seql

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> 293
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) light chain DNA

<400> 293
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccggttca gccagcgagc 60
atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120
tatctccaga aaccgggtca gagcccgag ctgctgatct accgtgtatc taagcgcttc 180
tccggcgcttc ctgatcgctt cagcgggttct ggatccggca ccgactttac tctgaaaatc 240
agccgtgtgg aagctgaaga cgttggcgct tactattgtc tgcagctgac ccatgaacca 300
tacaccttcg gtcaaggaac taaactggaa attaaacgta cggaggctgc accatctgtc 360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

eolf-seql

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	540
agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	600
gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt	657

<210> 294
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5D08) heavy chain DNA

<400> 294	
cagggtgcaat tgggttcaatc tgggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg	60
agctgcaaag catctgggta caccttcact gactatatca tgcactgggt tcgtcaggcc	120
ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc	300
tactactacg gttctgaact gtttgattac tggggccaag gtaccacggt gaccgtaagc	360
tctgctagca ccaaggcccc atcggcttc cccctggcac cctcctcaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tgggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960

eolf-seql

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat 1080
 gagctgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
 gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 295
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5D08) light chain

<400> 295

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
 20 25 30

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
 85 90 95

eolf-seql

Thr His Glu Pro Tyr Thr Phe Gly Gln 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> 296

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5D08) heavy chain

<400> 296

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

eolf-seql

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Glu Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

eolf-seq1

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

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

eolf-seql

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> 297
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) light chain DNA

<400> 297
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccggtca gccagcgagc 60
atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120
tatctccaga aaccgggtca gagcccgag ctgtgatct accgtgtatc taagcgcttc 180
tccggcgcttc ctgatcggtt cagcgggttct ggatccggca ccgactttac tctgaaaatc 240
agccgtgtgg aagctgaaga cggtggcgtc tactattgtc tgcagctgga ttcttaccga 300
aacaccttcg gtcaaggaac taaactggaa attaaacgta cgggtggctgc accatctgtc 360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480
tcgggtaact cccaggagag tgacacagag caggacagca aggacagcac ctacagcctc 540
agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
gtcaccatc agggcctgag ctgccccgtc acaaagagct tcaacagggg agagtgt 657

eolf-seql

<210> 298
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) heavy chain DNA

<400> 298
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 agctgcaaag catctgggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120
 ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180
 accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240
 atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300
 tactactacg gtccacagct gtttgattac tggggccaag gtaccacggg gaccgtaagc 360
 tctgctagca ccaaggggccc atcggctctc cccctggcac cctcctcaa gagcacctct 420
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag 600
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tgggtacgtg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
 aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggc ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca cagggtgaca ccctgcccc atcccgggat 1080
 gagctgacca agaaccaggc cagcctgacc tgcctgggtc aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200

eolf-seql

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 299
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) light chain

<400> 299

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
 20 25 30

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
 85 90 95

Asp Ser Tyr Pro Asn Thr Phe Gly Gln 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

eolf-seql

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> 300
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) heavy chain

<400> 300

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

eolf-seql

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

eolf-seql

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

eolf-seql

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 301
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5H09) light chain DNA

<400> 301
 gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccggttca gccagcgagc 60
 atttcttgca aatccagcca atctctggaa tcttccaccg gcaacacgta cctgaactgg 120
 tatctccaga aaccgggtca gagcccgag ctgctgatct accgtgtatc taagcgcttc 180
 tccggcgctt ctgatcgctt cagcgggttct ggatccggca ccgactttac tctgaaaatc 240
 agccgtgtgg aagctgaaga cggtggcgct tactattgtc tgcagctgat cgattaccca 300
 gttaccttcg gtcaaggaac taaactggaa attaaacgta cgggtggctgc accatctgtc 360
 ttcaccttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
 ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgccctccaa 480
 tcgggtaact cccaggagag tgacacagag caggacagca aggacagcac ctacagcctc 540
 agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600
 gtcacccatc agggcctgag ctgccccgtc acaaagagct tcaacagggg agagtgt 657

<210> 302
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5H09) heavy chain DNA

eolf-seql

<400> 302

caggtgcaat tggttcaatc tgggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagt	60
agctgcaaag catctgggta caccttcact gactatatca tgcactgggt tcgtcaggcc	120
ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc	300
tactactacg gttctgcact gtttgattac tggggccaag gtaccacggg gaccgtaagc	360
tctgctagca ccaaggggcc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaagggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat	1080
gagctgacca agaaccagggt cagcctgacc tgcctgggtc aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

eolf-seql

<210> 303
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5H09) light chain

<400> 303

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Ser Ser
 20 25 30

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
 85 90 95

Ile Asp Tyr Pro Val Thr Phe Gly Gln 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

eolf-seql

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> 304

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5H09) heavy chain

<400> 304

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

eolf-seql

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

eolf-seql

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

eolf-seql

<210> 305
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19(8B8-2B11) Fc hole chain DNA

<400> 305
 cagggtgcaat tgggttcaatc tgggtgctgaa gtaaaaaaac cgggcgcttc cggttaaagtg 60
 agctgcaaag catctgggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120
 ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180
 accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240
 atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300
 tactactacg gtccacagct gtttgattac tggggccaag gtaccacggt gaccgtaagc 360
 tctgctagca ccaagggcc ctcctgttc cccctggccc ccagcagcaa gagcaccagc 420
 ggccggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480
 tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540
 tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcaccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
 cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca cagggtgtgca ccctgcccc atcccgggat 1080
 gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200

eolf-seql

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 306
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19(8B8-2B11) Fc hole chain

<400> 306

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

eolf-seql

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

eolf-seq1

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 307
<211> 2514
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19(8B8-2B11) Fc hole dimeric ligand chain DNA

<400> 307
cagggtgcaat tgggttcaatc tgggtgctgaa gtaaaaaaac cggg'gcgttc cgttaaagtg

60

eolf-seq1

agctgcaaag catctgggta caccttcact gactatatca tgcactgggt tcgtcaggcc	120
ccgggcccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc	300
tactactacg gtccacagct gtttgattac tggggccaag gtaccacggg gaccgtaagc	360
tctgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcacag ccgctctggg ctgcctgggc aaggactact tccccgagcc cgtgaccgtg	480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt	540
tctggcctgt atagcctgag cagcgtgggc accgtgcctt ctagcagcct gggcaccagc	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag	660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	1440
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500

eolf-seql

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
agagtgggtg ccggcgaagg atctggctct gtgtctcttg ccctgcatct gcagcctctg	1680
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	1740
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	1800
aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag	1860
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct	1920
ccaagaagcg aaggcggagg cggatctggc ggccggaggat ctagagaggg acccgaactg	1980
tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctgggtg	2040
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca	2100
gggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct	2160
aaagctgggg tgtactatgt gttttttcag ctggaactga ggccgggtggg ggctggggag	2220
ggctcaggat ctgtgtccct ggctctgcat ctgcagccac tgcgctctgc tgctggcgca	2280
gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc	2340
ttcgggttcc aaggacgcct gctgcatctg agcgccggac agcgctggg agtgcatctg	2400
catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga	2460
ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaa	2514

<210> 308

<211> 1932

<212> DNA

<213> Artificial Sequence

<220>

<223> CD19(8B8-2B11) Fc knob monomeric ligand DNA

<400> 308

caggtgcaat tggttcaatc tgggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg	60
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agctgcaaag catctgggtta caccttcact gactatatca tgcaactgggt tcgtcaggcc	120
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eolf-seq1

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc	300
tactactacg gtccacagct gtttgattac tggggccaag gtaccacggg gaccgtaagc	360
tctgctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tgggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc ctgcagagat	1080
gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta cccagcgat	1140
atgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct	1200
gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	1440
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560

eolf-seql

aaagaactgg tggtaggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620
agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 1740
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 1800
aggctgggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 1920
ccaagaagcg aa 1932

<210> 309
<211> 838
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-2B11) Fc hole dimeric ligand chain

<400> 309

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

eolf-seql

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

eolf-seql

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

eolf-seql

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu
645 650 655

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
660 665 670

eolf-seql

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
675 680 685

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
690 695 700

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
705 710 715 720

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
725 730 735

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
740 745 750

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
755 760 765

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
770 775 780

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
785 790 795 800

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
805 810 815

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825 830

Pro Ser Pro Arg Ser Glu
835

<210> 310

<211> 644

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19(8B8-2B11) Fc knob monomeric ligand

<400> 310

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

eolf-seq1

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

eolf-seql

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

eolf-seql

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

Pro Arg Ser Glu

<210> 311
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19(8B8-2B11) Fc hole dimeric ligand (71-248) chain DNA

<400> 311
caggtgcaat tgggttcaatc tgggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 60
agctgcaaag catctgggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120
ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300
tactactacg gtccacagct gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

eolf-seq1

tctgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcacag ccgctctggg ctgcctgggtc aaggactact tccccgagcc cgtgaccgtg	480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt	540
tctggcctgt atagcctgag cagcgtgggtc accgtgcctt ctagcagcct gggcaccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag	660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccctgatgat cctgccggac tgctggacct gcggcaggga	1440
atgtttgccc agctgggtgg ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tgggtggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	1680
agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc	1740
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	1800

eolf-seql

aggctgggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag	1860
ggcgcctacag tgctgggcct gttcagagtg acccccgaga ttccagcagg cctgggaggc	1920
ggcggatctg gcggcggagg atctagagaa ggacccgagc tgtccccga cgatcccgt	1980
gggctgctgg atctgagaca gggcatgttc gctcagctgg tggctcagaa tgtgctgctg	2040
attgacggac ctctgagctg gtactccgac ccagggctgg cagggggtgtc cctgactggg	2100
ggactgtcct acaaagaaga tacaaaagaa ctggtggtgg ctaaagctgg ggtgtactat	2160
gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc	2220
ctggctctgc atctgcagcc actgcgtctt gcagcagggg ctgcagcact ggccctgact	2280
gtggacctgc cccagcttc ttccgaggcc agaaacagcg ccttcgggtt ccaaggacgc	2340
ctgctgcatc tgagcgccgg acagcgcttg ggagtgcac tgcatactga agccagagcc	2400
cggcatgctt ggcagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct	2460
gagatcccag ccgggctc	2478

<210> 312
 <211> 1914
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD19(8B8-2B11) Fc knob monomeric (71-248) ligand DNA

<400> 312	
caggtgcaat tggttcaatc tggctgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg	60
agctgcaaag catctgggta caccttcact gactatatca tgcactgggt tcgtcaggcc	120
ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat	180
accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac	240
atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcgtacc	300
tactactacg gtccacagct gtttgattac tggggccaag gtaccacggt gaccgtaagc	360
tctgctagca ccaagggcc atcggctctt cccctggcac cctcctccaa gagcacctct	420

eolf-seq1

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtaca ccctgcccc ctgcagagat	1080
gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta cccagcgat	1140
atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct	1200
gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccctgatgat cctgccggac tgctggacct gcggcaggga	1440
atgtttgccc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tgggtggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	1680
agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc	1740
gaggcccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	1800
aggctgggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag	1860

eolf-seql

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg gctc

1914

<210> 313

<211> 826

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19(8B8-2B11) Fc hole dimeric ligand (71-248) chain

<400> 313

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

eolf-seql

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

eolf-seql

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
 450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
 465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
 485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
 500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
 515 520 525

eolf-seql

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
645 650 655

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
660 665 670

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
675 680 685

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
690 695 700

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
705 710 715 720

eolf-seql

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
725 730 735

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
740 745 750

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
755 760 765

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
770 775 780

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
785 790 795 800

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
805 810 815

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825

<210> 314
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-2B11) Fc knob monomeric (71-248) ligand

<400> 314

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

eolf-seql

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

eolf-seq1

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

eolf-seql

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

eolf-seql

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
625 630 635

<210> 315
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19(8B8-018) heavy chain (huIgG1 PGLALA) DNA

<400> 315
cagggtccagc tgggtgcagtc cggcgccgag gtcaagaaac ccggggccttc tgtgaagggtt 60
tcatgcaagg caagcggata caccttcacc gactatatca tgcattgggt caggcaggcc 120
cctggccaag gtctcgaatg gatgggctac attaaccat ataatgatgg ctccaaatac 180
accgagaagt ttcagggaag agtcactatg acatctgaca ccagtatcag cactgcttac 240
atggagctgt cccgccttcg gtctgatgac accgcagtgt attactgtgc caggggcaca 300
tattactacg gctcagctct gttcgactat tgggggcagg gaaccacagt aaccgtgagc 360
tccgcaagta ctaaggcccc atcggcttcc cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agcagctggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca cctcatgat ctcccgacc 780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

eolf-seql

aaggagtaca agtgcaaggt ctccaacaaa gccctcggag ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat 1080
 gagctgacca agaaccaggt cagcctgacc tgcctgggtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
 gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtccccgggc aaa 1353

<210> 316
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19(8B8-018) heavy chain (huIgG1 PGLALA)

<400> 316

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

eolf-seql

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

eolf-seql

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 317

<211> 140

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-mu CEA T84.66 VH

<400> 317

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
1 5 10 15

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val
65 70 75 80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
85 90 95

Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135 140

<210> 318

<211> 131

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> anti-mu CEA T84.66 VL

<400> 318

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
20 25 30

Val Ser Leu Gly Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser
35 40 45

Val Asp Ile Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser
65 70 75 80

Gly Ile Pro Val Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr
85 90 95

Leu Ile Ile Asp Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys
100 105 110

Gln Gln Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys
130

<210> 319

<211> 392

<212> DNA

<213> Artificial Sequence

<220>

eolf-seql

<223> heavy chain framework acceptor sequence

<400> 319

taaggggctt cctagtccta aggctgagga agggatcctg gtttagttaa agaggatttt	60
attcaccctt gtgtcctctc cacagggtgtc cagtcccagg tccagctggg gcaatctggg	120
gctgagggtga agaagcctgg gtcctcgggtg aaggctctct gcaaggcttc tggaggcacc	180
ttcagcagct atactatcag ctgggtgcga caggcccctg gacaagggtt tgagtggatg	240
ggaaggatca tccctatcct tgggtacagca aactacgcac agaagttcca gggcagagtc	300
acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct	360
gaggacacgg ccgtgtatta ctgtgcgaga ga	392

<210> 320

<211> 797

<212> DNA

<213> Artificial Sequence

<220>

<223> light chain framework acceptor sequence

<400> 320

ctgcagctgg aagctcagct cccaccagc tgctttgcat gtccctccca gctgccctac	60
cttccagagc ccatatcaat gcctgtgtca gagccctggg gaggaactgc tcagttagga	120
cccagaggga accatggaag cccagctca gcttctcttc ctctgtctac tctggctccc	180
aggtgagggg aacatgaggt ggTTTTgcac attagtga aa actcttgcca cctctgtctca	240
gcaagaaata taattaaaa tcaaagtata tcaacaattt tggctctact caaagacagt	300
tggtttgatc ttgattacat gagtgcattt ctgttttatt tccaatttca gataccaccg	360
gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggg gaaagagcca	420
ccctctcctg cagggccagt cagagtgtta gcagctactt agcctgggtac caacagaaac	480
ctggccaggc tcccaggctc ctcatctatg atgcatcaa cagggccact ggcatcccag	540
ccaggttcag tggcagtggt tctgggacag acttcactct caccatcagc agcctagagc	600
ctgaagattt tgcagtttat tactgtcagc agcgtagcaa ctggcctccc acagtgattc	660

eolf-seql

cacatgaaac aaaaacccca acaagaccat cagtgtttac tagattatta taccagctgc 720
 ttcctttaca gacagctagt ggggtggcca ctcagtgtta gcatctcagc tctatttggc 780
 cattttggag ttcaagt 797

<210> 321
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA (T84.66-LCHA) CDR-H1

<400> 321

Asp Thr Tyr Met His
 1 5

<210> 322
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66-LCHA) CDR-H2

<400> 322

Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln
 1 5 10 15

Gly

<210> 323
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66-LCHA) CDR-H3

eolf-seql

<400> 323

Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr
1 5 10

<210> 324

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA(T84.66-LCHA) CDR-L1

<400> 324

Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly Phe Leu His
1 5 10 15

<210> 325

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA(T84.66-LCHA) CDR-L2

<400> 325

Arg Ala Ser Asn Arg Ala Thr
1 5

<210> 326

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA(T84.66-LCHA) CDR-L3

<400> 326

Gln Gln Thr Asn Glu Asp Pro Tyr Thr
1 5

eolf-seql

<210> 327
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Parental CEA binder VH

<400> 327

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
 1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
 50 55 60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
 115 120

<210> 328
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>

eolf-seql

<223> Parental CEA binder VL

<400> 328

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
20 25 30

Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
50 55 60

Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp
65 70 75 80

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 329

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA(T84.66-LCHA) VH

<400> 329

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

eolf-seql

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gln Val Gln Leu Val Gln Ser
115 120 125

Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys
130 135 140

Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His Trp Val Arg Gln
145 150 155 160

Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asn
165 170 175

Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Arg Val Thr Ile Thr
180 185 190

Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
195 200 205

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val
210 215 220

eolf-seql

Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
225 230 235 240

Ser Ser

<210> 330
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA(T84.66-LCHA) VL

<400> 330

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
20 25 30

Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

eolf-seql

<210> 331
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66-LCHA) Fc hole chain DNA

<400> 331
 caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaagggtg 60
 tcctgcaagg ccagcggcctt caacatcaag gacacctaca tgcactgggt gcgccaggcc 120
 cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac 180
 gtgcccgaagt tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac 240
 atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc ccccttcggc 300
 tactacgtgt ccgactacgc catggcctat tggggccagg gcacactcgt gaccgtgtcc 360
 tctgctagca ccaaggggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc 420
 ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480
 tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540
 tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcaccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaagggtggag 660
 cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tgggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaagggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atcccgggat 1080
 gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200

eolf-seql

gtgctggact cgcacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

<210> 332
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66-LCHA) light chain DNA

<400> 332	
gagatcgtgc tgacccagag ccctgccacc ctgtcactgt ctccaggcga gagagccacc	60
ctgagctgta gagccggcga gagcgtggac atcttcggcg tgggatttct gcactggtat	120
cagcagaagc ccggccaggc cccagactg ctgatctaca gagccagcaa ccgggccaca	180
ggcatccccg ccagattttc tggctctggc agcggcaccg acttcaccct gacaatcagc	240
agcctggaac ccgaggactt cgccgtgtac tactgccagc agaccaacga ggaccctac	300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggctgcacc atctgtcttc	360
atcttcccg catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg	420
aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg	480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc	540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	600
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt	654

<210> 333
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA (T84.66-LCHA) Fc hole chain

eolf-seql

<400> 333

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val 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

eolf-seql

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

eolf-seql

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 334
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA (T84.66-LCHA) light chain

<400> 334

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
20 25 30

Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
50 55 60

eolf-seq1

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp 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> 335

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA(T84.66-LCHA) Fc hole dimeric 4-1BBL(71-254) chain DNA

eolf-seq1

<400> 335

caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaagggtg	60
tcctgcaagg ccagcggcctt caacatcaag gacacctaca tgcactgggt gcgccaggcc	120
cctggacagg gactggaatg gatgggcaga atcgaccccc ccaacggcaa cagcaaatac	180
gtgcccgaagt tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac	240
atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc ccccttcggc	300
tactacgtgt ccgactacgc catggcctat tggggccagg gcacactcgt gaccgtgtcc	360
tctgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg	480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt	540
tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcacccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag	660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaagggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atccgggat	1080
gagctgacca agaaccagggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	1440

eolf-seql

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	1680
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	1740
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	1800
aggctgggag tgcattctga cacagaggcc agggctagac acgcctggca gctgacacag	1860
ggcgctacag tgctgggcct gttcagagt acccccgaga ttccagccgg cctgccttct	1920
ccaagaagcg aaggcggagg cggatctggc ggccggaggat ctagagaggg acccgaactg	1980
tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctggtg	2040
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca	2100
ggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct	2160
aaagctgggg tgtactatgt gttttttcag ctggaactga ggcgggtggt ggctggggag	2220
ggctcaggat ctgtgtccct ggctctgcat ctgcagccac tgcgctctgc tgctggcgca	2280
gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc	2340
ttcgggttcc aaggacgcct gctgcatctg agcgccggac agcgccctggg agtgcatctg	2400
catactgaag ccagagcccc gcatgcttgg cagctgactc agggggcaac tgtgctggga	2460
ctgtttcgcg tgacacctga gatccctgcc ggactgcca gccctagatc agaa	2514

<210> 336
 <211> 1932
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66-LCHA) Fc knob monomeric 41-BBL (71-254) DNA

<400> 336	
cagggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg	60

eolf-seq1

tcctgcaagg ccagcggcctt caacatcaag gacacctaca tgcactgggt gcgccaggcc	120
cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac	180
gtgccaagt tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac	240
atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc ccccttcggc	300
tactacgtgt ccgactacgc catggcctat tggggccagg gcacactcgt gaccgtgtcc	360
tctgctagca ccaagggccc atcggctctt cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc ctgcagagat	1080
gagctgacca agaaccaggt gtccctgtgg tgtctgggtc agggcttcta cccagcgat	1140
atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct	1200
gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	1440
atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500

eolf-seql

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 1560
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620
agagtgggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 1740
gaggccccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 1800
aggctggggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 1920
ccaagaagcg aa 1932

<210> 337
<211> 838
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA(T84.66-LCHA) Fc hole dimeric 41-BBL (71-254) chain
<400> 337

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

eolf-seq1

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

eolf-seql

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

eolf-seq1

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu
645 650 655

eolf-seq1

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
660 665 670

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
675 680 685

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
690 695 700

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
705 710 715 720

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
725 730 735

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
740 745 750

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
755 760 765

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
770 775 780

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
785 790 795 800

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
805 810 815

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825 830

Pro Ser Pro Arg Ser Glu
835

eolf-seql

<210> 338

<211> 644

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA(T84.66-LCHA) Fc knob monomeric 4-1BBL (71-254) chain

<400> 338

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

eolf-seql

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

eolf-seql

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

eolf-seql

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

Pro Arg Ser Glu

<210> 339

<211> 2478

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA (T84.66-LCHA) Fc hole dimeric 4-1BBL (71-248) chain DNA

<400> 339

caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg ccagcggctt caacatcaag gacacctaca tgcactgggt gcgccaggcc 120

cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccgaagt tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc ccccttcggc 300

eolf-seq1

tactacgtgt ccgactacgc catggcctat tggggccagg gcacactcgt gaccgtgtcc	360
tctgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcacag ccgctctggg ctgcctgggtc aaggactact tccccgagcc cgtgaccgtg	480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt	540
tctggcctgt atagcctgag cagcgtgggtc accgtgcctt ctagcagcct gggcaccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag	660
ccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccctgatgat cctgccggac tgctggacct gcggcaggga	1440
atgtttgccc agctggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tggtaggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	1680
agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc	1740

eolf-seq1

gaggccccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	1800
aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag	1860
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagcagg cctgggaggc	1920
ggcggatctg gcggcggagg atctagagaa ggacccgagc tgtccccga cgatcccgt	1980
gggctgctgg atctgagaca gggcatgttc gctcagctgg tggctcagaa tgtgctgtg	2040
attgacggac ctctgagctg gtactccgac ccagggtctg cagggtgtc cctgactggg	2100
ggactgtcct acaaagaaga taaaaaaga ctggtggtgg ctaaagctgg ggtgtactat	2160
gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc	2220
ctggctctgc atctgcagcc actgcgtct gcagcagggg ctgcagcact ggccctgact	2280
gtggacctgc cccagcttc ttccgaggcc agaaacagcg ccttcgggtt ccaaggacgc	2340
ctgctgcatac tgagcgccgg acagcgctg ggagtgcatac tgcatactga agccagagcc	2400
cggcatgctt ggcagctgac tcagggggca actgtgctgg gactgtttcg cgtgacacct	2460
gagatcccag ccgggctc	2478

<210> 340

<211> 1914

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA (T84.66-LCHA) Fc knob monomeric (71-248) 4-1BBL chain DNA

<400> 340

caggtgcagc tggcgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaagggtg	60
tcctgcaagg ccagcggctt caacatcaag gacacctaca tgcactgggt gcgccaggcc	120
cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac	180
gtgcccgaagt tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac	240
atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc ccccttcggc	300
tactacgtgt ccgactacgc catggcctat tggggccagg gcacactcgt gaccgtgtcc	360

eolf-seq1

tctgctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcaccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc	780
cctgaggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtag	900
aacagcacgt accgtgtgggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
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gagctgacca agaaccaggt gtccctgtgg tgtctgggtca agggcttcta cccagcgat	1140
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gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccctgatgat cctgccggac tgctggacct gcggcaggga	1440
atgtttgccc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tgggtggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	1680
agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc	1740
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	1800

eolf-seql

aggctgggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg gctc 1914

<210> 341

<211> 826

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA (T84.66-LCHA) Fc hole dimeric 4-1BBL (71-248) chain

<400> 341

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

eolf-seql

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

eolf-seql

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

eolf-seq1

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Gly Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro Glu Leu Ser Pro
645 650 655

Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln
660 665 670

Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr
675 680 685

Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr
690 695 700

eolf-seql

Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr
705 710 715 720

Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser
725 730 735

Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala
740 745 750

Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser
755 760 765

Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu
770 775 780

Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
785 790 795 800

Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe
805 810 815

Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825

<210> 342

<211> 638

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA (T84.66-LCHA) Fc knob monomeric (71-248) 4-1BBL chain

<400> 342

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

eolf-seql

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val 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

eolf-seql

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

eolf-seql

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

eolf-seql

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
625 630 635

<210> 343
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA(T84.66) Fc hole chain DNA

<400> 343
gagggtgcagc tgcagcagtc tggcgccgaa ctggtggaac ctggcgcctc tgtgaagctg 60
agctgtaccg ccagcggctt caacatcaag gacacctaca tgcactgggt caagcagcgg 120
cctgagcagg gcctggaatg gatcggcaga atcgaccccg ccaacggcaa cagcaaatac 180
gtgccaagt tccagggcaa ggccaccatc accgccgaca ccagcagcaa cacagcctac 240
ctgcagctga ccagcctgac ctccgaggac accgccgtgt actactgcgc ccccttcggc 300
tactacgtgt ccgactacgc catggcctat tggggccagg gcacaagcgt gaccgtgtcc 360
tctgctagca ccaaggggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc 420
ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540
tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcaccag 600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
ccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctccggacc 780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac 900

eolf-seql

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

<210> 344
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti- CEA(T84.66) light chain DNA

<400> 344	
gacatcgtgc tgaccagag ccctgcctct ctggccgtgt ctctgggaca gagggccacc	60
atgtcttgca gagccggcga gagcgtggac atcttcggcg tgggatttct gacttggtat	120
cagcagaagc ccggccagcc cccaagctg ctgatctaca gagccagcaa cctggaaagc	180
ggcatccccg tgcggtttag cggcaccggc agcagaaccg acttcaccct gatcatcgac	240
cccgtggaag ccgacgacgt ggccacctac tactgccagc agaccaacga ggaccctac	300
acctttggcg gaggcaccaa gctggaaatc aagcgtacgg tggctgcacc atctgtcttc	360
atcttcccg catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg	420
aataacttct atccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg	480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc	540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	600
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt	654

eolf-seql

<210> 345
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA (T84.66) Fc hole chain

<400> 345

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
 1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
 50 55 60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
 100 105 110

Gln Gly Thr 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

eolf-seq1

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

eolf-seq1

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 346
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA (T84.66) light chain

<400> 346

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
 20 25 30

eolf-seql

Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
50 55 60

Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp
65 70 75 80

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
85 90 95

Glu Asp Pro Tyr 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

eolf-seql

<210> 347
 <211> 2514
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66) Fc hole dimeric 4-1BBL (71-254) chain DNA

<400> 347
 gaggtgcagc tgcagcagtc tggcgccgaa ctggtggaac ctggcgccctc tgtgaagctg 60
 agctgtaccg ccagcggcctt caacatcaag gacacctaca tgcactgggt caagcagcgg 120
 cctgagcagg gcctggaatg gatcggcaga atcgaccccc ccaacggcaa cagcaaatac 180
 gtgcccgaagt tccagggcaa ggccaccatc accgccgaca ccagcagcaa cacagcctac 240
 ctgcagctga ccagcctgac ctccgaggac accgccgtgt actactgcgc ccccttcggc 300
 tactacgtgt ccgactacgc catggcctat tggggccagg gcacaagcgt gaccgtgtcc 360
 tctgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc 420
 ggcgggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480
 tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540
 tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcacccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
 cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctccgggacc 780
 cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atccgggat 1080
 gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

eolf-seql

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggaggcggcg gaagcggagg aggaggatcc	1380
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc	1440
atgtttgctc agctgggtggc ccagaacgtg ctgctgatcg atggccccct gtcctggtac	1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc	1560
aaagaactgg tgggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg	1620
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg	1680
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc	1740
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag	1800
aggctgggag tgcattctgca cacagaggcc agggctagac acgcctggca gctgacacag	1860
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct	1920
ccaagaagcg aaggcggagg cggatctggc ggccggaggat ctagagaggg acccgaactg	1980
tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctggtg	2040
gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca	2100
ggggtgtccc tgactggggg actgtcctac aaagaagata caaaagaact ggtggtggct	2160
aaagctgggg tgtactatgt gttttttcag ctggaactga ggcgggtggt ggctggggag	2220
ggctcaggat ctgtgtccct ggctctgcat ctgcagccac tgcgctctgc tgctggcgca	2280
gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc	2340
ttcgggttcc aaggacgcct gctgcatctg agcgccggac agcgcttggg agtgcatctg	2400
catactgaag ccagagcccc gcatgcttgg cagctgactc agggggcaac tgtgctggga	2460
ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaa	2514

eolf-seq1

<210> 348
 <211> 1932
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66) Fc knob monomeric 4-1BBL (72-254) chain DNA

<400> 348
 gaggtgcagc tgcagcagtc tggcgccgaa ctggtggaac ctggcgccctc tgtgaagctg 60
 agctgtaccg ccagcggcctt caacatcaag gacacctaca tgcactgggt caagcagcgg 120
 cctgagcagg gcctggaatg gatcggcaga atcgaccccg ccaacggcaa cagcaaatac 180
 gtgcccgaagt tccagggcaa ggccaccatc accgccgaca ccagcagcaa cacagcctac 240
 ctgcagctga ccagcctgac ctccgaggac accgccgtgt actactgcgc ccccttcggc 300
 tactacgtgt ccgactacgc catggcctat tggggccagg gcacaagcgt gaccgtgtcc 360
 tctgctagca ccaaggggccc atcggctctt cccctggcac cctcctcaa gagcacctct 420
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag 600
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780
 cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tggtagctgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggc ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc ctgcagagat 1080
 gagctgacca agaaccaggc gtccctgtgg tgtctgggtc agggcttcta cccagcgat 1140
 atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct 1200

eolf-seql

```

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg      1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac      1320
accagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc      1380
agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc      1440
atgtttgctc agctgggtgg ccagaacgtg ctgctgatcg atggccccct gtcctggtac      1500
agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc      1560
aaagaactgg tgggtggcaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg      1620
agagtgggtg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg      1680
agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc      1740
gaggccccga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag      1800
aggctgggag tgcattctga cacagaggcc agggctagac acgcctggca gctgacacag      1860
ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct      1920
ccaagaagcg aa                                                                1932

```

<210> 349
 <211> 838
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA(T84.66) Fc hole dimeric 4-1BBL(71-254) chain

<400> 349

```

Glu Val Gln Leu Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
1           5           10           15

```

```

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20           25           30

```

```

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35           40           45

```

eolf-seql

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

Gln Gly Thr 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 Ala Ala Gly
225 230 235 240

eolf-seql

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

eolf-seql

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

eolf-seql

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

Pro Arg Ser Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu
645 650 655

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
660 665 670

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
675 680 685

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
690 695 700

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
705 710 715 720

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
725 730 735

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
740 745 750

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
755 760 765

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
770 775 780

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
785 790 795 800

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
805 810 815

eolf-seql

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
820 825 830

Pro Ser Pro Arg Ser Glu
835

<210> 350
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA(T84.66) Fc knob monomeric 4-1BBL (71-254) chain

<400> 350

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly
100 105 110

eolf-seql

Gln 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 Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

eolf-seq1

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Glu Gly Pro
450 455 460

Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly
465 470 475 480

Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro
485 490 495

eolf-seq1

Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly
500 505 510

Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala
515 520 525

Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala
530 535 540

Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu
545 550 555 560

Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro
565 570 575

Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg
580 585 590

Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr
595 600 605

Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val
610 615 620

Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser
625 630 635 640

Pro Arg Ser Glu

<210> 351
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> hu NA3B3A2-avi His DNA

eolf-seql

<400> 351

cagctgacca ccgagtccat gcccttcaac gtggccgagg gcaaagaggt gctgctgctg	60
gtccacaacc tgccccagca gctgttcggc tacagctgggt acaagggcga gcgggtggac	120
ggcaaccggc agatcgtggg ctacgccatc ggcacccagc aggccacacc cggccctgcc	180
aatagcggca gagagacaat ctaccccaac gccagcctgc tgatccagaa cgtgaccag	240
aacgacaccg gcttctacac actccaagtc atcaagagcg acctgggtcaa cgaggaagcc	300
accggccagt tccacgtgta ccccgagctg cccaagccca gcatcagcag caacaacagc	360
aagcccgtgg aagataagga cgccgtggcc tttacctgcg agcccagggc ccagaacacc	420
acctacctgt ggtgggtcaa cgccagagc ctgcccgtgt ccccagact ccagctgagc	480
aacggcaaca gaacctgac cctgttcaac gtgaccgga atgacgccag agcctacgtg	540
tgcggcatcc agaacagcgt gtccgccaac cgcagcgacc ccgtgaccct ggatgtgctg	600
tacggccccg acacccccat catcagcccc cctgacagca gctacctgag cggcgccaac	660
ctgaacctga gctgccacag cgccagcaac cccagccctc agtacagctg gcggatcaac	720
ggcatcccc agcagcacac ccaggtgctg tttatcgcca agatcacccc caacaacaac	780
ggcacctacg cctgcttcgt gtccaacctg gccaccggcc ggaacaacag catcgtgaag	840
tccatcaccg tgtccgcctc cctgagcccc gtggtggcca agcctcagat caaggccagc	900
aagaccaccg tgaccggcga caaggacagc gtgaacctga cctgctccac caacgatacc	960
ggcatcagca tccggtgggt cttcaagaat cagtccctgc ccagcagcga gcggatgaag	1020
ctgagccagg gcaacatcac cctgtccatc aaccccgtga aaagagagga cgccggcacc	1080
tattggtgcg aggtgttcaa ccccatcagc aagaaccaga gcgaccccat catgctgaac	1140
gtgaactaca acgccctgcc ccaagaaaac ctgatcaatg ttgatctgga agtgctgttc	1200
cagggcccag gcagcggcct gaacgacatc ttcgaagccc agaaaatcga gtggcacgag	1260
gccagagccc accaccacca tcaccac	1287

<210> 352

<211> 429

eolf-seql

<212> PRT

<213> Artificial Sequence

<220>

<223> hu NA3B3A2-avi-His

<400> 352

Gln Leu Thr Thr Glu Ser Met Pro Phe Asn Val Ala Glu Gly Lys Glu
1 5 10 15

Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly Tyr Ser
20 25 30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val Gly Tyr
35 40 45

Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser Gly Arg
50 55 60

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65 70 75 80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
85 90 95

Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
100 105 110

Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp Ala
115 120 125

Val Ala Phe Thr Cys Glu Pro Glu Ala Gln Asn Thr Thr Tyr Leu Trp
130 135 140

Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145 150 155 160

eolf-seql

Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp Ala
165 170 175

Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser Val Ser Ala Asn Arg Ser
180 185 190

Asp Pro Val Thr Leu Asp Val Leu Tyr Gly Pro Asp Thr Pro Ile Ile
195 200 205

Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala Asn Leu Asn Leu Ser
210 215 220

Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn
225 230 235 240

Gly Ile Pro Gln Gln His Thr Gln Val Leu Phe Ile Ala Lys Ile Thr
245 250 255

Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr
260 265 270

Gly Arg Asn Asn Ser Ile Val Lys Ser Ile Thr Val Ser Ala Ser Leu
275 280 285

Ser Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr Val
290 295 300

Thr Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp Thr
305 310 315 320

Gly Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser Ser
325 330 335

Glu Arg Met Lys Leu Ser Gln Gly Asn Ile Thr Leu Ser Ile Asn Pro
340 345 350

eolf-seql

Val Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn Pro
355 360 365

Ile Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr Asn
370 375 380

Ala Leu Pro Gln Glu Asn Leu Ile Asn Val Asp Leu Glu Val Leu Phe
385 390 395 400

Gln Gly Pro Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
405 410 415

Glu Trp His Glu Ala Arg Ala His His His His His His
420 425

<210> 353
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<223> Dimeric hu OX40L (51-183) - CL* Fc knob chain DNA

<400> 353
caggtgtccc acagataccc cagaatccag agcatcaagg tgcagttcac cgagtacaag 60
aaagagaagg gcttcatcct gaccagccag aaagaggacg agatcatgaa ggtgcaggac 120
aacagcgtga tcatcaactg cgacggcttc tacctgatca gcctgaaggg ctacttcagc 180
caggaagtgg acatcagcct gcactaccag aaggacgagg aaccctgtt ccagctgaag 240
aaagtgcgga gcgtaacag cctgatgggtg gccagcctga cctacaagga caaggtgtac 300
ctgaacgtga ccaccgacaa caccagcctg gacgacttcc acgtgaacgg cggcgagctg 360
atcctgattc accagaaccc cggcgagttc tgcgtgctgg gaggcggagg atctggcgga 420
ggcggatctc aggtgtcaca ccgctacccc cggattcagt ccattaaggt gcagtttaca 480
gagtataaga aagaaaaagg ctttattctg acttcccaga aagaagatga gattatgaag 540
gtgcaggata attctgtgat catcaattgt gacggcttct acctgatcag cctgaagggc 600

eolf-seql

tacttcagcc aggaagtgga catcagcctg cactaccaga aggacgagga acccctgttc	660
cagctgaaga aagtgcggag cgtgaacagc ctgatggtgg ccagcctgac ctacaaggac	720
aaggtgtacc tgaacgtgac caccgacaac accagcctgg acgacttcca cgtgaacggc	780
ggcgagctga tcctgatcca ccagaaccct ggcgagtctt gcgtgctggg aggcggaggc	840
tccggagggg gaggatctcg tacggtggct gcaccatctg tctttatctt cccaccacagc	900
gaccggaagc tgaagtctgg cacagccagc gtcgtgtgcc tgctgaataa cttctacccc	960
cgcgaggcca aggtgcagtg gaagggtggac aatgccctgc agagcggcaa cagccaggaa	1020
agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg	1080
agcaaggccg actacgagaa gcacaagggtg tacgcctgcg aagtgaccca ccagggcctg	1140
tctagccccg tgaccaagag cttcaaccgg ggcgagtgcg acaagaccca cacctgtcct	1200
ccatgccctg cccctgaagc tgctggcggc cctagcgtgt tcctgttccc cccaaagccc	1260
aaggacaccc tgatgatcag ccggacccct gaagtgacct gcgtggtggt ggatgtgtcc	1320
cacgaggacc ctgaagtgaa gttcaattgg tacgtggacg gcgtggaagt gcacaatgcc	1380
aagaccaagc cgcgggagga gcagtacaac agcacgtacc gtgtgggtcag cgtcctcacc	1440
gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggcttc caacaaagcc	1500
ctcggcgccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag	1560
gtgtacaccc tgcccccatg ccgggatgag ctgaccaaga accaggtcag cctgtggtgc	1620
ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg	1680
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac	1740
agcaagctca ccgtggacaa gagcagggtgg cagcagggga acgtcttctc atgctccgtg	1800
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa	1860

<210> 354

<211> 738

<212> DNA

<213> Artificial Sequence

eolf-seql

<220>

<223> Monomeric hu OX40L (51-183) - CH1* DNA

<400> 354

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cagggtgtccc acagataccc cagaatccag agcatcaagg tgcagttcac cgagtacaag      60
aaagagaagg gcttcatcct gaccagccag aaagaggacg agatcatgaa ggtgcaggac      120
aacagcgtga tcatcaactg cgacggcttc tacctgatca gcctgaaggg ctacttcagc      180
caggaagtgg acatcagcct gcactaccag aaggacgagg aaccctgtt ccagctgaag      240
aaagtgcgga gcgtgaacag cctgatgggtg gccagcctga cctacaagga caaggtgtac      300
ctgaacgtga ccaccgacaa caccagcctg gacgacttcc acgtgaacgg cggcgagctg      360
atcctgattc accagaaccc cggcgagttc tgcgtgctgg gaggcggagg ttccggaggc      420
ggaggatctg ctagcacaaa gggccccagc gtgttccctc tggcccctag cagcaagagc      480
acatctggcg gaacagccgc cctgggctgc ctggtggaag attacttccc cgagcccgtg      540
accgtgtcct ggaattcttg cgccctgaca agcggcgtgc acacctttcc agccgtgctg      600
cagagcagcg gcctgtactc tctgagcagc gtcgtgacag tgcccagcag ctctctgggc      660
accagacct acatctgcaa cgtgaaccac aagcccagca acaccaaggt ggacgagaag      720
gtggaaccca agtcctgc                                     738

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<210> 355

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Dimeric hu OX40L (51-183) - CL* Fc knob chain

<400> 355

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Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe
1           5           10          15

```

```

Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu
20          25          30

```

eolf-seql

Asp Glu Ile Met Lys Val Gln Asp Asn Ser Val Ile Ile Asn Cys Asp
 35 40 45

Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asp
 50 55 60

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
 65 70 75 80

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
 85 90 95

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp
 100 105 110

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
 115 120 125

Glu Phe Cys Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 130 135 140

Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr
 145 150 155 160

Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp
 165 170 175

Glu Ile Met Lys Val Gln Asp Asn Ser Val Ile Ile Asn Cys Asp Gly
 180 185 190

Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asp Ile
 195 200 205

Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
 210 215 220

eolf-seql

Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp
225 230 235 240

Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe
245 250 255

His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
260 265 270

Phe Cys Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr
275 280 285

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Arg Lys Leu
290 295 300

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
305 310 315 320

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
325 330 335

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
340 345 350

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
355 360 365

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
370 375 380

Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp Lys Thr His Thr Cys Pro
385 390 395 400

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
405 410 415

eolf-seql

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
420 425 430

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
435 440 445

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
450 455 460

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
465 470 475 480

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
485 490 495

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
500 505 510

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
515 520 525

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
530 535 540

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
545 550 555 560

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
565 570 575

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
580 585 590

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
595 600 605

eolf-seql

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615 620

<210> 356

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Monomeric hu OX40L (51-183) - CH1*

<400> 356

Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe
1 5 10 15

Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu
20 25 30

Asp Glu Ile Met Lys Val Gln Asp Asn Ser Val Ile Ile Asn Cys Asp
35 40 45

Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asp
50 55 60

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
65 70 75 80

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
85 90 95

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp
100 105 110

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
115 120 125

eolf-seql

Glu Phe Cys Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
130 135 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145 150 155 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Glu Asp Tyr Phe
165 170 175

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
180 185 190

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
195 200 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
210 215 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Glu Lys
225 230 235 240

Val Glu Pro Lys Ser Cys
245

<210> 357
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) VH

<400> 357

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

eolf-seql

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 358
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-2B11) VL

<400> 358

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
 20 25 30

Thr Gly Thr Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

eolf-seql

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
85 90 95

Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 359

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-7H07) VH

<400> 359

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

eolf-seql

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Glu Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 360
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-7H07) VL

<400> 360

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
 20 25 30

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Ala
 85 90 95

Thr His Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

eolf-seql

<210> 361
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-2B03) VH

<400> 361

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ile Thr His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Asp Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 362
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>

eolf-seql

<223> CD19 (8B8-2B03) VL

<220>

<221> misc_feature

<222> (107)..(107)

<223> Xaa can be any naturally occurring amino acid

<400> 362

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Thr	Pro	Gly
1				5				10					15		

Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Glu	Thr	Ser
			20				25						30		

Thr	Gly	Asn	Thr	Tyr	Leu	Asn	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35				40						45			

Pro	Gln	Leu	Leu	Ile	Tyr	Arg	Val	Ser	Lys	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	Val	Gly	Val	Tyr	Tyr	Cys	Leu	Gln	Leu
			85					90						95	

Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Xaa	Lys	Leu	Glu	Ile	Lys
			100					105					110		

<210> 363

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) VH

<400> 363

eolf-seql

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 364

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) VL

<400> 364

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

eolf-seql

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Pro
85 90 95

Gly His Tyr Pro Gly Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 365
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) VH

<400> 365

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

eolf-seql

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Glu Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 366

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5D08) VL

<400> 366

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
85 90 95

eolf-seql

Thr His Glu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 367
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) VH

<400> 367

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

eolf-seql

<210> 368
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5B08) VL

<400> 368

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
 20 25 30

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
 85 90 95

Asp Ser Tyr Pro Asn Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 369
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 (8B8-5H09) VH

<400> 369

eolf-seql

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Ala Leu Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 370

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> CD19 (8B8-5H09) VL

<400> 370

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Ser Ser
20 25 30

eolf-seql

Thr Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys 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 Val Gly Val Tyr Tyr Cys Leu Gln Leu
85 90 95

Ile Asp Tyr Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 371
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> dimeric huOX40L (51-183) connected by (G4S)₂ linker

<400> 371

Gln Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe
1 5 10 15

Thr Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu
20 25 30

Asp Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp
35 40 45

Gly Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn
50 55 60

eolf-seq1

Ile Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys
65 70 75 80

Lys Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys
85 90 95

Asp Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp
100 105 110

Phe His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly
115 120 125

Glu Phe Cys Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr
145 150 155 160

Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp
165 170 175

Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly
180 185 190

Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile
195 200 205

Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
210 215 220

Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp
225 230 235 240

Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe
245 250 255

eolf-seq1

His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
260 265 270

Phe Cys Val Leu
275

<210> 372

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> dimeric huOX40L (52-183) connected by (G4S)₂ linker

<400> 372

Val Ser His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr
1 5 10 15

Glu Tyr Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp
20 25 30

Glu Ile Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly
35 40 45

Phe Tyr Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile
50 55 60

Ser Leu His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys
65 70 75 80

Val Arg Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp
85 90 95

Lys Val Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe
100 105 110

His Val Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu
115 120 125

eolf-seql

Phe Cys Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Ser
 130 135 140

His Arg Tyr Pro Arg Ile Gln Ser Ile Lys Val Gln Phe Thr Glu Tyr
 145 150 155 160

Lys Lys Glu Lys Gly Phe Ile Leu Thr Ser Gln Lys Glu Asp Glu Ile
 165 170 175

Met Lys Val Gln Asn Asn Ser Val Ile Ile Asn Cys Asp Gly Phe Tyr
 180 185 190

Leu Ile Ser Leu Lys Gly Tyr Phe Ser Gln Glu Val Asn Ile Ser Leu
 195 200 205

His Tyr Gln Lys Asp Glu Glu Pro Leu Phe Gln Leu Lys Lys Val Arg
 210 215 220

Ser Val Asn Ser Leu Met Val Ala Ser Leu Thr Tyr Lys Asp Lys Val
 225 230 235 240

Tyr Leu Asn Val Thr Thr Asp Asn Thr Ser Leu Asp Asp Phe His Val
 245 250 255

Asn Gly Gly Glu Leu Ile Leu Ile His Gln Asn Pro Gly Glu Phe Cys
 260 265 270

Val Leu

<210> 373

<211> 164

<212> PRT

<213> Artificial Sequence

<220>

eolf-seql

<223> hu 4-1BBL (85-248)

<400> 373

Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val
1 5 10 15

Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala
20 25 30

Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu
35 40 45

Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu
50 55 60

Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala
65 70 75 80

Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala
85 90 95

Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala
100 105 110

Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu
115 120 125

Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu
130 135 140

Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile
145 150 155 160

Pro Ala Gly Leu

eolf-seql

<210> 374
 <211> 169
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hu 4-1BBL (80-248)

<400> 374

Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
 1 5 10 15

Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
 20 25 30

Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
 35 40 45

Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
 50 55 60

Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
 65 70 75 80

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 85 90 95

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
 100 105 110

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 115 120 125

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 130 135 140

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 145 150 155 160

eolf-seql

Val Thr Pro Glu Ile Pro Ala Gly Leu
165

<210> 375
<211> 197
<212> PRT
<213> Artificial Sequence

<220>
<223> hu 4-1BBL (52-248)

<400> 375

Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser
1 5 10 15

Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly
20 25 30

Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn
35 40 45

Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu
50 55 60

Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys
65 70 75 80

Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu
85 90 95

Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu
100 105 110

Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu
115 120 125

eolf-seq1

Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser
 130 135 140

Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg
 145 150 155 160

Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp Gln
 165 170 175

Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu
 180 185 190

Ile Pro Ala Gly Leu
 195