LISTADO DE SECUENCIAS

<110> F. Hoffmann-La Roche AG

<120> “MOLÉCULAS DE UNIÓN A ANTÍGENO QUE COMPRENDEN UN TRÍMERO DE LIGANDO DE LA FAMILIA DE TNF”

<130> P32429-WO

<150> EP14193260.8

<151> 14-11-2014

<150> EP15183736.6

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<151> 02-10-2015

<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

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

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

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

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

<213> Secuencia artificial

<220>

<223> hu 4-1BBL (71-254) conectado mediante el enlazador (G4S)2 a 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

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

355 360 365

Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu

370 375

<210> 6

<211> 194

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL (71-254) más (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

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> 13

<211> 10

<212> PRT

<213> Secuencia artificial

<220>

<223> enlazador peptídico (G4S)2

<400> 13

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10

<210> 14

<211> 718

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-254) más CH1 más cadena Fc pomo

<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

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

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

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

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> Secuencia artificial

<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

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 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser

195 200 205

Asp Glu Gln 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> 28

<211> 702

<212> PRT

<213> Homo sapiens

<400> 28

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

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

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

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
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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<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

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

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

<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

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

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

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

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

<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

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

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

<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

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

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

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

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

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
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

145 150 155 160

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

<210> 42

<211> 254

<212> PRT

<213> Homo sapiens

<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 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

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

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

<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

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

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

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

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

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

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 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

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
1 5 10 15

Met Leu Pro Glu His Gly Ser Cys Arg Pro Lys Ala Arg Ser Ser Ser
20 25 30

Ala Arg Trp Ala Leu Thr Cys Cys Leu Val Leu Leu Pro Phe Leu Ala
35 40 45

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

Ala Cys Val Gln Phe Gln Ala Leu Lys Gly Gln Glu Phe Ala Pro Ser
65 70 75 80

His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
85 90 95

Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Phe Lys Asn

100 105 110

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

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

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

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

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

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

<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

<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> Secuencia artificial

<220>

<223> Enlazador peptídico (SG4)2

<400> 55

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

1 5 10

<210> 56

<211> 14

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<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> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 57

Gly Ser Pro Gly Ser Ser Ser Ser Gly Ser

1 5 10

<210> 58

<211> 20

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 58

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser

20

<210> 59

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 59

Gly Ser Gly Ser Gly Asn Gly Ser

1 5

<210> 60

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 60

Gly Gly Ser Gly Ser Gly Ser Gly

1 5

<210> 61

<211> 6

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 61

Gly Gly Ser Gly Ser Gly

1 5

<210> 62

<211> 4

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 62

Gly Gly Ser Gly

1

<210> 63

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 63

Gly Gly Ser Gly Asn Gly Ser Gly
1 5

<210> 64

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 64

Gly Gly Asn Gly Ser Gly Ser Gly
1 5

<210> 65

<211> 6

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador pept+AO0-dico

<400> 65

Gly Gly Asn Gly Ser Gly

1 5

<210> 66

<211> 2154

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico(71-254)-CH1 Fc de cadena de pomo

<400> 66

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag 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 agcgcctggg agtgcatctg 1020

catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 1080

ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaagggggc 1140

ggaggaagcg gagggggagg aagtgctagc accaagggcc ctagcgtgtt ccctctggcc 1200

cctagcagca agagcacaag tggaggaaca gccgccctgg gctgcctggt caaggactac 1260

ttccccgagc ccgtgaccgt gtcctggaat tctggcgccc tgacaagcgg cgtgcacaca 1320

tttccagccg tgctgcagag cagcggcctg tactctctga gcagcgtcgt gaccgtgccc 1380

tctagctctc tgggcaccca gacctacatc tgcaacgtga accacaagcc cagcaacacc 1440

aaagtggaca agaaggtgga acccaagagc tgcgacaaga cccacacctg tccccccttgc 1500

cctgcccctg aagctgctgg tggcccttcc gtgttcctgt tccccccaaa gcccaaggac 1560

accctgatga tcagccggac ccccgaagtg acctgcgtgg tggtcgatgt gtcccacgag 1620

gaccctgaag tgaagttcaa ttggtacgtg gacggcgtgg aagtgcacaa tgccaagacc 1680

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1740

caccaggact ggctgaatgg caaggagtac aagtgcaagg 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

<210> 67

<211> 903

<212> ADN

<213> Secuencia artificial

<220>

<223> Hu 4-1BBL monomérico (71-254)-CL

<400> 67

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atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 480

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 540

ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctcgtacggt ggctgcacca 600

tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 660

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 720

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 780

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 840

tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 900

tgt 903

<210> 70

<211> 309

<212> PRT

<213> Mus musculus

<400> 70

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

Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His

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

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> ADN

<213> Secuencia artificial

<220>

<223> 4-1BBL dimérico (71-254) -CH1-cadena Fc pomo

<400> 71

agaaccgagc ccagacccgc cctgaccatc accaccagcc ctaacctggg caccagagag 60

aacaacgccg accaagtgac ccccgtgtcc cacatcggca gccccaatac cacacagcag 120

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

ttccccagca gcatggaaaa caagctggtg gatcggagct ggtcccagct tctgctgctg 480

aaggccggac acagactgag cgtgggcctg agggcttatc tgcacggcgc ccaggacgcc 540

tacagagact gggagctgag ctaccccaac acaaccagct tcggcctgtt cctcgtgaag 600

cccgacaacc cttgggaagg cggcggagga tctggcggag gcggatctag aacagagcct 660

cggcctgccc tgacaattac cacatccccc aatctgggca cccgggaaaa caatgcagat 720

caagtgacac ctgtgtctca tattggctcc ccaaacacta cccagcaggg ctcccccgtg 780

tttgctaaac tgctggctaa aaatcaggcc tccctgtcta acacaacact gaactggcac 840

tcccaggacg gcgctggcag ctcttacctg agtcagggac tgcgctatga ggaagataag 900

aaagaactgg tggtggattc ccccggactg tactatgtgt ttctggaact gaaactgtcc 960

cctaccttta caaataccgg gcacaaagtg cagggatggg tgtccctggt gctgcaggct 1020

aagcctcagg tggacgattt tgataatctg gctctgacag tggaactgtt tcctagcagc 1080

atggaaaaca agctggtgga cagaagctgg tcccagctcc tgctgctgaa ggccggacac 1140

agactgagcg tgggcctgag agcctatctg cacggcgccc aggacgccta cagagactgg 1200

gagctgagct accccaacac aaccagcttc ggcctgttcc tcgtgaagcc cgacaaccct 1260

tgggaaggcg gcggaggatc tggcggaggc ggatccagag ctgatgctgc ccctaccgtg 1320

tccatcttcc cacccagcag cgagcagctg acatctgggg gagctagcgt cgtgtgcttc 1380

ctgaacaact tctaccccaa ggacatcaac gtgaagtgga agatcgacgg cagcgagcgg 1440

cagaacggcg tgctgaatag ctggaccgac caggacagca aggactccac ctacagcatg 1500

agcagcaccc tgaccctgac caaggacgag tacgagcggc acaacagcta cacatgcgag 1560

gccacccaca agaccagcac cagccccatc gtgaagtcct tcaaccggaa cgagtgcgtg 1620

cccagagact gcggctgcaa gccttgcatc tgcaccgtgc ctgaggtgtc cagcgtgttc 1680

atcttcccac ccaagcccaa ggacgtgctg accatcaccc tgacacccaa agtgacctgc 1740

gtggtggtgg ccatcagcaa ggatgacccc gaggtgcagt tcagttggtt cgtggacgac 1800

gtggaagtgc acaccgctca gaccaagccc agagaggaac agatcaacag caccttcaga 1860

agcgtgtccg agctgcccat catgcaccag gactggctga acggcaaaga attcaagtgc 1920

agagtgaaca gcgccgcctt tggcgccccc atcgagaaaa ccatctccaa gaccaagggc 1980

agacccaagg ccccccaggt gtacacaatc cccccaccca aagaacagat ggccaaggac 2040

aaggtgtccc tgacctgcat gatcaccaat ttcttcccag aggatatcac cgtggaatgg 2100

cagtggaacg gccagcccgc cgagaactac gacaacaccc agcctatcat ggacaccgac 2160

ggctcctact tcgtgtacag cgacctgaac gtgcagaagt ccaactggga ggccggcaac 2220

accttcacct gtagcgtgct gcacgagggc ctgcacaacc accacaccga gaagtccctg 2280

tcccacagcc ctggcaag 2298

<210> 72

<211> 954

<212> ADN

<213> Secuencia artificial

<220>

<223> fusión de mu 4-1BBL monomérico (71-254) -CL

<400> 72

agaaccgagc ccagacccgc cctgaccatc accaccagcc ctaacctggg caccagagag 60

aacaacgccg accaagtgac ccccgtgtcc cacatcggca gccccaatac cacacagcag 120

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

ttccccagca gcatggaaaa caagctggtg gatcggagct ggtcccagct tctgctgctg 480

aaggccggac acagactgag cgtgggcctg agggcctatc tgcatggcgc ccaggacgcc 540

tacagagact gggagctgag ctaccccaac acaaccagct tcggcctgtt cctcgtgaag 600

cccgacaacc cttgggaagg cggcggaggc tccggaggag gcggaagcgc taagaccacc 660

ccccccagcg tgtaccctct ggcccctgga tctgccgccc agaccaacag catggtgacc 720

ctgggctgcc tggtgaaggg ctacttcccc gagcctgtga ccgtgacctg gaacagcggc 780

agcctgagca gcggcgtgca cacctttcca gccgtgctgc agagcgacct gtacaccctg 840

agcagctccg tgaccgtgcc tagcagcacc tggcccagcc agacagtgac ctgcaacgtg 900

gcccaccctg ccagcagcac caaggtggac aagaaaatcg tgccccggga ctgc 954

<210> 75

<211> 766

<212> PRT

<213> Secuencia artificial

<220>

<223> mu 4-1BBL dimérico (71-254)-CH1-cadena pesada Fc DD

<400> 75

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

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

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

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

<210> 76

<211> 318

<212> PRT

<213> Secuencia artificial

<220>

<223> fusión de mu 4-1BBL monomérico (71-254) -CL

<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

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> 79

<211> 1335

<212> ADN

<213> Secuencia artificial

<220>

<223> cadena pesada de DP47 Fc agujero

<400> 79

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc 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 ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct 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

gtggtggacg 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 ccatcccggg atgagctgac caagaaccag 1080

gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtaaa 1335

<210> 80

<211> 645

<212> ADN

<213> Secuencia artificial

<220>

<223> cadena ligera de DP47

<400> 80

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta 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

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 81

<211> 445

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena pesada de DP47 Fc agujero

<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

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

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

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> Secuencia artificial

<220>

<223> cadena ligera de DP47

<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

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

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> Cinomolgo

<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

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

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> ADN

<213> Secuencia artificial

<220>

<223> cadena Fc agujero

<400> 86

gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg 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> ADN

<213> Secuencia artificial

<220>

<223> fusión de hu 4-1BB Fc pomo

<400> 87

ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag 60

atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac 120

atctgcagac agtgcaaggg cgtgttcaga acccggaaag agtgcagcag caccagcaac 180

gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag 240

caggactgca agcagggcca ggaactgacc aagaagggct gcaaggactg ctgcttcggc 300

accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc 360

aagagcgtgc tggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct 420

gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac 480

tctcctcagg tcgacgaaca gttatatttt cagggcggct cacccaaatc tgcagacaaa 540

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 600

ttcccccaa 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 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 gtaaatccgg aggcctgaac gacatcttcg aggcccagaa gattgaatgg 1260

cacgag 1266

<210> 88

<211> 1266

<212> ADN

<213> Secuencia artificial

<220>

<223> Fusión de 4-1BB de cinomolgo Fc pomo

<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 agggtatcac tgcctggggg cagagtgcag catgtgtgaa 240

caggattgta aacaaggtca agaattgaca aaaaaaggtt gtaaagactg ttgctttggg 300

acatttaatg accagaaacg tggcatctgt cgcccctgga caaactgttc tttggatgga 360

aagtctgtgc ttgtgaatgg gacgaaggag agggacgtgg tctgcggacc atctccagcc 420

gacctctctc caggagcatc ctctgcgacc ccgcctgccc ctgcgagaga gccaggacac 480

tctccgcagg tcgacgaaca gttatatttt cagggcggct cacccaaatc tgcagacaaa 540

actcacacat gcccaccgtg 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 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 gtaaatccgg aggcctgaac gacatcttcg aggcccagaa gattgaatgg 1260

cacgag 1266

<210> 89

<211> 1269

<212> ADN

<213> Secuencia artificial

<220>

<223> Fusión de 4-1BB murino Fc pomo

<400> 89

gtgcagaaca gctgcgacaa ctgccagccc ggcaccttct gccggaagta caaccccgtg 60

tgcaagagct gccccccccag caccttcagc agcatcggcg gccagcccaa ctgcaacatc 120

tgcagagtgt gcgccggcta cttccggttc aagaagttct gcagcagcac ccacaacgcc 180

gagtgcgagt gcatcgaggg cttccactgc ctgggccccc agtgcaccag atgcgagaag 240

gactgcagac ccggccagga actgaccaag cagggctgta agacctgcag cctgggcacc 300

ttcaacgacc agaacgggac cggcgtgtgc cggccttgga ccaattgcag cctggacggg 360

agaagcgtgc tgaaaaccgg caccaccgag aaggacgtcg tgtgcggccc tcccgtggtg 420

tccttcagcc ctagcaccac catcagcgtg acccctgaag gcggccctgg cggacactct 480

ctgcaggtcc tggtcgacga acagttatat tttcagggcg gctcacccaa atctgcagac 540

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 600

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga 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 cccagccccc atcgagaaaa ccatctccaa agccaaaggg 900

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 960

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1020

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1080

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1140

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1200

tccctgtctc cgggtaaatc cggaggcctg aacgacatct tcgaggccca gaagattgaa 1260

tggcacgag 1269

<210> 90

<211> 227

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena Fc agujero

<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

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> Secuencia artificial

<220>

<223> Fusión de 4-1BB humano Fc pomo

<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

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

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> Secuencia artificial

<220>

<223> Fusión de 4-1BB de cinomolgo Fc pomo

<400> 92

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

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

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

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> Secuencia artificial

<220>

<223> Fusión de 4-1BB murino Fc pomo

<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

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

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> ADN

<213> Secuencia artificial

<220>

<223> 4-1BB humano marcado con His

<400> 94

ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag 60

atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac 120

atctgcagac agtgcaaggg cgtgttcaga acccggaaag agtgcagcag caccagcaac 180

gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag 240

caggactgca agcagggcca ggaactgacc aagaagggct gcaaggactg ctgcttcggc 300

accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc 360

aagagcgtgc tggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct 420

gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac 480

tctcctcagg tcgacgaaca gttatatttt cagggcggct caggcctgaa cgacatcttc 540

gaggcccaga agatcgagtg gcacgaggct cgagctcacc accatcacca tcac 594

<210> 95

<211> 198

<212> PRT

<213> Secuencia artificial

<220>

<223> 4-1BB humano marcado con His

<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

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

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> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico conectado mediante (G4S)2

<400> 97

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

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

355 360 365

<210> 98

<211> 360

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (80-254) conectado mediante enlazador (G4S)2

<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

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

<211> 416

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (52-254) conectado mediante enlazador (G4S)2

<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

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

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> 108

<211> 718

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-254) - CH1* cadena Fc pomo

<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

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

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

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> Secuencia artificial

<220>

<223> Hu 4-1BBL monomérico (71-254)-CL*

<400> 109

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

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> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (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

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 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

225 230 235 240

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser

245 250 255

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys

260 265 270

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

275 280 285

Lys Ser Phe Asn Arg Gly Glu Cys

290 295

<210> 111

<211> 756

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (52-254) - CH1* cadena Fc pomo

<400> 111

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

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

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

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

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> Secuencia artificial

<220>

<223> Hu 4-1BBL monomérico (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

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

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> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (80-254) - CH1* cadena Fc pomo

<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

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

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

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

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> Secuencia artificial

<220>

<223> Hu 4-1BBL monomérico (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

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

275 280 285

Arg Gly Glu Cys

290

<210> 115

<211> 722

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-254) - CL* cadena Fc pomo

<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

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

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

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

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> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (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

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

<211> 722

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-254) - CL cadena Fc pomo

<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

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

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 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

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

<210> 118

<211> 297

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (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

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 Lys

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 Lys Lys Val Glu Pro Lys Ser Cys

290 295

<210> 119

<211> 710

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-248) - CL* cadena Fc pomo

<400> 119

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

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

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

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> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-248) - CH1*

<400> 120

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 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 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> 128

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<223> Enlazador peptídico G4S

<400> 128

Gly Gly Gly Gly Ser

1 5

<210> 129

<211> 2166

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-254) - CL* cadena Fc pomo

<400> 129

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag 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 agcgcctggg agtgcatctg 1020

catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 1080

ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaaaggggc 1140

ggaggttccg gagggggagg atctcgtacg gtggctgcac catctgtctt tatcttccca 1200

cccagcgacc ggaagctgaa gtctggcaca gccagcgtcg tgtgcctgct gaataacttc 1260

taccccgcg aggccaaggt gcagtggaag gtggacaatg ccctgcagag cggcaacagc 1320

caggaaagcg tgaccgagca ggacagcaag gactccacct acagcctgag cagcaccctg 1380

accctgagca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag 1440

ggcctgtcta gccccgtgac caagagcttc aaccggggcg agtgcgacaa gacccacacc 1500

tgtcctccat gccctgcccc tgaagctgct ggcggcccta gcgtgttcct gttccccca 1560

aagcccaagg acaccctgat gatcagccgg acccctgaag tgacctgcgt ggtggtggat 1620

gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac 1680

aatgccaaga ccaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1740

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1800

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tggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1980

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 2040

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 2100

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 2160

ggtaaa 2166

<210> 130

<211> 891

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-254) -CH1*

<400> 130

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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag 420

agactgggag tgcatctgca cacagaggcc agagccaggc acgcctggca gctgacacag 480

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg cctgcctagc 540

cctagatctg aaggcggcgg aggttccgga ggcggaggat ctgctagcac aaagggcccc 600

agcgtgttcc ctctggcccc tagcagcaag agcacatctg gcggaacagc cgccctgggc 660

tgcctggtgg aagattactt ccccgagccc gtgaccgtgt cctggaattc tggcgccctg 720

acaagcggcg tgcacacctt tccagccgtg ctgcagagca gcggcctgta ctctctgagc 780

agcgtcgtga cagtgcccag cagctctctg ggcacccaga cctacatctg caacgtgaac 840

cacaagccca gcaacaccaa ggtggacgag aaggtggaac ccaagtcctg c 891

<210> 131

<211> 2154

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-254) - CH1* cadena Fc pomo

<400> 131

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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag 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 agcgcctggg agtgcatctg 1020

catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 1080

ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaaaggggc 1140

ggaggaagcg gagggggagg aagtgctagc accaagggcc cctccgtgtt ccccctggcc 1200

cccagcagca agagcaccag cggcggcaca gccgctctgg gctgcctggt cgaggactac 1260

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tctagcagcc tgggcaccca gacctacatc tgcaacgtga accacaagcc cagcaacacc 1440

aaggtggacg agaaggtgga gcccaagagc tgcgacaaaa ctcacacatg cccaccgtgc 1500

ccagcacctg aagctgcagg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1560

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1620

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1680

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caccaggact ggctgaatgg caaggagtac aagtgcaagg 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

<210> 132

<211> 903

<212> ADN

<213> Secuencia artificial

<220>

<223> Hu 4-1BBL monomérico (71-254)-CL*

<400> 132

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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 480

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 540

ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctcgtacggt ggctgcacca 600

tctgtcttca tcttcccgcc atctgatcgg aagttgaaat ctggaactgc ctctgttgtg 660

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 720

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 780

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 840

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tgt 903

<210> 137

<211> 1572

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-254) - CH1* cadena Fc pomo

<400> 137

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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag 420

agactgggag tgcatctgca cacagaggcc agagccaggc acgcctggca gctgacacag 480

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg cctgcctagc 540

cctagatctg aaggcggcgg aggttccgga ggcggaggat ctgctagcac caagggcccc 600

tccgtgttcc ccctggcccc cagcagcaag agcaccagcg gcggcacagc cgctctgggc 660

tgcctggtcg aggactactt ccccgagccc gtgaccgtgt cctggaacag cggagccctg 720

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agcgtggtca ccgtgccttc tagcagcctg ggcacccaga cctacatctg caacgtgaac 840

cacaagccca gcaacaccaa ggtggacgag aaggtggagc ccaagagctg cgacaaaact 900

cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc 960

cccccaaaac ccaaggacac cctcatgatc 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 gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1380

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1440

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1500

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1560

tctccgggta aa 1572

<210> 138

<211> 1485

<212> ADN

<213> Secuencia artificial

<220>

<223> Hu 4-1BBL dimérico (71-254)-CL*

<400> 138

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atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag 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

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ggctcaggat ctgtgtccct ggctctgcat ctgcagccac tgcgctctgc tgctggcgca 900

gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc 960

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catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 1080

ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaagggggc 1140

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tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 1320

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 1380

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 1440

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 1485

<210> 139

<211> 718

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-254) - CL* cadena Fc pomo

<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

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

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

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

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> Secuencia artificial

<220>

<223> Hu 4-1BBL dimérico (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

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

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 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

<210> 143

<211> 888

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-254) -(G4S)1- CL*

<400> 143

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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga 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 aaggtggata acgccctcca atcgggtaac 720

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 780

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 840

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<210> 150

<211> 2268

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (52-254) - CH1* cadena Fc pomo

<400> 150

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ttcgcccagc tggtggccca gaacgtgctg ctgatcgatg gccccctgtc ctggtacagc 180

gatcctggac tggctggcgt gtcactgaca ggcggcctga gctacaaaga ggacaccaaa 240

gaactggtgg tggccaaggc cggcgtgtac tacgtgttct ttcagctgga actgcggaga 300

gtggtggccg gcgagggatc tggatctgtg tctctggccc tgcatctgca gcccctgaga 360

agcgctgctg gcgctgcagc tctggcactg acagtggatc tgcctcctgc cagctccgag 420

gcccggaata gcgcatttgg gtttcaaggc agactgctgc acctgtctgc cggccagagg 480

ctgggagtgc atctgcacac agaggccagg gctagacacg cctggcagct gacacagggc 540

gctacagtgc tgggcctgtt cagagtgacc cccgagattc cagccggact gcccagccct 600

agatctgaag gcggcggagg aagcggaggc ggaggatccc cttgggctgt gtctggcgct 660

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<210> 151

<211> 960

<212> ADN

<213> Secuencia artificial

<220>

<223> Hu 4-1BBL monomérico (52-254)-CL*

<400> 151

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caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 840

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<210> 152

<211> 2100

<212> ADN

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (80-254) - CH1* cadena Fc pomo

<400> 152

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ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1920

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agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 2040

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<210> 153

<211> 876

<212> ADN

<213> Secuencia artificial

<220>

<223> Hu 4-1BBL monomérico (80-254)-CL*

<400> 153

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gtgctgctga tcgatggccc cctgagctgg tacagcgatc ctggactggc tggcgtgtca 120

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gtgtactacg tgttctttca gctggaactg cggagagtgg tggccggcga aggatctggc 240

tctgtgtctc tggccctgca tctgcagccc ctgagaagcg ctgctggcgc tgcagctctg 300

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gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 720

gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc 780

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tcgcccgtca caaagagctt caacagggga gagtgt 876

<210> 154

<211> 1317

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena KK de Fc de DP47

<400> 154

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caccctgcca gcagcaccaa ggtggacaag aaaatcgtgc cccgggactg cggctgcaag 660

ccctgcatct gcaccgtgcc cgaggtgtcc agcgtgttca tcttcccacc caagcccaag 720

gacgtgctga ccatcaccct gacccccaaa gtgacctgcg tggtggtggc catcagcaag 780

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gagaactaca agaacaccca gcccatcatg aagaccgacg gcagctactt cgtgtacagc 1200

aagctgaacg tgcagaagtc caactgggag gccggcaaca ccttcacctg tagcgtgctg 1260

cacgagggcc tgcacaacca ccacaccgag aagtccctga gccactcccc cggcaag 1317

<210> 155

<211> 645

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de DP47

<400> 155

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ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct gacgttcggc 300

caggggacca aagtggaaat caaacgtgcc gatgctgcac caactgtatc gattttccca 360

ccatccagtg agcagttaac atctggaggt gcctcagtcg tgtgcttctt gaacaacttc 420

taccccaaag acatcaatgt caagtggaag attgatggca gtgaacgaca aaatggcgtc 480

ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc 540

acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag 600

acatcaactt cacccattgt caagagcttc aacaggaatg agtgt 645

<210> 156

<211> 439

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena KK de Fc de DP47

<400> 156

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

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

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> Secuencia artificial

<220>

<223> cadena ligera de DP47

<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

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> ADN

<213> Secuencia artificial

<220>

<223> 4-1BBL murino dimérico (104-309, C160S) +IBM- cadena DD de Fc de CL

<400> 158

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gaagaggaca agaaagaact ggtggtggac agccctggcc tgtactacgt gttcctggaa 300

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<210> 159

<211> 954

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de 4-1BBL murino monomérico (104-309, C160S) - CH1

<400> 159

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gaagaggaca agaaagaact ggtggtggac agccctggcc tgtactacgt gttcctggaa 300

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ctgggctgcc tggtgaaggg ctacttcccc gagcctgtga ccgtgacctg gaacagcggc 780

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agcagctccg tgaccgtgcc tagcagcacc tggcccagcc agacagtgac ctgcaacgtg 900

gcccaccctg ccagcagcac caaggtggac aagaaaatcg tgccccggga ctgc 954

<210> 160

<211> 766

<212> PRT

<213> Secuencia artificial

<220>

<223> 4-1BBL murino dimérico (104-309, C160S) +IBM- cadena DD de Fc de CL

<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
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

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

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

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> Secuencia artificial

<220>

<223> ADN de 4-1BBL murino monomérico (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

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

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> 165

<211> 2166

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu 4-1BBL dimérico (71-254) - CL cadena Fc pomo

<400> 165

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag 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 agcgcctggg agtgcatctg 1020

catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 1080

ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaagggggc 1140

ggaggttccg gagggggagg atctcgtacg gtggccgctc cctccgtgtt tatctttccc 1200

ccatccgatg aacagctgaa aagcggcacc gcctccgtcg tgtgtctgct gaacaatttt 1260

taccctaggg aagctaaagt gcagtggaaa gtggataacg cactgcagtc cggcaactcc 1320

caggaatctg tgacagaaca ggactccaag gacagcacct actccctgtc ctccaccctg 1380

acactgtcta aggctgatta tgagaaacac aaagtctacg cctgcgaagt cacccatcag 1440

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtgacaa gacccacacc 1500

tgtccccctt gtcctgcccc tgaagctgct ggcggccctt ctgtgttcct gttccccccа 1560

aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt ggtggtggat 1620

gtgtcccacg aggaccctga agtgaagttc aattggtacg tggacggcgt ggaagtgcac 1680

aatgccaaga ccaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1740

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1800

aaagccctcg gcgcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1860

ccacaggtgt acaccctgcc cccatgccgg gatgagctga ccaagaacca ggtcagcctg 1920

tggtgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1980

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 2040

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 2100

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 2160

ggtaaa 2166

<210> 166

<211> 891

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu 4-1BBL monomérico (71-254) - CH1

<400> 166

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agaagcgctg ctggcgctgc agctctggct ctgacagtgg atctgcctcc tgccagctcc 360

gaggcccgga atagcgcatt tgggtttcaa ggccggctgc tgcacctgtc tgccggccag 420

agactgggag tgcatctgca cacagaggcc agagccaggc acgcctggca gctgacacag 480

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttcctgccgg cctgcctagc 540

cctagatctg aaggcggcgg aggttccgga ggcggaggat ctgctagcac caaaggccct 600

tccgtgtttc ctctggctcc tagctccaag tccacctctg gaggcaccgc tgctctcgga 660

tgcctcgtga aggattattt tcctgagcct gtgacagtgt cctggaatag cggagcactg 720

acctctggag tgcatacttt ccccgctgtg ctgcagtcct ctggactgta cagcctgagc 780

agcgtggtga cagtgcccag cagcagcctg ggcacccaga cctacatctg caacgtgaac 840

cacaagccca gcaacaccaa ggtggacaag aaggtggaac ccaagtcttg t 891

<210> 169

<211> 2130

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu 4-1BBL dimérico (71-248) - CL* cadena de Fc pomo

<400> 169

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 360

gaggcccgga 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

attgacggac ctctgagctg gtactccgac ccagggctgg caggggtgtc cctgactggg 720

ggactgtcct acaaagaaga tacaaaagaa ctggtggtgg ctaaagctgg ggtgtactat 780

gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc 840

ctggctctgc atctgcagcc actgcgctct gcagcagggg ctgcagcact ggccctgact 900

gtggacctgc ccccagcttc ttccgaggcc agaaacagcg ccttcgggtt ccaaggacgc 960

ctgctgcatc tgagcgccgg acagcgcctg ggagtgcatc tgcatactga agccagagcc 1020

cggcatgctt ggcagctgac tcaggggggca actgtgctgg gactgtttcg cgtgacacct 1080

gagatccccg ctggactggg cggaggcggt tccggagggg gaggatctcg tacggtggct 1140

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 gcacaaggtg 1380

tacgcctgcg aagtgaccca ccagggcctg tctagccccg tgaccaagag cttcaaccgg 1440

ggcgagtgcg acaagaccca cacctgtcct ccatgccctg cccctgaagc tgctggcggc 1500

cctagcgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccct 1560

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 1620

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac 1680

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1740

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1800

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatg ccgggatgag 1860

ctgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc 1920

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1980

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 2040

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 2100

cagaagagcc tctccctgtc tccgggtaaa 2130

<210> 170

<211> 873

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu 4-1BBL monomérico (71-248) - CH1*

<400> 170

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 480

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg actgggaggc 540

ggaggttccg gaggcggagg atctgctagc acaaagggcc ccagcgtgtt ccctctggcc 600

cctagcagca agagcacatc tggcggaaca gccgccctgg gctgcctggt ggaagattac 660

ttccccgagc ccgtgaccgt gtcctggaat tctggcgccc tgacaagcgg cgtgcacacc 720

tttccagccg tgctgcagag cagcggcctg tactctctga gcagcgtcgt gacagtgccc 780

agcagctctc tgggcaccca gacctacatc tgcaacgtga accacaagcc cagcaacacc 840

aaggtggacg agaaggtgga acccaagtcc tgc 873

<210> 171

<211> 2130

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu 4-1BBL dimérico (71-248) - CL cadena Fc pomo

<400> 171

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccct gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 360

gaggcccgga 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

attgacggac ctctgagctg gtactccgac ccagggctgg caggggtgtc cctgactggg 720

ggactgtcct acaaagaaga tacaaaagaa ctggtggtgg ctaaagctgg ggtgtactat 780

gtgtttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc 840

ctggctctgc atctgcagcc actgcgctct gcagcagggg ctgcagcact ggccctgact 900

gtggacctgc ccccagcttc ttccgaggcc agaaacagcg ccttcgggtt ccaaggacgc 960

ctgctgcatc tgagcgccgg acagcgcctg ggagtgcatc tgcatactga agccagagcc 1020

cggcatgctt ggcagctgac tcaggggca actgtgctgg gactgtttcg cgtgacacct 1080

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gctccctccg tgtttatctt tcccccatcc gatgaacagc tgaaaagcgg caccgcctcc 1200

gtcgtgtgtc tgctgaacaa tttttaccct agggaagcta aagtgcagtg gaaagtggat 1260

aacgcactgc agtccggcaa ctcccaggaa tctgtgacag aacaggactc caaggacagc 1320

acctactccc tgtcctccac cctgacactg tctaaggctg attatgagaa acacaaagtc 1380

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 1440

ggagagtgtg acaagaccca cacctgtccc ccttgtcctg cccctgaagc tgctggcggc 1500

ccttctgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc 1560

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 1620

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac 1680

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1740

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1800

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatg ccgggatgag 1860

ctgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc 1920

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1980

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 2040

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 2100

cagaagagcc tctccctgtc tccgggtaaa 2130

<210> 172

<211> 873

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu 4-1BBL monomérico (71-248) - CH1

<400> 172

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 60

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 120

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 180

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 240

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 300

agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 360

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 420

aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 480

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg actgggaggc 540

ggaggttccg gaggcggagg atctgctagc accaaaggcc cttccgtgtt tcctctggct 600

cctagctcca agtccacctc tggaggcacc gctgctctcg gatgcctcgt gaaggattat 660

tttcctgagc ctgtgacagt gtcctggaat agcggagcac tgacctctgg agtgcatact 720

ttccccgctg tgctgcagtc ctctggactg tacagcctga gcagcgtggt gacagtgccc 780

agcagcagcc tgggcaccca gacctacatc tgcaacgtga accacaagcc cagcaacacc 840

aaggtggaca agaaggtgga acccaagtct tgt 873

<210> 173

<211> 710

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL dimérico (71-248) - CL cadena Fc pomo

<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

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

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

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

705 710

<210> 174

<211> 291

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (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

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

b

<210> 177

<211> 2496

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena de Fc agujero de DP47 fusionada a hu 4-1BBL dimérico (71-254)

<400> 177

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 cgagtgctag caccaagggc 360

ccctccgtgt tccccctggc ccccagcagc aagagcacca gcggcggcac agccgctctg 420

ggctgcctgg tcaaggacta cttccccgag cccgtgaccg tgtcctggaa cagcggagcc 480

ctgacctccg gcgtgcacac cttccccgcc gtgctgcaga gttctggcct gtatagcctg 540

agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg 600

aaccacaagc ccagcaacac caaggtggac aagaaggtgg agcccaagag ctgcgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttcccccaa 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 caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgtg caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtggaggcgg 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 ggagagtggt ggccggcgaa 1620

ggatctggct ctgtgtctct ggccctgcat ctgcagcctc tgagaagcgc tgctggcgct 1680

gcagctctgg cactgacagt ggatctgcct cctgccagct ccgaggcccg gaatagcgca 1740

tttgggtttc aaggcaggct gctgcacctg tctgccggcc agaggctggg agtgcatctg 1800

cacacagagg ccagggctag acacgcctgg cagctgacac agggcgctac agtgctgggc 1860

ctgttcagag tgacccccga gattccagcc ggcctgcctt ctccaagaag cgaaggcgga 1920

ggcggatctg gcggcggagg atctagagag ggacccgaac tgtcccctga cgatccagcc 1980

gggctgctgg atctgagaca gggaatgttc gcccagctgg tggctcagaa tgtgctgctg 2040

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 ccttcgggtt ccaaggacgc 2340

ctgctgcatc tgagcgccgg acagcgcctg ggagtgcatc tgcatactga agccagagcc 2400

cggcatgctt ggcagctgac tcaggggggca actgtgctgg gactgtttcg cgtgacacct 2460

gagatccctg ccggactgcc aagccctaga tcagaa 2496

<210> 178

<211> 1914

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena de Fc pomo de DP47 fusionada a hu 4-1BBL monomérico (71-254)

<400> 178

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc 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 ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct 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

ttcccccaa 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 caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccctgcagag atgagctgac caagaaccag 1080

gtgtccctgt ggtgtctggt caagggcttc taccccagcg atatcgccgt ggagtgggag 1140

agcaacggcc agcctgagaa caactacaag accacccccc ctgtgctgga cagcgacggc 1200

agcttcttcc tgtactccaa actgaccgtg gacaagagcc ggtggcagca gggcaacgtg 1260

ttcagctgca gcgtgatgca cgaggccctg cacaaccact acacccagaa 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 ggagagtggt ggccggcgaa 1620

ggatctggct ctgtgtctct ggccctgcat ctgcagcctc tgagaagcgc tgctggcgct 1680

gcagctctgg cactgacagt ggatctgcct cctgccagct ccgaggcccg gaatagcgca 1740

tttgggtttc aaggcaggct gctgcacctg tctgccggcc agaggctggg agtgcatctg 1800

cacacagagg ccagggctag acacgcctgg cagctgacac agggcgctac agtgctgggc 1860

ctgttcagag tgacccccga gattccagcc ggcctgcctt ctccaagaag cgaa 1914

<210> 179

<211> 834

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena de Fc agujero de DP47 fusionada a hu 4-1BBL dimérico (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

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

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

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

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> Secuencia artificial

<220>

<223> cadena de Fc pomo de DP47 fusionada a hu 4-1BBL monomérico (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
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

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

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

625 630 635 640

<210> 181

<211> 1335

<212> ADN

<213> Secuencia artificial

<220>

<223> DP47 heavy chain (hu IgG1 PGLALA) DNA

<400> 181

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc 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 ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct 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

ttcccccaa 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 caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt 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> Secuencia artificial

<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

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

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> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-254) más enlazador (G4S)1

<400> 183

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

180 185

<210> 184

<211> 188

<212> PRT

<213> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-248) más enlazador (G4S)2

<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

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> Secuencia artificial

<220>

<223> hu 4-1BBL monomérico (71-248) más enlazador (G4S)1

<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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena de Fc pomo de ant+AO0-geno CD19 humano marcador avi

<400> 186

cccgaggaac ccctggtcgt gaaggtggaa gagggcgaca atgccgtgct gcagtgcctg 60

aagggcacct ccgatggccc tacccagcag ctgacctggt ccagagagag ccccctgaag 120

cccttcctga agctgtctct gggcctgcct ggcctgggca tccatatgag gcctctggcc 180

atctggctgt tcatcttcaa cgtgtcccag cagatgggcg gcttctacct gtgtcagcct 240

ggcccccccat ctgagaaggc ttggcagcct ggctggaccg tgaacgtgga aggatccggc 300

gagctgttcc ggtggaacgt gtccgatctg ggcggcctgg gatgcggcct gaagaacaga 360

tctagcgagg gccccagcag ccccagcggc aaactgatga gccccaagct gtacgtgtgg 420

gccaaggaca gacccgagat ctgggagggc gagcctcctt gcctgccccc tagagacagc 480

ctgaaccaga gcctgagcca ggacctgaca atggcccctg gcagcacact gtggctgagc 540

tgtggcgtgc cacccgactc tgtgtctaga ggccctctga gctggaccca cgtgcaccct 600

aagggcccta agagcctgct gagcctggaa ctgaaggacg acaggcccgc cagagatatg 660

tgggtcatgg aaaccggcct gctgctgcct agagccacag cccaggatgc cggcaagtac 720

tactgccaca gaggcaacct gaccatgagc ttccacctgg aaatcaccgc cagacccgtg 780

ctgtggcact ggctgctgag aacaggcggc tggaaggtcg acgctagcgg tggtagtccg 840

acacctccga cacccggggg tggttctgca gacaaaactc acacatgccc accgtgccca 900

gcacctgaag ccgcaggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 960

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1020

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1080

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1140

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcggagcc 1200

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1260

ctgcccccat gccgggatga gctgaccaag aaccaggtca gcctgtggtg cctggtcaaa 1320

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1380

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1440

accgtggaca agagcaggtg 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> Secuencia artificial

<220>

<223> cadena de Fc pomo de ant+AO0-geno CD19 humano marcador avi

<400> 187

Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val

1 5 10 15

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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena de Fc pomo de ant+AO0-geno CD19 de cinomolgo marcador avi

<400> 188

ccccaggaac ccctggtcgt gaaggtggaa gagggcgaca atgccgtgct ccagtgcctg 60

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 ccccagcggc aagctgaata gcagccagct gtacgtgtgg 420

gccaaggaca gacccgagat gtgggagggc gagcctgtgt gtggcccccc tagagatagc 480

ctgaaccaga gcctgagcca ggacctgaca atggcccctg gcagcacact gtggctgagc 540

tgtggcgtgc cacccgactc 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 cggtggtagt 840

ccgacacctc cgacacccgg gggtggttct gcagacaaaa ctcacacatg cccaccgtgc 900

ccagcacctg aagccgcagg gggaccgtca gtcttcctct tccccccaaa acccaaggac 960

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1020

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1080

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1140

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctcgga 1200

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1260

accctgcccc catgccggga tgagctgacc aagaaccagg tcagcctgtg gtgcctggtc 1320

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1380

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1440

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1500

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatccgga 1560

ggcctgaacg acatcttcga ggcccagaag attgaatggc acgag 1605

<210> 189

<211> 535

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena de Fc pomo de ant+AO0-geno CD19 de cinomolgo marcador avi

<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

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

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

515 520 525

Gln Lys Ile Glu Trp His Glu

530 535

<210> 190

<211> 6

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 humanizado (8B8) HVR-L1

<400> 190

Asn Ser Asn Gly Asn Thr

1 5

<210> 191

<211> 4

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 humanizado (8B8) HVR-H2

<400> 191

Lys Phe Asn Gly

1

<210> 192

<211> 10

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 humanizado (8B8) var. 1 a 9 HVR-H2

<400> 192

Thr Glu Lys Phe Gln Gly Arg Val Thr Met
1 5 10

<210> 193

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 (8B8) humanizado var.5 HVR-L1

<400> 193

Leu Glu Asn Pro Asn Gly Asn Thr
1 5

<210> 194

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 (8B8) humanizado var.9 HVR-L1

<400> 194

Leu Glu Asn Pro Ser Gly Asn Thr
1 5

<210> 195

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 (8B8-018) CDR-H1

<400> 195

Asp Tyr Ile Met His
1 5

<210> 196

<211> 17

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-018) CDR-L2

<400> 199

Arg Val Ser Lys Arg Phe Ser

1 5

<210> 200

<211> 9

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<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
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> Secuencia artificial

<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

Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100 105 110

<210> 203

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena Fc agujero de anti-CD19(8B8-018)

<400> 203

caggtccagc tggtgcagtc 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 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 gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660

cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de anti-CD19(8B8-018)

<400> 204

gacatcgtca tgacccagac acccctgtcc ctctctgtga cccctggcca gccagcctca 60

attagctgca agtcctctca aagtctggag aaccccaatg ggaacactta ccttaattgg 120

tatctgcaga aacccggaca atcccctcaa ctcctgatct acagggtctc taagagattc 180

tcaggcgtgc cagatcgctt tagcggttcc gggtctggca 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 acaaggtgta cgcctgcgaa 600

gtgacccacc agggcctgtc cagccccgtg accaagtcct tcaaccgggg cgagtgc 657

<210> 205

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena Fc agujero de anti-CD19(8B8-018)

<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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Lys

450

<210> 206

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de anti-CD19(8B8-018)

<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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena Fc agujero ligando dimérico de anti-CD19(8B8-018)

<400> 207

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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 gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660

cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

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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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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

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gctcagaatg tgctgctgat tgacggacct ctgagctggt actccgaccc agggctggca 2100

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catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 2460

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<210> 208

<211> 1932

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de anti-CD19(8B8-018) ligando monomérico de Fc pomo

<400> 208

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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 atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

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aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccccct 1200

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tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320

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aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860

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ccaagaagcg aa 1932

<210> 209

<211> 838

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena Fc agujero ligando dimérico de anti-CD19(8B8-018)

<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

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly 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

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

Pro Ser Pro Arg Ser Glu

835

<210> 210

<211> 644

<212> PRT

<213> Secuencia artificial

<220>

<223> anti-CD19(8B8-018) ligando monomérico de Fc pomo

<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

130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena Fc agujero ligando dimérico (71-248) de anti-CD19(8B8-018)

<400> 211

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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 gggcacccag 600

acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660

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tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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

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aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagcagg cctgggaggc 1920

ggcggatctg gcggcggagg atctagagaa ggacccgagc tgtcccccga cgatcccgct 1980

gggctgctgg atctgagaca gggcatgttc gctcagctgg tggctcagaa tgtgctgctg 2040

attgacggac ctctgagctg gtactccgac ccagggctgg caggggtgtc cctgactggg 2100

ggactgtcct acaaagaaga tacaaaagaa ctggtggtgg ctaaagctgg ggtgtactat 2160

gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc 2220

ctggctctgc atctgcagcc actgcgctct gcagcagggg ctgcagcact ggccctgact 2280

gtggacctgc ccccagcttc ttccgaggcc agaaacagcg ccttcgggtt ccaaggacgc 2340

ctgctgcatc tgagcgccgg acagcgcctg ggagtgcatc tgcatactga agccagagcc 2400

cggcatgctt ggcagctgac tcaggggggca actgtgctgg gactgtttcg cgtgacacct 2460

gagatcccag ccgggctc 2478

<210> 212

<211> 1914

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de anti-CD19(8B8-018) ligando monomérico (71-248) de Fc pomo

<400> 212

caggtccagc tggtgcagtc 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 gttcgactat tgggggcagg gaaccacagt aaccgtgagc 360

tccgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccct 1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320

acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc 1380

agagagggcc ctgagctgag ccctgatgat cctgccggac tgctggacct gcggcaggga 1440

atgtttgccc agctggtggc ccagaacgtg ctgctgatcg atggcccct gtcctggtac 1500

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 1560

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680

agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 1740

gaggcccgga 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> Secuencia artificial

<220>

<223> cadena Fc agujero ligando dimérico (71-248) de anti-CD19(8B8-018)

<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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

115 120 125

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

130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly 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 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

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> Secuencia artificial

<220>

<223> anti-CD19(8B8-018) ligando monomérico (71-248) de Fc pomo

<400> 214

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

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 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

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

625 630 635

<210> 215

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de secuencia nucleot+AO0-dica CD19 (8B8) VH clon progenitor

<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> ADN

<213> Secuencia artificial

<220>

<223> ADN de secuencia nucleot+AO0-dica CD19 (8B8) VL clon progenitor

<400> 216

gatgctgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca ggtctagtca gagccttgaa aacagtaatg gaaacaccta tttgaactgg 120

tacctccaga aaccaggcca gtctccacaa ctcctgatct acagggtttc caaacgattt 180

tctggggtcc tagacaggtt cagtggtagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tatttctgcc tacaacttac acatgtcccg 300

tacacgttcg gaggggggac caagctggaa ataaaa 336

<210> 217

<211> 94

<212> ADN

<213> Secuencia artificial

<220>

<223> 43-45: 40+AKAAJQ- Y, 6+AKAAJQ- A/S/T/G/P/D/N/E/Q/V, 49-51: 40+AKAAJQ- N, 6 +ACU-

A/S/T/Y/G/P/D/E/Q/V, 55-57: 25+AKAAJQ- S/T/Q/E, 61-63: 25+AKAAJQ- S/T/Q/E

<220>

<221> misc+AF8-feature

<222> (43)..(45)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (49)..(51)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (55)..(57)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (61)..(63)

<223> n es a, c, g o t

<400> 217

cagctgcggg ctctgacccg gtttctggag ataccagttc agnnncgtnn ngccnnngga 60

nnnttccaga gattggctgg atttgcaaga aatg 94

<210> 218

<211> 99

<212> ADN

<213> Secuencia artificial

<220>

<223> 40-42: 30+AKAAJQ- R, 20+AKAAJQ- E, 5+AKAAJQ- A/S/T/Y/G/P/D/N/Q/V. 49-51: 30+AKAAJQ- K, 20+AKAAJQ- S,

5+AKAAJQ- A/N/T/Y/G/P/D/E/Q/V, 55-57: 40+AKAAJQ- F, 5+AKAAJQ- A/S/T/Y/G/P/D/E/Q/V/I/L,

58-60: 40+AKAAJQ- S, 6,6+AKAAJQ- A/T/Y/G/P/D/E/Q/V, 67-69: 50+AKAAJQ- P, 50+AKAAJQ- L

<220>

<221> misc+AF8-feature

<222> (40)..(42)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (49)..(51)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (55)..(57)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (58)..(60)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (67)..(69)

<223> n es a, c, g o t

<400> 218

ctccagaaac cgggtcagag cccgcagctg ctgatctacn nngtatctnn ncgcnnnnnn 60

ggcgttnnng atcgtttcag cggttctgga tccggcacc 99

<210> 219

<211> 99

<212> ADN

<213> Secuencia artificial

<220>

<223> 40-42: 52+AKAAJQ- H, 4+AKAAJQ- G/A/S/P/T/N/Y/D/E/Q/V/I 46-48: 30+AKAAJQ- I, 15+AKAAJQ- Y, 5+AKAAJQ-

G/A/S/T/P/N/H/D/E/Q/V, 49-51: 52+AKAAJQ- Y, 4+AKAAJQ- G/A/S/P/T/N/H/D/E/Q/V/I,

52-54: 30+AKAAJQ- D, 15+AKAAJQ- G, 5+AKAAJQ- A/S/P/Y/N/H/D/E/Q/V/I, 55-57: 52+AKAAJQ- T, 4+AKAAJQ-

G/A/S/P/Y/N/H/D/E/Q/V/I, 61-63: 52+AKAAJQ- T, 4+AKAAJQ- G/A/S/P/Y/N/H/D/E/Q/V/I

<220>

<221> misc+AF8-feature

<222> (40)..(42)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (46)..(48)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (49)..(51)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (52)..(54)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (55)..(57)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (61)..(63)

<223> n es a, c, g o t

<400> 219

catccactcc agaccctggc ccggggcctg acgaacccan nncatnnnnn nnnnnnngaa 60

nnngtaacca gatgctttgc agctcacttt aacggaagc 99

<210> 220

<211> 99

<212> ADN

<213> Secuencia artificial

<220>

<223> 34-36: 45+AKAAJQ- Y, 5+ACU- otros, 40-42: 52+AKAAJQ- N, 4+AKAAJQ- otros, 46-48: 40+AKAAJQ- Y,

5+ACU- otros, 49-51: 30+AKAAJQ- N, 15+AKAAJQ- S, 5+ACU- otros, 52-54: 30+AKAAJQ- D, 15+AKAAJQ- G,

5+ACU- otros, 55-57: 52+AKAAJQ- G, 4+AKAAJQ- otros, 61-63: 30+AKAAJQ- K, 15+AKAAJQ- N, 4+AKAAJQ-

otros, 70-72: 30+AKAAJQ- E, 15+AKAAJQ- Q, 5+ACU- otros

<220>

<221> misc+AF8-feature

<222> (34)..(36)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (40)..(42)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (46)..(48)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (49)..(51)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (52)..(54)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (55)..(57)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (61)..(63)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (70)..(72)

<223> n es a, c, g o t

<400> 220

caggccccgg gccagggtct ggagtggatg ggcnnnattn nnccannnnn nnnnnnntcc 60

nnntataccn nnaaattcca gggccgcgtc acgatgacc 99

<210> 221

<211> 33

<212> ADN

<213> Secuencia artificial

<220>

<223> CD19 H3 inverso constante

<400> 221

cgtcaccggt tcggggaagt agtccttgac cag 33

<210> 222

<211> 26

<212> ADN

<213> Secuencia artificial

<220>

<223> LMB3

<400> 222

caggaaacag ctatgaccat gattac 26

<210> 223

<211> 33

<212> ADN

<213> Secuencia artificial

<220>

<223> CD19 L1 directo constante

<400> 223

tggtatctcc agaaaccggg tcagagcccg cag 33

<210> 224

<211> 84

<212> ADN

<213> Secuencia artificial

<220>

<223> 34-36: 52+AKAAJQ- Y, 4+AKAAJQ- otros, 37-39: 52+AKAAJQ- P, 4+AKAAJQ- otros, 40-42: 42+AKAAJQ- V,

10+AKAAJQ- L, 4+AKAAJQ- otros, 43-45: 52+AKAAJQ- H, 4+AKAAJQ- otros, 46-48: 42+AKAAJQ- T, 10+AKAAJQ- I,

4+AKAAJQ- otros, 49-51: 45+AKAAJQ- L, 11+AKAAJQ- G, 4+AKAAJQ- otros

<220>

<221> misc+AF8-feature

<222> (34)..(36)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (37)..(39)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (40)..(42)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (43)..(45)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (46)..(48)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (49)..(51)

<223> n es a, c, g o t

<400> 224

tttaatttcc agtttagttc cttgaccgaa ggtnnnnnnn nnnnnnnnnn nctgcagaca 60

atagtagacg ccaacgtctt cagc 84

<210> 225

<211> 35

<212> ADN

<213> Secuencia artificial

<220>

<223> CD19 L3 directo constante

<400> 225

accttcggtc aaggaactaa actggaaatt aaacg 35

<210> 226

<211> 107

<212> ADN

<213> Secuencia artificial

<220>

<223> pos. 59-61: 50+AKAAJQ- L, 3,8+AKAAJQ- otros, 62-64: 50+AKAAJQ- A, 4,2+AKAAJQ- otros, 65-67:

50+AKAAJQ- S, 4,2+AKAAJQ- otros, 68-70: 50+AKAAJQ- G, 4,2+AKAAJQ- otros, 71-73: 50+AKAAJQ- Y, 4,2+AKAAJQ-

otros, 74-76: 50+AKAAJQ- Y, 4,2+AKAAJQ- otros, 77-79: 50+AKAAJQ- Y, 4,2+AKAAJQ- otros,

80-82: 50+AKAAJQ- T, 4,2+AKAAJQ- otros, 83-85: 50+AKAAJQ- G, 4,2+AKAAJQ- otros.

<220>

<221> misc+AF8-feature

<222> (54)..(58)

<223> n es a, c, g, o t

<220>

<221> misc+AF8-feature

<222> (59)..(61)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (62)..(64)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (65)..(67)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (68)..(70)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (71)..(73)

<223> n es a, c, g o t

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<222> (74)..(76)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (77)..(79)

<223> n es a, c, g o t

<220>

<221> misc+AF8-feature

<222> (80)..(82)

<223> n es a, c, g o t

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<222> (83)..(85)

<223> n es a, c, g o t

<400> 226

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nnnnnnnnnn nnnnnnnnnn gcgtgcacaa tagtaaacag cggtgtc 107

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<211> 1615

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<400> 227

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actgtctggg tgcgaacagg gcctgcacga gatcaagctg ctgggcaaag gaacatctgc 180

cgccgacgcc gtggaagtgc ctgccccagc cgccgtgctg ggcggaccag agccactgat 240

gcaggccacc gcctggctca acgcctactt tcaccagcct gaggccatcg aggagttccc 300

tgtgccagcc ctgcaccacc cagtgttcca gcaggagagc tttacccgcc aggtgctgtg 360

gaaactgctg aaagtggtga agttcggaga ggtcatcagc taccagcagc tggccgccct 420

ggccggcaat cccgccgcca ccgccgccgt gaaaaccgcc ctgagcggaa atcccgtgcc 480

cattctgatc ccctgccacc gggtggtgtc tagctctggc gccgtggggg gctacgaggg 540

cgggctcgcc gtgaaagagt ggctgctggc ccacgagggc cacagactgg gcaagcctgg 600

gctgggtgat atccccgagg aacccctggt cgtgaaggtg gaagagggcg acaatgccgt 660

gctgcagtgc ctgaagggca cctccgatgg ccctacccag cagctgacct ggtccagaga 720

gagccccctg aagcccttcc tgaagctgtc tctgggcctg cctggcctgg gcatccatat 780

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<400> 228

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gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 180

gccgccgacg ccgtggaagt gcctgcccca gccgccgtgc tgggcggacc agagccactg 240

atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagttc 300

cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccaggtgctg 360

tggaaactgc tgaaagtggt gaagttcgga gaggtcatca gctaccagca gctggccgcc 420

ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg 480

cccattctga tcccctgcca ccgggtggtg tctagctctg gcgccgtggg gggctacgag 540

ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 600

gggctgggtg atatccccca ggaacccctg gtcgtgaagg tggaagaggg cgacaatgcc 660

gtgctccagt gtctcgaggg cacctccgat ggccctacac agcagctcgt gtggtgcaga 720

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atgggccctc tgggcatctg gctgctgatc ttcaacgtgt ccaaccagac cggcggcttc 840

tacctgtgtc agcctggcct gccaagcgag aaggcttggc agcctggatg gaccgtgtcc 900

gtggaaggat ctggcgagct gttccggtgg aacgtgtccg atctgggcgg cctgggatgc 960

ggcctgaaga acagaagcag cgagggccct agcagcccca gcggcaagct gaatagcagc 1020

cagctgtacg tgtgggccaa 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

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atcaccgcca gacccgccct gtggcactgg ctgctgagaa tcggaggctg gaaggtcgac 1440

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> Secuencia artificial

<220>

<223> marcador SNAP ECD de CD19 humano-PDGFR

<400> 229

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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

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

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

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> Secuencia artificial

<220>

<223> marcador SNAP ECD de CD19 de cinomolgo-PDGFR

<400> 230

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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

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

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

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> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-5H09) CDR-L3

<400> 233

Leu Gln Leu Ile Asp Tyr Pro Val Thr

1 5

<210> 234

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 (8B8-5H09) CDR-H1

<400> 234

Asp Tyr Ile Met His

1 5

<210> 235

<211> 17

<212> PRT

<213> Secuencia artificial

<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

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<400> 236

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

1 5 10

<210> 237

<211> 16

<212> PRT

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<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> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-7H07) CDR-L3

<400> 239

Leu Gln Ala Thr His Ile Pro Tyr Thr

1 5

<210> 240

<211> 5

<212> PRT

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<220>

<223> CD19 (8B8-7H07) CDR-H1

<400> 240

Asp Tyr Ile Met His

1 5

<210> 241

<211> 17

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<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

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<220>

<223> CD19 (8B8-2B03) CDR-H1

<400> 246

Asp Tyr Ile Thr His

1 5

<210> 247

<211> 17

<212> PRT

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<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

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<400> 248

Gly Thr Tyr Tyr Tyr Gly Pro Asp Leu Phe Asp Tyr

1 5 10

<210> 249

<211> 16

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<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

<210> 250

<211> 7

<212> PRT

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<223> CD19 (8B8-2B11) CDR-L2

<400> 250

Arg Val Ser Lys Arg Phe Ser

1 5

<210> 251

<211> 9

<212> PRT

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<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> Secuencia artificial

<220>

<223> CD19 (8B8-2B11) CDR-H1

<400> 252

Asp Tyr Ile Met His

1 5

<210> 253

<211> 17

<212> PRT

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<220>

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<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> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-5A07) CDR-L2

<400> 256

Arg Val Ser Lys Arg Phe Ser

1 5

<210> 257

<211> 9

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-5A07) CDR-H1

<400> 258

Asp Tyr Ile Met His

1 5

<210> 259

<211> 17

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<400> 259

Tyr Ile Asn Pro Tyr Asn Asp Gly Ser Lys Tyr Thr Glu Lys Phe Gln

1 5 10 15

Gly

<210> 260

<211> 12

<212> PRT

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<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> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-5B08) CDR-L2

<400> 262

Arg Val Ser Lys Arg Phe Ser

1 5

<210> 263

<211> 9

<212> PRT

<213> Secuencia artificial

<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

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<220>

<223> CD19 (8B8-5B08) CDR-H1

<400> 264

Asp Tyr Ile Met His

1 5

<210> 265

<211> 17

<212> PRT

<213> Secuencia artificial

<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

<212> PRT

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<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

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<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
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<210> 268

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Arg Val Ser Lys Arg Phe Ser
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<210> 269

<211> 9

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<220>

<223> CD19 (8B8-5D08) CDR-L3

<400> 269

Leu Gln Leu Thr His Glu Pro Tyr Thr

1 5

<210> 270

<211> 5

<212> PRT

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<220>

<223> CD19 (8B8-5D08) CDR-H1

<400> 270

Asp Tyr Ile Met His

1 5

<210> 271

<211> 17

<212> PRT

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<220>

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<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

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<220>

<223> CD19 (8B8-5D08) CDR-H3

<400> 272

Gly Thr Tyr Tyr Tyr Gly Ser Glu Leu Phe Asp Tyr

1 5 10

<210> 273

<211> 657

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de CD19 (8B8) cadena ligera progenitora

<400> 273

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atctcttgca ggtctagtca gagccttgaa aacagtaatg gaaacaccta tttgaactgg 120

tacctccaga aaccaggcca gtctccacaa ctcctgatct acagggtttc caaacgattt 180

tctggggtcc tagacaggtt cagtggtagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tatttctgcc tacaacttac acatgtcccg 300

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tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 274

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de CD19 (8B8) cadena pesada progenitora

<400> 274

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

tcggctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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

<210> 275

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> CD19 (8B8) cadena ligera progenitora

<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

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> Secuencia artificial

<220>

<223> CD19 (8B8) cadena pesada progenitora

<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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CD19 (8B8-2B11)

<400> 277

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atttcttgca aatccagcca atctctggaa acctccaccg gcaccacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc 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

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 278

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena pesada de CD19 (8B8-2B11)

<400> 278

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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

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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

<210> 279

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de CD19 (8B8-2B11)

<400> 279

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 280

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena pesada de CD19 (8B8-2B11)

<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

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

130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CD19 (8B8-7H07)

<400> 281

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atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcaggcaac ccatatccca 300

tacaccttcg gtcaaggaac taaactggaa 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

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 282

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena pesada de CD19 (8B8-7H07)

<400> 282

caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 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 gttctgaact gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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

<210> 283

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de CD19 (8B8-7H07)

<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

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

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena pesada de CD19 (8B8-7H07)

<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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CD19 (8B8-2B03)

<220>

<221> misc+AF8-feature

<222> (320)..(321)

<223> n es a, c, g, o t

<400> 285

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atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagttgac ccacgttccg 300

tacaccttcg gtcaaggaan naaactggaa 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

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 286

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena pesada de CD19 (8B8-2B03)

<400> 286

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agctgcaaag catctggtta caccttcact gactatatca cgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300

tactactacg gtccagatct gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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

<210> 287

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de CD19 (8B8-2B03)

<220>

<221> misc+AF8-feature

<222> (107)..(107)

<223> Xaa puede ser cualquier amino+AOE-cido de origen natural

<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

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

<210> 288

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena pesada de CD19 (8B8-2B03)

<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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CD19 (8B8-5A07)

<400> 289

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atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagccagg tcattaccca 300

ggtaccttcg gtcaaggaac taaactggaa 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

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 290

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena pesada de CD19 (8B8-5A07)

<400> 290

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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 acgcggtact 300

tactactacg gttccgccct ctttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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

<210> 291

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de CD19 (8B8-5A07)

<400> 291

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 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> Secuencia artificial

<220>

<223> cadena pesada de CD19 (8B8-5A07)

<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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CD19 (8B8-5D08)

<400> 293

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atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgac ccatgaacca 300

tacaccttcg gtcaaggaac taaactggaa 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

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 294

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena pesada de CD19 (8B8-5D08)

<400> 294

caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 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 gttctgaact gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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

<210> 295

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de CD19 (8B8-5D08)

<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

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> Secuencia artificial

<220>

<223> cadena pesada de CD19 (8B8-5D08)

<400> 296

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

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

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> 297

<211> 657

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CD19 (8B8-5B08)

<400> 297

gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc 60

atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgga ttcttaccca 300

aacaccttcg gtcaaggaac taaactggaa 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

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 298

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena pesada de CD19 (8B8-5B08)

<400> 298

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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

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

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<210> 299

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de CD19 (8B8-5B08)

<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

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> Secuencia artificial

<220>

<223> cadena pesada de CD19 (8B8-5B08)

<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

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser

355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Lys

450

<210> 301

<211> 657

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CD19 (8B8-5H09)

<400> 301

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tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgat cgattaccca 300

gttaccttcg gtcaaggaac taaactggaa 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

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 302

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena pesada de CD19 (8B8-5H09)

<400> 302

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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 gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

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cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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

<210> 303

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de CD19 (8B8-5H09)

<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

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> Secuencia artificial

<220>

<223> cadena pesada de CD19 (8B8-5H09)

<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

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

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

<210> 305

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena Fc agujero de CD19(8B8-2B11)

<400> 305

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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 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 cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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> 306

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena Fc agujero de CD19(8B8-2B11)

<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

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

130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Lys

450

<210> 307

<211> 2514

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena de ligando dimérico de Fc agujero de CD19(8B8-2B11)

<400> 307

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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 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 cccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

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aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

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ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 1920

ccaagaagcg aaggcggagg cggatctggc ggcggaggat ctagagaggg acccgaactg 1980

tcccctgacg atccagccgg gctgctggat ctgagacagg gaatgttcgc ccagctggtg 2040

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gctgcactgg ctctgactgt ggacctgcca ccagcctcta gcgaggccag aaacagcgcc 2340

ttcgggttcc aaggacgcct gctgcatctg agcgccggac agcgcctggg agtgcatctg 2400

catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 2460

ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaa 2514

<210> 308

<211> 1932

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de ligando mon+APM-erico de Fc pomo de CD19(8B8-2B11)

<400> 308

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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

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

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aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccccct 1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320

acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc 1380

agagagggcc ctgagctgag ccccgatgat cctgctggac tgctggacct gcggcagggc 1440

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 1500

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 1560

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 1740

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 1800

aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 1920

ccaagaagcg aa 1932

<210> 309

<211> 838

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena de ligando dimérico de Fc agujero de CD19(8B8-2B11)

<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

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

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

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

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

<212> PRT

<213> Secuencia artificial

<220>

<223> ligando mon+APM-erico de Fc pomo de CD19(8B8-2B11)

<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

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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena de ligando dimérico (71-248) de Fc agujero de CD19(8B8-2B11)

<400> 311

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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

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 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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

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aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620

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agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 1740

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ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagcagg cctgggaggc 1920

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ggactgtcct acaaagaaga tacaaaagaa ctggtggtgg ctaaagctgg ggtgtactat 2160

gtgttttttc agctggaact gaggcgggtg gtggctgggg agggctcagg atctgtgtcc 2220

ctggctctgc atctgcagcc actgcgctct gcagcagggg ctgcagcact ggccctgact 2280

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gagatcccag ccgggctc 2478

<210> 312

<211> 1914

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de ligando mon+APM-erico de Fc pomo (71-248) de CD19(8B8-2B11)

<400> 312

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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

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccct 1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260

tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320

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agagagggcc ctgagctgag ccctgatgat cctgccggac tgctggacct gcggcaggga 1440

atgtttgccc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 1500

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 1560

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680

agatctgctg ctggcgccgc tgctctggca ctgacagtgg atctgcctcc tgccagcagc 1740

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<210> 313

<211> 826

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena de ligando dimérico (71-248) de Fc agujero de CD19(8B8-2B11)

<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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly 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 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

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> Secuencia artificial

<220>

<223> ligando mon+APM-erico de Fc pomo (71-248) de CD19(8B8-2B11)

<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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Gly Gly 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

625 630 635

<210> 315

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> CD19(8B8-018) heavy chain (huIgG1 PGLALA) DNA

<400> 315

caggtccagc tggtgcagtc 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 gttcgactat tgggggcagg gaaccacagt aaccgtgagc 360

tccgcaagta ctaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agcagctggg 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 gccctcggag cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca 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 gtccccgggc aaa 1353

<210> 316

<211> 451

<212> PRT

<213> Secuencia artificial

<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

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

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

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<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> ADN

<213> Secuencia artificial

<220>

<223> Secuencia de armaz+APM-n aceptor de cadena pesada

<400> 319

taaggggctt cctagtccta aggctgagga agggatcctg gtttagttaa agaggatttt 60

attcacccct gtgtcctctc cacaggtgtc cagtcccagg tccagctggt gcaatctggg 120

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 180

ttcagcagct atactatcag ctgggtgcga caggcccctg gacaagggct tgagtggatg 240

ggaaggatca tccctatcct tggtacagca aactacgcac agaagttcca gggcagagtc 300

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 360

gaggacacgg ccgtgtatta ctgtgcgaga ga 392

<210> 320

<211> 797

<212> ADN

<213> Secuencia artificial

<220>

<223> Secuencia de armaz+APM-n aceptor de cadena ligera

<400> 320

ctgcagctgg aagctcagct cccacccagc tgctttgcat gtccctccca gctgccctac 60

cttccagagc ccatatcaat gcctgtgtca gagccctggg gaggaactgc tcagttagga 120

cccagaggga accatggaag ccccagctca gcttctcttc ctcctgctac tctggctccc 180

aggtgagggg aacatgaggt ggttttgcac attagtgaaa actcttgcca cctctgctca 240

gcaagaaata taattaaaat tcaaagtata tcaacaattt tggctctact caaagacagt 300

tggtttgatc ttgattacat gagtgcattt ctgttttatt tccaatttca gataccaccg 360

gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggg gaaagagcca 420

ccctctcctg cagggccagt cagagtgtta gcagctactt agcctggtac caacagaaac 480

ctggccaggc tcccaggctc ctcatctatg atgcatccaa cagggccact ggcatcccag 540

ccaggttcag tggcagtggg tctgggacag acttcactct caccatcagc agcctagagc 600

ctgaagattt tgcagtttat tactgtcagc agcgtagcaa ctggcctccc acagtgattc 660

cacatgaaac aaaaacccca acaagaccat cagtgtttac tagattatta taccagctgc 720

ttcctttaca gacagctagt ggggtggcca ctcagtgtta gcatctcagc tctatttggc 780

cattttggag ttcaagt 797

<210> 321

<211> 5

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66-LCHA) CDR-H1

<400> 321

Asp Thr Tyr Met His

1 5

<210> 322

<211> 17

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CEA(T84.66-LCHA) CDR-H3

<400> 323

Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr
1 5 10

<210> 324

<211> 15

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CEA(T84.66-LCHA) CDR-L3

<400> 326

Gln Gln Thr Asn Glu Asp Pro Tyr Thr

1 5

<210> 327

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> VH de uni+APM-n a CEA progenitora

<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> Secuencia artificial

<220>

<223> VL de uni+APM-n a CEA progenitora

<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> Secuencia artificial

<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

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

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> Secuencia artificial

<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

<210> 331

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena Fc agujero de CEA(T84.66-LCHA)

<400> 331

caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg ccagcggctt caacatcaag gacacctaca tgcactgggt gcgccaggcc 120

cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt 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 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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> 332

<211> 654

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de CEA(T84.66-LCHA)

<400> 332

gagatcgtgc tgacccagag ccctgccacc ctgtcactgt ctccaggcga gagagccacc 60

ctgagctgta gagccggcga gagcgtggac atcttcggcg tgggatttct gcactggtat 120

cagcagaagc ccggccaggc ccccagactg ctgatctaca gagccagcaa ccgggccaca 180

ggcatccccg ccagattttc tggctctggc agcggcaccg acttcaccct gacaatcagc 240

agcctggaac ccgaggactt cgccgtgtac tactgccagc agaccaacga ggacccctac 300

acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggctgcacc atctgtcttc 360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga 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

<210> 333

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66-LCHA) cadena de Fc agujero

<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

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Lys

450

<210> 334

<211> 218

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66-LCHA) cadena ligera

<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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de CEA (T84.66-LCHA) cadena de 4-1BBL dimérico de Fc agujero (71-254)

<400> 335

caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg ccagcggctt caacatcaag gacacctaca tgcactgggt gcgccaggcc 120

cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt 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 cccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

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<210> 336

<211> 1932

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de anti-CEA (T84.66-LCHA) Fc pomo 41-1BBL (71-254) monomérico

<400> 336

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cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc ccccttcggc 300

tactacgtgt ccgactacgc catggcctat tggggccagg gcacactcgt gaccgtgtcc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

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tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

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ccaagaagcg aa 1932

<210> 337

<211> 838

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66-LCHA) cadena de 4-1BBL dimérico de Fc agujero (71-254)

<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

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

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

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

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

<210> 338

<211> 644

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena anti-CEA (T84.66-LCHA) Fc pomo 4-1BBL (71-254) monomérico

<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

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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de CEA (T84.66-LCHA) cadena de 4-1BBL dimérico de Fc agujero (71-248)

<400> 339

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cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt 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

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gagatcccag ccgggctc 2478

<210> 340

<211> 1914

<212> ADN

<213> Secuencia artificial

<220>

<223> cadena de ADN de anti-CEA (T84.66-LCHA) Fc pomo 4-1BBL (71-248) monomérico

<400> 340

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tcctgcaagg ccagcggctt caacatcaag gacacctaca tgcactgggt gcgccaggcc 120

cctggacagg gactggaatg gatgggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt tccagggcag agtgaccatc accgccgaca ccagcacctc caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc ccccttcggc 300

tactacgtgt ccgactacgc catggcctat tggggccagg gcacactcgt gaccgtgtcc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

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aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

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gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

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<210> 341

<211> 826

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66-LCHA) cadena de 4-1BBL dimérico de Fc agujero (71-248)

<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

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

130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly 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 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

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> Secuencia artificial

<220>

<223> cadena de anti-CEA (T84.66-LCHA) Fc pomo 4-1BBL (71-248) monomérico

<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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Gly Gly 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

625 630 635

<210> 343

<211> 1353

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena Fc agujero de CEA(T84.66)

<400> 343

gaggtgcagc tgcagcagtc tggcgccgaa ctggtggaac ctggcgcctc tgtgaagctg 60

agctgtaccg ccagcggctt caacatcaag gacacctaca tgcactgggt caagcagcgg 120

cctgagcagg gcctggaatg gatcggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt 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

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 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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> 344

<211> 654

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de cadena ligera de anti-CEA(T84.66)

<400> 344

gacatcgtgc tgacccagag ccctgcctct ctggccgtgt ctctgggaca gagggccacc 60

atgtcttgca gagccggcga gagcgtggac atcttcggcg tgggatttct gcactggtat 120

cagcagaagc ccggccagcc ccccaagctg ctgatctaca gagccagcaa cctggaaagc 180

ggcatccccg tgcggtttag cggcaccggc agcagaaccg acttcaccct gatcatcgac 240

cccgtggaag ccgacgacgt ggccacctac tactgccagc agaccaacga ggacccctac 300

acctttggcg gaggcaccaa gctggaaatc aagcgtacgg tggctgcacc atctgtcttc 360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga 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

<210> 345

<211> 451

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66) cadena de Fc agujero

<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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly Lys

450

<210> 346

<211> 218

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66) cadena ligera

<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

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

<210> 347

<211> 2514

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de CEA (T84.66) cadena de 4-1BBL dimérico de Fc agujero (71-254)

<400> 347

gaggtgcagc tgcagcagtc tggcgccgaa ctggtggaac ctggcgcctc tgtgaagctg 60

agctgtaccg ccagcggctt caacatcaag gacacctaca tgcactgggt caagcagcgg 120

cctgagcagg gcctggaatg gatcggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt 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

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 cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgccccc 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 ccccgatgat cctgctggac tgctggacct gcggcagggc 1440

atgtttgctc agctggtggc ccagaacgtg ctgctgatcg atggcccccc gtcctggtac 1500

agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 1560

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 1740

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 1800

aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 1920

ccaagaagcg aaggcggagg cggatctggc ggcggaggat 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 agcgcctggg agtgcatctg 2400

catactgaag ccagagcccg gcatgcttgg cagctgactc agggggcaac tgtgctggga 2460

ctgtttcgcg tgacacctga gatccctgcc ggactgccaa gccctagatc agaa 2514

<210> 348

<211> 1932

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de CEA (T84.66) cadena de 4-1BBL monomérico de Fc pomo (72-254)

<400> 348

gaggtgcagc tgcagcagtc tggcgccgaa ctggtggaac ctggcgcctc tgtgaagctg 60

agctgtaccg ccagcggctt caacatcaag gacacctaca tgcactgggt caagcagcgg 120

cctgagcagg gcctggaatg gatcggcaga atcgaccccg ccaacggcaa cagcaaatac 180

gtgcccaagt tccagggcaa ggccaccatc accgccgaca ccagcagcaa cacagcctac 240

ctgcagctga ccagcctgac ctccgaggac accgccgtgt actactgcgc ccccttcggc 300

tactacgtgt ccgactacgc catggcctat tggggccagg gcacaagcgt gaccgtgtcc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccccaaaa 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 cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc ctgcagagat 1080

gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta ccccagcgat 1140

atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cacccccccct 1200

gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260

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acccagaagt ccctgagcct gagccccggc ggaggcggcg gaagcggagg aggaggatcc 1380

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agcgatcctg gactggctgg cgtgtcactg acaggcggcc tgagctacaa agaggacacc 1560

aaagaactgg tggtggccaa ggccggcgtg tactacgtgt tctttcagct ggaactgcgg 1620

agagtggtgg ccggcgaagg atctggctct gtgtctctgg ccctgcatct gcagcctctg 1680

agaagcgctg ctggcgctgc agctctggca ctgacagtgg atctgcctcc tgccagctcc 1740

gaggcccgga atagcgcatt tgggtttcaa ggcaggctgc tgcacctgtc tgccggccag 1800

aggctgggag tgcatctgca cacagaggcc agggctagac acgcctggca gctgacacag 1860

ggcgctacag tgctgggcct gttcagagtg acccccgaga ttccagccgg cctgccttct 1920

ccaagaagcg aa 1932

<210> 349

<211> 838

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66) cadena de 4-1BBL dimérico de Fc agujero (71-254)

<400> 349

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

145 150 155 160

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

165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val

180 185 190

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

195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys

210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly

225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

260 265 270

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

275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305 310 315 320

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

325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

340 345 350

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

355 360 365

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

370 375 380

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

385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val

405 410 415

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

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

435 440 445

Pro Gly 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

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

Pro Ser Pro Arg Ser Glu

835

<210> 350

<211> 644

<212> PRT

<213> Secuencia artificial

<220>

<223> CEA (T84.66) cadena de 4-1BBL monomérico de Fc pomo (71-254)

<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

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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu NA3B3A2-avi His

<400> 351

cagctgacca ccgagtccat gcccttcaac gtggccgagg gcaaagaggt gctgctgctg 60

gtccacaacc tgccccagca gctgttcggc tacagctggt acaagggcga gcgggtggac 120

ggcaaccggc agatcgtggg ctacgccatc ggcacccagc aggccacacc cggccctgcc 180

aatagcggca gagagacaat ctaccccaac gccagcctgc tgatccagaa cgtgacccag 240

aacgacaccg gcttctacac actccaagtc atcaagagcg acctggtcaa cgaggaagcc 300

accggccagt tccacgtgta ccccgagctg cccaagccca gcatcagcag caacaacagc 360

aagcccgtgg aagataagga cgccgtggcc tttacctgcg agcccgaggc ccagaacacc 420

acctacctgt ggtgggtcaa cggccagagc ctgcccgtgt cccccagact ccagctgagc 480

aacggcaaca gaaccctgac cctgttcaac gtgacccgga atgacgccag agcctacgtg 540

tgcggcatcc agaacagcgt gtccgccaac cgcagcgacc ccgtgaccct ggatgtgctg 600

tacggccccg acacccccat catcagcccc cctgacagca gctacctgag cggcgccaac 660

ctgaacctga gctgccacag cgccagcaac cccagccctc agtacagctg gcggatcaac 720

ggcatccccc 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 tccggtggtt 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

<212> PRT

<213> Secuencia artificial

<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

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

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> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu OX40L dimérico (51-183) - CL* cadena de Fc pomo

<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 aacccctgtt ccagctgaag 240

aaagtgcgga gcgtgaacag cctgatggtg 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

tacttcagcc aggaagtgga catcagcctg cactaccaga aggacgagga acccctgttc 660

cagctgaaga aagtgcggag cgtgaacagc ctgatggtgg ccagcctgac ctacaaggac 720

aaggtgtacc tgaacgtgac caccgacaac accagcctgg acgacttcca cgtgaacggc 780

ggcgagctga tcctgatcca ccagaaccct ggcgagttct gcgtgctggg aggcggaggc 840

tccggagggg gaggatctcg tacggtggct gcaccatctg tctttatctt cccacccagc 900

gaccggaagc tgaagtctgg cacagccagc gtcgtgtgcc tgctgaataa cttctacccc 960

cgcgaggcca aggtgcagtg gaaggtggac aatgccctgc agagcggcaa cagccaggaa 1020

agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgaccctg 1080

agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgaccca ccagggcctg 1140

tctagccccg tgaccaagag cttcaaccgg ggcgagtgcg acaagaccca cacctgtcct 1200

ccatgccctg cccctgaagc tgctggcggc cctagcgtgt tcctgttccc cccaaagccc 1260

aaggacaccc tgatgatcag ccggaccccc gaagtgacct gcgtggtggt ggatgtgtcc 1320

cacgaggacc ctgaagtgaa gttcaattgg tacgtggacg gcgtggaagt gcacaatgcc 1380

aagaccaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1440

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1500

ctcggcgccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1560

gtgtacaccc tgcccccatg ccgggatgag ctgaccaaga accaggtcag cctgtggtgc 1620

ctggtcaaag gcttctatcc agcgacatc gccgtggagt gggagagcaa tgggcagccg 1680

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1740

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1800

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1860

<210> 354

<211> 738

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de hu OX40L monomérico (51-183) - CH1*

<400> 354

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 aacccctgtt ccagctgaag 240

aaagtgcgga gcgtgaacag cctgatggtg 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 ggaattctgg cgccctgaca agcggcgtgc acacctttcc agccgtgctg 600

cagagcagcg gcctgtactc tctgagcagc gtcgtgacag tgcccagcag ctctctgggc 660

acccagacct acatctgcaa cgtgaaccac aagcccagca acaccaaggt ggacgagaag 720

gtggaaccca agtcctgc 738

<210> 355

<211> 620

<212> PRT

<213> Secuencia artificial

<220>

<223> hu OX40L dimérico (51-183) - CL* cadena de Fc pomo

<400> 355

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

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

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

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

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

610 615 620

<210> 356

<211> 246

<212> PRT

<213> Secuencia artificial

<220>

<223> hu OX40L monomérico (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

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> Secuencia artificial

<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

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> Secuencia artificial

<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

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> Secuencia artificial

<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

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> Secuencia artificial

<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

<210> 361

<211> 121

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-2B03) VL

<220>

<221> misc+AF8-feature

<222> (107)..(107)

<223> Xaa puede ser cualquier amino+AOE-cido de origen natural

<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> Secuencia artificial

<220>

<223> CD19 (8B8-5A07) VH

<400> 363

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> Secuencia artificial

<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

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> Secuencia artificial

<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

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> Secuencia artificial

<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

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> Secuencia artificial

<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

<210> 368

<211> 112

<212> PRT

<213> Secuencia artificial

<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> Secuencia artificial

<220>

<223> CD19 (8B8-5H09) VH

<400> 369

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> Secuencia artificial

<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

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> Secuencia artificial

<220>

<223> hu OX40L dimérico (51-183) conectado mediante el enlazador (G4S)2

<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

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

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> Secuencia artificial

<220>

<223> hu OX40L dimérico (52-183) conectado mediante el enlazador (G4S)2

<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

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> Secuencia artificial

<220>

<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

<210> 374

<211> 169

<212> PRT

<213> Secuencia artificial

<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

Val Thr Pro Glu Ile Pro Ala Gly Leu

165

<210> 375

<211> 197

<212> PRT

<213> Secuencia artificial

<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

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