

LISTADO DE SECUENCIAS

<110> FIVE PRIME THERAPEUTICS, INC.
BRISTOL-MYERS SQUIBB COMPANY
SCHEBYE, Xiao Min, et al.

<120> ANTICUERPOS DE UNIÓN A ILT4

<130> 01134-0060-00PCT

<140> PCT/US2019/040820

<141> 2019-07-08

<150> US 62/695,600

<151> 2018-07-09

<150> US 62/744,611

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<160> 193

<170> PatentIn versión 3.5

<210> 1

<211> 214

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 kappa LC (aka. ILT4.1-kappa)

<400> 1

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

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

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

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

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

Glu Asp Phe Ala Gly Tyr Tyr Cys Gln Gln Arg Ser Tyr Trp Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 2

<211> 446

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4-IgG1.1f HC (aka. ILT4.1-IgG1.1f)

<400> 2

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

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

Lys Val Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
 325 330 335

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

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

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

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

420 425 430

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

435 440 445

<210> 3

<211> 214

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 kappa LC ILT4.2-kappa

<400> 3

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala

20 25 30

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

35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Phe

85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly

115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

Phe Asn Arg Gly Glu Cys

210

<210> 4

<211> 455

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8-IgG1.1f HC ILT4.2-IgG1.1f

<400> 4

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 Ser Ser
20 25 30

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

Gly Trp Met Asn Pro Asn Ser Gly His Thr Gly Tyr Ala Gln Lys Phe
50 55 60

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

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

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

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

225 230 235 240
 Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 245 250 255
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 290 295 300
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 420 425 430
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 5

<211> 214

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2 kappa LC ILT4.3-kappa

<400> 5

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 Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 6

<211> 458

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2-IgG1.1fHC ILT4.3-IgG1.1f

<400> 6

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Phe Thr Ser Ser 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 Lys Ser Ser Ile Thr Met Ile Arg Gly Ala Tyr Leu Tyr Tyr Tyr
 100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 145 150 155 160

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

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 195 200 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 210 215 220

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

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

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

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

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

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 325 330 335

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

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

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 7

<211> 215

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5 kappa LC ILT4.4-kappa

<400> 7

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

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Trp 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> 8

<211> 451

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5-IgG1.1f HC ILT4.4-IgG1.1f

<400> 8

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

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

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

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

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

Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85	90	95
Ala Arg Asp Pro Phe Tyr Gly Ser Gly Asn Tyr Phe Asp 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 Arg Val Glu Pro Lys Ser Cys		
210	215	220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly		
225	230	235
240		
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
245	250	255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		
260	265	270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
275	280	285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		
290	295	300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
305	310	315
320		
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser 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 Glu Glu Met 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> 9

<211> 214

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 kappa LC ILT4.5-kappa

<400> 9

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
 20 25 30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 10

<211> 451

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5-IgG1.1 HC ILT4.5-IgG1.1f

<400> 10

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

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

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

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

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

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

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

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser 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 Glu Glu Met 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> 11

<211> 215

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 kappa LC ILT4.6-kappa

<400> 11

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 Gly 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> 12

<211> 455
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9-IgG1.1f HC ILT4.6-IgG1.1f

<400> 12

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

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

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

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

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

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

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

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

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

245 250 255
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 290 295 300
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 420 425 430
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 13

<211> 454

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.e.IgG1.3 HC ILT4.8.IgG1.3

<400> 13

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 Asn Tyr
 20 25 30

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 420 425 430
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 Leu Ser Leu Ser Pro Gly
 450

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

<220>
 <223> Sintético: 21A5 kappa LC

<400> 14

Glu Ile Ala 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 Thr Phe

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

<210> 15
 <211> 453
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5.IgG1.3 HC

<400> 15

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
 Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Phe His Pro Ser Gly Asp Ile Thr Ser Ser Ala Gln Asn Phe
 50 55 60
 Gln Gly Arg Val Thr Met Ile Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

385 390 395 400
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 405 410 415
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 420 425 430
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 435 440 445
 Ser Leu Ser Pro Gly
 450

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

<220>
 <223> Sintético: 21A5.1 kappa LC (ILT4.9.1K)
 <400> 16

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 Thr Phe
 85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
 100 105 110

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

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
 130 135 140

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

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

165 170 175
 Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
 180 185 190
 Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 195 200 205
 Arg Gly Glu Cys
 210

<210> 17
 <211> 453
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5.a.IgG1.3 HC (ILT4.9.IgG1.3)

<400> 17

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

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

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

 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

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

 Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly
 450

<210> 18
 <211> 214
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10 kappa LC

<400> 18

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

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

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 19
 <211> 445

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.IgG1.3 HC ILT4.10.IgG1.3

<400> 19

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

Ala Ile Ile Ser Tyr Asp Glu Tyr Asn Lys 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 Arg Glu Trp Val Gly Ile Arg Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

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

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

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

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

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 20

<211> 214

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.1 kappa LC

<400> 20

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 21

<211> 214

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.3 kappa LC

<400> 21

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

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

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

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

<210> 22
 <211> 645
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 9G4 LC ADN ILT4.1-kappa ADN

<400> 22
 gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgtagc agctacttag cctggtacca acagaaacct 120
 ggccaggctc ccaggctcct catctatgat gcgtccaaca gggccactgg catcccagcc 180
 aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag cctagagcct 240
 gaagattttg caggttatta ctgtcagcag cgtagctact ggccgtggac gttcggccaa 300
 gggaccaagg tggaaatcaa acgtacgggtg gctgcaccaa ctgtcttcat ctcccgcca 360
 tctgatgagc agttgaaatc tggaaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 23

<211> 1341

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 IgG1.1f HC ADN ILT4.1-IgG1.1f ADN

<400> 23

cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc ctgcggagac cctgtccctc 60
 acctgcactg tctctggtgg ctccatcagt agttactact ggaactggat tcggcagccc 120
 ccaggggaagg gactggagtg gcttggttac atctattaca gtgggagtac caagtacaac 180
 ccctccctca agagtgcagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
 aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt attgtgccag cagtggctgg 300
 tactactttg actattgggg ccaggggaacc ctggtcaccg tctcctcagc tagcaccaag 360
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tggtaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540
 ctgagcagcg tggtagaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac 660
 aaaactcaca catgcccacc gtgccagca cctgaagccg aaggggcccc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggaggtgc ataagccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cccaagcagc atcgagaaaa ccatctcaa agccaaaggg 1020
 cagccccgag aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca ggcacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tccctgtccc cgggtaaag a 1341

<210> 24
<211> 645
<212> ADN
<213> Secuencia Artificial

<220>
<223> Sintético: 9C8 kappa LC ADN ILT4.2-kappa ADN

<400> 24
gccatccagt tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattagc agtgcttag cctggatca gcagaaacca 120
gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caactatta ctgtcaacag ttaatatgtt acccattcac ttccggcct 300
gggaccaaag tgatatcaa acgtacgggtg gctgcacat ctgtctcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taactctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 25
<211> 1368
<212> ADN
<213> Secuencia Artificial

<220>
<223> Sintético: 9C8 IgG1.1f ADN ILT4.2-IgG1.1f ADN

<400> 25
cagggtcaac tgggtcagtc tggggctgag gttaaagaagc ctggggcctc agtgaaggtc 60
tcctgaagg cttctggata cacctcacc agctctgata tcaactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgaacccta acagtgggtca cacaggctat 180
 gcacagaagt tccaggacag agtcaccttg acccgggaca cctccataag cacagcctac 240
 atggagctga gcagcctgag atctgaggac tcggccgtgt attactgtgc gagaggtggg 300
 aatagcattg actgggggtt ctcctactac ggtctggacg tctggggcca agggaccacg 360
 gtcaccgtct cctcagctag caccaagggc ccatcgtct tccccctggc accctcctcc 420
 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
 ccggtgacgg tgcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt 540
 gtctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600
 ttgggcaccc agacctacat ctgaacgtg aatcacaagc ccagcaacac caaggtggac 660
 aagagagttg agcccaaate ttgtgacaaa actcacacat gccaccgtg cccagcacct 720
 gaagccgaag gggccccgtc agtcttctc tccccccaa aaccaagga caccctcatg 780
 atctccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840
 gtcaagtca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900
 gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 960
 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc aagcagcatc 1020
 gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080
 ccatccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140
 tatccagcg acatcgccgt ggagtgggag agcaatggc agccggagaa caactacaag 1200
 accacgcctc ccgtgctgga ctccgacggc tccttcttc tctatagcaa gtcaccgtg 1260
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
 cacaaccact acacgcagaa gagcctctcc ctgtccccgg gtaaatga 1368

<210> 26

<211> 645

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2 kappa LC ADN ILT4.3-kappa ADN

<400> 26

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcgtacac tttggccag 300
 gggaccaagc tggagatcaa acgtacgggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
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<210> 27

<211> 1377

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2 IgG1.1f HC ADN ILT4.3-IgG1.1f ADN

<400> 27

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 tcttgaagg cttctggggg caccttcagc aactatgcta tcagctgggt gcgacaggcc 120
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 gcaccgaagt tccagggcag agtcacgatt accgcggacg aattcacgag ctcagcttac 240
 atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaagtctagt 300
 attactatga ttcggggagc ctatctttac tactacgacg gtatggacgt ctggggccaa 360
 gggaccacgg tcaccgtctc ctcagctagc accaagggcc catcggtctt ccccctggca 420
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<210> 28

<211> 648

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5 kappa LC ADN ILT4.4-kappa ADN

<400> 28

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 ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catccagcc 180
 aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
 gaagattttg cagtttatta ctgtcagcag cgtagcaact ggctccgtg gacgttcggc 300
 caagggaaca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgctgct gaataacttc 420
 tatccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggtactcc 480
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 acgtgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
 ggctgagct cgcccgctac aaagagcttc aacaggggag agtgtag 648

<210> 29

<211> 1356
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2E5 IgG1.1f HC ADN ILT4.4-IgG1.1f ADN

<400> 29
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 tcctgtacag cgtctggatt caccttcagt aactatggca tgcactgggt ccgccaggct 120
 ccaggcaagg gactggagtg ggtggcagtt atctggtatg atggaagtaa tgaatactat 180
 gcagaatccg tgaagggccg actcaccatc tccagagaca attccaagaa cacgctgtat 240
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 ttctatgggt cggggaatta cttgactac tggggccagg gaaccctggt caccgtctcc 360
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 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgaaggg 720
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 cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
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 gtgtggact ccgacggctc ctcttctc tatagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtccccgggt aatatga 1356

<210> 30
 <211> 645
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Sintético: 24E5 kappa LC ADN ILT4.5-kappa ADN

<400> 30
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 atcactgttc gggcgagtca gggtagtag agctggtag cctggtagc gcagaaacca 120
 gagaaagccc ctaagtcct gatctatgct gcatccagtt tgcaaagtg ggtccatca 180
 aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240
 gaagatttg caactatta ctgccaacag tataatagtt accctctcac ttccggcgga 300
 gggaccaagg tggagatcaa acgtacgggt gctgcacat ctgtctcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgtgtgt gcctgctgaa taactctat 420
 cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagctcaac aggggagagt gttag 645

<210> 31
 <211> 1356
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Sintético: 24E5 IgG1.1f HC ADN ILT4.5-IgG1.1f ADN

<400> 31
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
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 ccagggaagg ggctggagt ggtctcaggt attagtggta gtggtgtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
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 gatattatag cagcatacta cttgtctac tggggccagg gaaccctgg caccgtctcc 360
 tcagctagca ccaagggccc atcggtcttc cccctggcac cctctccaa gagcacctct 420

gggggcacag cggccctggg ctgctggtc aaggactact tccccgaacc ggtgacgggtg 480
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 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agccgaaggg 720
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 gtgctggact ccgacggctc ctctctctc tatagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcatgctcc gtgatgatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtccccgggt aaatga 1356

<210> 32

<211> 648

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 kappa LC ADN ILT4.6-kappa ADN

<400> 32

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 ctctctgca gggccagtca gagtgttagc agcagctact tagcctggtta ccagcagaaa 120
 cctggccagg ctccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgagtgta ttactgtcag cagtatggta gctcacctct cactttcggc 300
 ggagggacca aggtggagat caaacgtacg gtggctgcac catctgtt catcttccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgtt tgtgctgct gaataactc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
 ggctgagct cgcccgctac aaagagcttc aacaggggag agtggttag 648

<210> 33

<211> 1368

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 IgG1.1f HC ADN ILT4.6-IgG1.1f ADN

<400> 33

gagggacagc tggtggagtc tgggggagac ttgtacagc ctggggggtc cctgagactc 60
 tcctgtgcaa cctctggatt caccttagc aactatgcca tgaactgggt ccgccaggct 120
 ccaggggaagg ggctggagtg gatctcagtt attagtgtta gtggtggttag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga atagcctgag agccgaggac acggccgtat attactgtgc gaaagattat 300
 tactatgatt cggggagtta ttatgactct ttcttgact actggggcca gggaaccctg 360
 gtcaccgtct cctcagctag caccaagggc ccatcggtct tccccctggc accctcctcc 420
 aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
 ccggtgacgg tgcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggt 540
 gtctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
 aagagagttg agcccaaatc ttgtgacaaa actcacacat gccaccgtg cccagcacct 720
 gaagccgaag gggccccgtc agtcttcctc ttcccccaa aaccaagga caccctcatg 780
 atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 840
 gtcaagtca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 900
 gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 960
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ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140
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 accacgcctc ccgtgctgga ctccgacggc tcctttctcc tctatagcaa gtcaccgtg 1260
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
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<210> 34

<211> 1365

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.IgG1.3 HC ADN ILT4.6-IgG1.3 HC ADN

<400> 34

gagggacagc tggtggagtc tgggggagac ttgtacagc ctggggggtc cctgagactc 60
 tcctgtgcaa cctctggatt cacctttagc aactatgcc a tgaactgggt ccgccaggct 120
 ccaggggaagg ggtctggagt gatctcagtt attagtgtta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
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 tactatgatt cgggggagtta ttatgactct ttctttgact actggggcca gggaaccctg 360
 gtcaccgtct cctcagctag caccaagggc ccatcggctt tccccctggc accctcctcc 420
 aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
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 aagagagttg agcccaaact ttgtgacaaa actcacacat gccaccgtg ccagcacct 720
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<210> 35
 <211> 1365
 <212> ADN
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<220>
 <223> Sintético: 21D9.b.IgG1.3 HC ADN

<400> 35
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 cctggcaagg gactggagtg gatctctgtg atctctgtga gcggcggctc tacctactat 180
 gccgacagcg tgaagggccg gttcaccatc agcagagata actccaagaa tacactgtat 240
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<210> 36

<211> 454

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.b.IgG1.3 HC

<400> 36

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly
 450

<210> 37
 <211> 1365
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9.c.IgG1.3 HC ADN

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 gagaaaacca tctcaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1080
 ccatcccgga aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1140
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 accagcctc ccgtgtgga ctccgacggc tccttctcc tctatagcaa gtcaccgtg 1260
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
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<210> 38
 <211> 454
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9.c.IgG1.3 HC

<400> 38

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly
 450

<210> 39

<211> 1365

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.d.IgG1.3 HC ADN

<400> 39

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 cctggcaagg gactggagtg ggtgtctgtg atctctgtga gcggcggctc tacctactat 180
 gccgacagcg tgaagggccg gttcaccatc agcagagata actccaagaa tacactgtat 240
 ctgcagatga acagcctgcg ggccgaggac acagccgtgt actattgtgc caaggactac 300
 tattacgatt ccggctctta ttacgactcc ttcttgatt actggggcca gggcaccctg 360
 gtgacagtga gtcgcgtag caccaagggc ccatcggctt tccccctggc accctcctcc 420
 aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480
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 gtctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 600
 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
 aagagagttg agcccaaac ttgtgacaaa actcacacat gccaccgtg cccagcacct 720
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 accacgctc ccgtgctgga ctccgacggc tccttcttc tctatagcaa gtcaccgtg 1260
 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1320
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<210> 40

<211> 454

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.d.IgG1.3 HC

<400> 40

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly
450

<210> 41

<211> 1413

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.e.IgG1.3 HC ADN ILT4.8.IgG1.3 HC ADN con señal de péptido

<400> 41

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gcctctggat tcaccttag caactatgcc atgaactggg tccgccaggc tccagggaag 180

gggctggagt gggctcagt tattagtgtt agtggtggtg gcacatacta cgcagactcc 240

gtgaagggcc gggtcaccat ctccagagac aattccaaga acacgctgta tctgcaaagt 300

aatagcctga gagccgagga cacggccgta tattactgtg cgaaagatta ttactatgat 360

tcggggagtt attatgactc ttctttgac tactggggcc agggaaccct ggtcaccgtc 420

tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
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 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgcctacag 600
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 cccgtgctgg actccgacgg ctccttctc ctctatagca agctcaccgt ggacaagagc 1320
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 tacacgcaga agagcctctc cctgtccccg ggt 1413

<210> 42

<211> 1020

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5 LC ADN

<400> 42

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 ccaggacagg cacctaggct gctgatctac ggagccagct ccagggaac cggcatccct 180
 gaccgcttca gcggctccgg ctctggcaca gacttcccc tgacaatctc taggctggag 240
 cccgaggact tcgccgtgta ctattgtcag cagtatggct ccaccttgg cggcggcaca 300

aaggtggaga tcaaggaatt cgccaccatg agggcttgga tcttcttct gctctgcctg 360
 gccgggcgcg ccctcgaga gatcgtgtg acccagagcc caggcacact gtctctgagc 420
 ccaggagaga gggccaccct gtcctgcaga gcctccagct ctgtgagctc ctcttacctg 480
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 acctttggcg gcggcacaaa ggtggagatc aagcgtacgg tggccgcccc gtccgtgttt 720
 atcttcctc catcgagca gcagctcaag tccggtaccg cgagcgtggt ctgcctgctg 780
 aacaattct acccgcgga agctaaagt caatggaagg tcgataacgc acttcagtcc 840
 gggaacagcc aggaatctgt gaccgagcag gactccaagg attcgaccta ttcctgtcc 900
 tcgacttca ccctgtcaa ggccgactac gagaagcaca aggtctacgc ctgcgaagtg 960
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<210> 43

<211> 1362

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5.IgG1.3 HC ADN

<400> 43

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 agctgcaagg cctccggcta cacctcaca gattactatc tgactgggt gcggcaggca 120
 ccaggacagg gactggagt gatgggcatc ttccaccctt ctggcgacat cacaagctcc 180
 gccagaact tcagggccg ggtgaccatg acaagagata ccagcacatc caccgtgtac 240
 atggagctgt ctgacctgag gtctgaggac accgccgtgt actattgtgc aaggggaggc 300
 gtgctgaggt atctggactg gagccacgcc ttgatatct ggggccaggg cacaatgggt 360
 accgtgtcct ctgctagcac caaaggacct tcagtgtcc cgctcgccc gtcaccaag 420
 tccacctccg gcggaaccgc tgcctggga tgccttga aggactactt ccctgagcct 480
 gtgactgtgt cctggaactc cggagccctg acctccggcg tgcatactt ccctgctgtg 540
 ctgcaatcaa gcggcctcta ctattgagc tccgtctga ccgtgccgag ctccagcctc 600
 ggtactcaaa cctacatctg caatgtcaac cacaagccca gcaacaccaa ggtcgataag 660

agagtggagc ccaagtcgtg cgacaagact cacactgtc ccccatgccc ggcccccgag 720
 gccgaggggg ccccgagcgt cttctgttc ccgcctaagc ccaaggatac cctgatgatt 780
 tcgcggaact ccgaagtgc ctgtgtcgtg gtggacgtgt cccacgaaga tcccgaagtc 840
 aagttcaact ggtacgtgga cggagtcgag gtgcacaacg caaagaccaa gcctcgcgag 900
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 aaccactaca ccagaagtc tctgagcctt tccccgggat ga 1362

<210> 44

<211> 687

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5.1 kappa LC ADN (ILT4.9.1K) ADN con señal de péptido

<400> 44

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 ttgacgcagt ctccaggcac cctgtctttg tctccagggg aaagagccac cctctcctgc 120
 agggccagtc agagtgttag cagcagctac ttgacctggt accagcagaa acctggccag 180
 gctcccaggc tctcatcta tggatcatcc agcagggcca ctggcatccc agacagggtc 240
 agtggcagtg ggtctgggac agacttact ctaccatca gcagactgga gcctgaagat 300
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 gtacagtgga aggtggataa cgccctccaa tcgggtaact cccaggagag tgtcacagag 540
 caggacagca aggacagcac ctacagcctc agcagcacc tgacgctgag caaagcagac 600

tacgagaaac acaaagtcta cgctgcgaa gtcacccatc agggcctgag ctgcccgtc 660

acaagagct tcaacagggg agagtgt 687

<210> 45

<211> 1410

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5.a.IgG1.3 HC ADN (ILT4.9.IgG1.3) ADN con señal de péptido

<400> 45

atgagggtt ggatcttctt tctgctctgc ctggccggga gagcgctgc acaggtgcag 60

ctggtgcagt ctggggctga ggtgaagaag cctggggcct cagtgaaggt ttctgcaag 120

gcactctggat acaccttcac cgactactat ttgactggg tgcgacaggc ccctggacaa 180

gggcttgagt ggatgggaat attccaccct agtggtgata tcacaagctc cgacacagaac 240

ttccagggca gattcaccat gaccagggac acgtccacga gcacagtcta catggagctg 300

agcagcctga gatctgagga cacggccgtg tattactgtg cgagaggagg cgtgctgagg 360

tatctggact ggagccatgc tttgatatc tggggccaag ggacaatggc caccgtctct 420

tcagctagca ccaagggccc atcgggtctc ccctggcac cctctccaa gagcacctct 480

gggggcacag cggccctggg ctgcctggtc aaggactact tcccgaacc ggtgacggtg 540

tcgtggaact caggcgccct gaccagcggc gtgcacacct tccggctgt cctacagtcc 600

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag 660

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aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080

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gagatgacca agaaccaggt cagcctgacc tgcttggtca aaggcttcta tccagcgac 1200

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 acgcagaaga gcctctccct gtccccgggt 1410

<210> 46
 <211> 693
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10 kappa LC ADN ILT4.10K ADN con señal de péptido

<400> 46
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 ctgacccagt ctctagctc cctgtctgcc agcgtgggcg acaggggtgac catcacatgc 120
 agagcctccc agggaaatctc tagcgccctg gcctgggtcc agcagaagcc aggcaaggcc 180
 cctaagctgc tgatctacga tgcctctct ctggagagcg gagtgccatc cagggtcacc 240
 ggctccggct ctggcacaga cttaccctg acaatcagct ccctgcagcc agaggatttt 300
 gccacatact attgtcagca gttcaacagc tatcccatca ctttggcca gggcacacgg 360
 ctggagatca agcgtacggg ggccgccccg tccgtgttta tcttcctcc atcggacgag 420
 cagctcaagt ccggtaccgc gagcgtggtc tgctgtctga acaatttcta cccgcgcgaa 480
 gctaaagtgc aatggaaggt cgataacgca cttcagtccg ggaacagcca ggaatctgtg 540
 accgagcagg actccaagga ttgacctat tcctgtcct cgactctcac cctgtcaaag 600
 gccgactacg agaagcaciaa ggtctacgcc tgcaagtga cccatcaggg cttgtcctca 660
 cccgtgacta agagctcaa ccgggggagag tgt 693

<210> 47
 <211> 1386
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10.IgG1.3 HC ADN ILT4.10.IgG1.3 ADN con señal de péptido

<400> 47
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 gccagcggct tcacctttag ctctacgca atgcactggg tgaggcaggc acctggcaag 180
 ggactggagt ggggtggccat catcagctac gacgagtata acaagtacta tgccgattcc 240
 gtgaagggca ggttcacat cccccgcgac aactctaaga atacactgta cctgcagatg 300
 aatagcctga gagccgagga tacagccgtg tactattgtg cccgggagtg ggtgggcatc 360
 agatattggg gccagggcac cctggtgaca gtgtctagcg ctagcaccaa aggacattca 420
 gtgttccgc tcgcgcgctc atccaagtcc acctccggcg gaaccgctgc cctgggatgc 480
 ctgtgaagg actacttccc tgagcctgtg actgtgtcct ggaactccgg agccctgacc 540
 tccggcgtgc atacctccc tgctgtgtg caatcaagcg gccttactc attgagctcc 600
 gtctgaccg tgccgagctc cagcctcggg actcaaacct acatctgcaa tgtcaaccac 660
 aagcccagca acaccaaggc cgataagaga gtggagccca agtcgtgcga caagactcac 720
 actgtcccc catgcccggc ccccgaggcc gagggggccc cgagcgtctt tctgttccg 780
 cctaagcca aggataccct gatgatttcg cggactcccg aagtgacctg tgcgtggtg 840
 gacgtgtccc acgaagatcc cgaagtcaag ttcaactggg acgtggacgg agtcgaggtg 900
 cacaacgcaa agaccaagcc tcgcgaggaa cagtacaact cgacctatcg ggtggtgtcc 960
 gtgtgacag tgctgcatca ggactggctc aacggaaagg agtacaagtg caaagtgtcc 1020
 aacaaggccc tgccagcgcc cattgaaaag actatcagca aggccaaggg gcagccaagg 1080
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 ctgacgtgct tggtaaggg cttttaccct tccgacatcg ccgtggagtg ggagtcgaac 1200
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<210> 48

<211> 642

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.1 kappa LC ADN

<400> 48

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 ggcaaggccc ctaagctgct gatctatgat gcctcctctc tggagagcgg agtgccatcc 180
 aggttcaccg gctccggctc tggcacagac ttaccctga caatcagctc cctgcagcca 240
 gaggatttcg ccacatacta ttgtcagcag ttcaacagct accccatcac ctttgccag 300
 ggacacggc tggagatcaa gcgtacggg gccgccccgt ccgtgtttat cttccctcca 360
 tcggacgagc agctcaagtc cggtagcgcg agcgtggtct gcctgctgaa caattctac 420
 ccgcgcgaag ctaaagtga atggaaggct gataacgcac ttacgtccgg gaacagccag 480
 gaatctgtga ccgagcagga ctccaaggat tcgacctatt ccctgtcctc gactctacc 540
 ctgtcaaagg ccgactacga gaagcacaag gtctacgcct gcgaagtgc ccatcagggc 600
 ttgtcctcac ccgtgactaa gagcttcaac cggggagaggt gt 642

<210> 49

<211> 693

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.3 kappa LC ADN ILT4.11K ADN con señal de péptido

<400> 49

atgagggtt ggatcttctt tctgctctgc ctggccgggc gcgccctgc agccatccag 60
 ctgaccagtc ctctagctc cctgtctgcc agcgtgggcg acagggtgac catcacatgc 120
 agagcctccc agggatctc tagcgccctg gcctggtacc agcagaagcc aggcaaggcc 180
 cctaagctgc tgatctatga tgcctcctct ctggagagcg gagtgccatc cagggtcagc 240
 ggctccggct ctggcacaga cttaccctg acaatcagct ccctgcagcc agaggatttc 300
 gccacatact attgtcagca gttcaacagc taccatca ccttgccca gggcacacgg 360
 ctggagatca agcgtacggg ggccgccccg tccgtgttta tctccctcc atcggacgag 420
 cagctcaagt ccggtaccgc gagcgtggc tgctgctga acaatttcta cccgcgcgaa 480
 gctaaagtgc aatggaaggc cgataacgca cttcagtcg ggaacagcca ggaatctgtg 540
 accgagcagg actccaagga ttgacctat tccctgtcct cgactctcac cctgtcaaag 600
 gccgactacg agaagcaca ggtctacgcc tgcaagtga cccatcaggg cttgtcctca 660

cccgtagacta agagcttcaa ccggggagag tgt

693

<210> 50

<211> 125

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VL ILT4.1K VL (incluyendo la secuencia de señal, residuos 1-18)

<400> 50

Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro Asp Thr
1 5 10 15

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

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

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

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

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
85 90 95

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

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

<210> 51

<211> 135

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4.IgG1.1 VH ILT4.1.IgG1.1 VH (incluyendo la secuencia de señal, residuos 1-19)

<400> 51

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys

20 25 30
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
 35 40 45

Ser Ser Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Leu Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Lys Tyr Asn Pro
 65 70 75 80

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

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
 100 105 110

Tyr Cys Ala Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
 115 120 125

Thr Leu Val Thr Val Ser Ser
 130 135

<210> 52

<211> 375

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VL ADN ILT4.1K VL ADN

<400> 52

gccccagctc agcttctctt cctcctgcta ctctggctcc cagataccac cggagaaatt 60

gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctctcc 120

tgcagggcca gtcagagtgt tagcagctac ttagcctggt accaacagaa acctggccag 180

gctcccaggc tcctcatcta tgatgcgtcc aacagggcca ctggcatccc agccagggtc 240

agtggcagtg ggtctgggac agacttcaact ctaccatca gcagcctaga gcctgaagat 300

tttcaggtt attactgtca gcagcgtagc tactggccgt ggacgttcgg ccaagggacc 360

aaggtgaaa tcaaa 375

<210> 53

<211> 405

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4.IgG1.1 VH ADN ILT4.1.IgG1.1 VH ADN

<400> 53

atgaaacatc tgtggttctt ccttctcctg gtggcagctc ccagatgggt cctgtcccag 60
 gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 120
 tgcactgtct ctggtggctc catcagtagt tactactgga actggatccg gcagccccc 180
 ggggaaggac tggagtggct tgggtacatc tattacagtg ggagtaccaa gtacaacccc 240
 tccctcaaga gtcgagtcac catatcagta gacacgtcca agaaccagtt ctcctgaag 300
 ctgagctctg tgaccgctgc ggacacggcc gtgtattatt gtgccagcag tggctggtac 360
 tactttgact attggggcca gggaaccctg gtcaccgtct cctca 405

<210> 54

<211> 107

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 kappa VL ILT4.2K VL

<400> 54

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala

20 25 30

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

35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Phe

85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100 105

<210> 55

<211> 125

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8.IgG1.1 VH ILT4.2.IgG1.1 VH

<400> 55

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 Ser Ser
 20 25 30

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

Gly Trp Met Asn Pro Asn Ser Gly His Thr Gly Tyr Ala Gln Lys Phe
 50 55 60

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

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

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

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 56

<211> 321

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 kappa VL ADN ILT4.2K VL ADN

<400> 56

gccatccagt tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattagc agtgctttag cctggtatca gcagaaacca 120

gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

agggtcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag ttaatatgtt acccattcac ttccggccct 300

gggaccaaag tggatatcaa a 321

<210> 57

<211> 375

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8.IgG1.1 VH ADN ILT4.2.IgG1.1 VH ADN

<400> 57

caggtgcaac tgggtgcagtc tggggctgag gtaaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc agctctgata tcaactgggt gcgacaggcc 120

actggacaag ggcttgagtg gatgggatgg atgaacccta acagtgggtca cacaggctat 180

gcacagaagt tccaggacag agtcaccttg acccgggaca cctccataag cacagcctac 240

atggagctga gcagcctgag atctgaggac tcggccgtgt attactgtgc gagaggtggg 300

aatagcattg actgggggtt ctcctactac ggtctggacg tctggggcca agggaccacg 360

gtcaccgtct cctca 375

<210> 58

<211> 128

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2.IgG1.1 VH ILT4.3.IgG1.1 VH

<400> 58

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Phe Thr Ser Ser 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 Lys Ser Ser Ile Thr Met Ile Arg Gly Ala Tyr Leu Tyr Tyr Tyr
 100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 59

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

<220>
 <223> Sintético: 2H2 kappa VL ILT4.3K VL

<400> 59

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 Tyr
 85 90 95

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

<210> 60
 <211> 384
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2H2.IgG1.1 VH ADN ILT4.3.IgG1.1 VH ADN

<400> 60

cagggtccagt tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtggaggtc 60

tctgcaagg ctctggggg caccttcagc aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagt gatgggaggg atcatcccca tctggctac agcaaactac 180

gcaccgaagt tccagggcag agtcacgatt accgcggacg aattcacgag ctcagcttac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaagtctagt 300

attactatga ttcggggagc ctatctttac tactacgacg gtatggacgt ctggggccaa 360

gggaccacgg tcaccgtctc ctca 384

<210> 61
 <211> 321
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2H2 kappa VL ADN ILT4.3K VL ADN

<400> 61
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcgtacac ttttgccag 300
 gggaccaagc tggagatcaa a 321

<210> 62
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2E5 kappa VL ILT4.4K VL

<400> 62

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
 85 90 95
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 63

<211> 121
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2E5.IgG1.1 VH ILT4.4.IgG1.1 VH

<400> 63

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 64
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2E5 kappa VL ADN ILT4.4K VL

<400> 64

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgtagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag cgtagcaact ggctccgtg gacgttcggc 300

caagggacca agtggaat caaa

324

<210> 65

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5.IgG1.1 VH ADN ILT4.4.IgG1.1 VH

<400> 65

caggtgcagc tggaggagtc tgggggaggc gtgtccagc ctgggaggtc cctgagactc 60

tcctgtacag cgtctggatt caccttcagt aactatggca tgcactgggt ccgccaggct 120

ccaggcaagg gactggagtg ggtggcagtt atctggtatg atggaagtaa tgaatactat 180

gcagaatccg tgaagggccg actcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaagtga acagcctgag agccgaggac acggctgtgt attattgtgc gagagatcct 300

ttctatgggt cggggaatta cttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 66

<211> 107

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 kappa VL ILT4.5K VL

<400> 66

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
35 40 45Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 67

<211> 121

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5.IgG1.1 VH ILT4.5.IgG1.1 VH

<400> 67

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

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

Ser Gly 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 Asp Gln Asp Ile Ile Ala Ala Tyr Tyr Phe Val Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 68

<211> 321

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 kappa VL ADN ILT4.5K VL

<400> 68

gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60

atcactgtc gggcgagtca gggtagtagc agctggtag cctggtagc gcagaaacca 120

gagaaagccc ctaagtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

agggtcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240

gaagattttg caactatta ctgccaacag tataatagtt accctctcac ttccggcgga 300

gggaccaagg tggagatcaa a 321

<210> 69
 <211> 363
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 24E5.IgG1.1 VH ADN ILT4.5.IgG1.1 VH

<400> 69
 gaggtgcagc tgttggagtc tgggggaggc ttgttacagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttagc agctatgtca tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcaggt attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagatcag 300
 gatattatag cagcatacta ctttgtctac tggggccagg gaaccctggt caccgtctcc 360
 tca 363

<210> 70
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9K kappa VL ILT4.6K VL

<400> 70

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 Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 71
 <211> 125
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9.IgG1.1 VH ILT4.6.IgG1.1 VH
 <400> 71

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

<210> 72
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9K kappa VL ADN ILT4.6K VL ADN

<400> 72
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacctct cactttcggc 300

ggagggacca aggtggagat caaa 324

<210> 73

<211> 375

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.IgG1.1 VH ADN ILT4.6.IgG1.1 VH ADN

<400> 73

gagggacagc tgttgagtc tgggggagac ttgtacagc ctgggggggc cctgagactc 60

tcctgtgcaa cctctggatt caccttagc aactatgcca tgaactgggt ccgccaggct 120

ccaggggaagg ggctggagtg gatctcagtt attagtgtta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga atagcctgag agccgaggac acggccgtat attactgtgc gaaagattat 300

tactatgatt cggggagtta ttatgactct ttcttgact actggggcca gggaaccctg 360

gtcaccgtct cctca 375

<210> 74

<211> 125

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.b.IgG1.3 VH

<400> 74

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 Thr Ser Gly Phe Thr Phe Ser Asn Tyr

20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

<210> 75
 <211> 125
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9.c.IgG1.3 VH

<400> 75

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

<210> 76
 <211> 375
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9.b.IgG1.3 VH ADN

<400> 76

gaggtgcagc tgctggagtc tggaggagga ctggtgcagc caggaggcag cctgaggctg 60

tcctgcgcca cctctggctt cacattttcc aactatgcca tgaattgggt gcgccaggca 120
 cctggcaagg gactggagtg gatctctgtg atctctgtga gcggcggctc tacctactat 180
 gccgacagcg tgaagggccg gttcaccatc agcagagata actccaagaa tacactgtat 240
 ctgcagatga acagcctgcg ggccgaggac acagccgtgt actattgtgc caaggactac 300
 tattacgatt ccggctctta ttacgactcc ttctttgatt actggggcca gggcaccctg 360
 gtgacagtga gctcc 375

<210> 77

<211> 375

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.c.IgG1.3 VH ADN

<400> 77

gaggtgcagc tgctggagtc tggaggagac ctggtgcagc caggaggcag cctgaggctg 60
 tcctgcgccc cctctggctt cacattttcc aactatgcca tgaattgggt gcgccaggca 120
 cctggcaagg gactggagtg gatctctgtg atctctgtga gcggcggctc tacctactat 180
 gccgacagcg tgaagggccg gttcaccatc agcagagata actccaagaa tacactgtat 240
 ctgcagatga acagcctgcg ggccgaggac acagccgtgt actattgtgc caaggactac 300
 tattacgatt ccggctctta ttacgactcc ttctttgatt actggggcca gggcaccctg 360
 gtgacagtga gctcc 375

<210> 78

<211> 125

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.d.IgG1.3 VH

<400> 78

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

<210> 79

<211> 375

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.d.IgG1.3 VH ADN

<400> 79

gaggtgcagc tgctggagtc tggaggagac ctggtgcagc caggaggcag cctgaggctg 60

tcctgcgcca cctctggctt cacattttcc aactatgcca tgaattgggt gcgccaggca 120

cctggcaagg gactggagtg ggtgtctgtg atctctgtga gcggcggtc tacctactat 180

gccgacagcg tgaagggccg gttcaccatc agcagagata actccaagaa tacactgtat 240

ctgcagatga acagcctgcg ggccgaggac acagccgtgt actattgtgc caaggactac 300

tattacgatt ccggctctta ttacgactcc ttcttgatt actggggcca gggcaccctg 360

gtgacagtga gctcc 375

<210> 80

<211> 125

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.e.IgG1.3 VH ILT4.8.IgG1.3 VH

<400> 80

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
 100 105 110

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

<210> 81

<211> 375

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.e.IgG1.3 VH ADN ILT4.8.IgG1.3 VH ADN

<400> 81

gaggtgcagc tgctggagtc tggaggagga ctggtgcagc caggaggcag cctgaggctg 60

tcctgcgccg cctctggcct cacattttcc aactatgccca tgaattgggt gcgccaggca 120

cctggcaagg gactggagtg ggtgtctgtg atctctgtga gcggcggctc tacctactat 180

gccgacagcg tgaagggccg gttcaccatc agcagagata actccaagaa tacactgtat 240

ctgcagatga acagcctgcg ggccgaggac acagccgtgt actattgtgc caaggactac 300

tattacgatt ccggctctta ttacgactcc ttctttgatt actggggcca gggcaccctg 360

gtgacagtga gctcc 375

<210> 82

<211> 105

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5 kappa VL

<400> 82

Glu Ile Ala 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 Thr Phe
 85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 83

<211> 124

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5.IgG1.3 VH

<400> 83

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

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

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

Gln Gly Arg Val Thr Met Ile Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

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

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 84
 <211> 315
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5 kappa VL ADN

<400> 84
 gaaattgcgt tgacgcagtc tccaggcacc ctgtcttgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
 gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gcacttcgg cggaggggacc 300
 aaggtggaga tcaaa 315

<210> 85
 <211> 372
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5.IgG1.3 VH ADN

<400> 85
 caggtgcagc tggcgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaagggt 60
 tctgcaagg catctggata caccttcacc gactactatt tacactgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggaata ttccacccta gtggtgatat cacaagcagc 180
 gcacagaact tccagggcag agtcacatg atcagggaca cgtccacgag caccgtctac 240
 atggaactga gcagcctgag atctgaagac acggccgtgt attactgtgc gagagggggt 300
 gtattacgat atcttgactg gtccatgct ttgatatct ggggccaagg gacaatggtc 360
 accgtctctt ca 372

<210> 86
 <211> 105
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5.a kappa VL 21A5.1K ILT4.9K VL

<400> 86

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 Thr Phe
85 90 95

Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 87

<211> 124

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5.a.IgG1.3 VH ILT4.9.IgG1.3 VH

<400> 87

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

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

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

115

120

<210> 88

<211> 315

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5.a kappa VL ADN 21A5.1K ILT4.9K VL

<400> 88

gagatcgtgc tgaccagag cccaggcaca ctgtctctga gccaggaga gagggccacc 60

ctgtctctga gagcctocca gtctgtgagc tctcttacc tggcctggta tcagcagaag 120

ccaggacagg cacctaggct gctgatctac ggagccagct ccagggaac cgcatccct 180

gaccgctca gcggctccgg ctctggcaca gacttcaccc tgacaatctc taggctggag 240

cccaggagct tcgccgtgta ctattgtcag cagtatggct ccaccttgg cggcggcaca 300

aaggtggaga tcaag

315

<210> 89

<211> 372

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 21A5.a.IgG1.3 VH ADN ILT4.9.IgG1.3 VH

<400> 89

caggtgcagc tggcgcagtc cggagcagag gtgaagaagc caggagcctc tgtgaaggag 60

agctgcaagg cctccggcta cacctcaca gattactatc tgactgggt gcggcaggca 120

ccaggacagg gactggagtg gatgggcatc ttccaccctt ctggcgacat cacaagctcc 180

gccagaact ttcaggggccg ggtgacatg acaagagata ccagcacatc caccgtgtac 240

atggagctgt ctgcctgag gtctgaggac accgccgtgt actattgtgc aaggggaggc 300

gtgctgaggt atctggactg gagccacgcc ttgatatct ggggccaggg cacaatggag 360

accgtgtcct ct

372

<210> 90

<211> 107

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10 kappa VL ILT4.10K VL

<400> 90

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

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

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Ile
85 90 95
Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 91

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.IgG1.3 VH ILT4.10.IgG1.3 VH

<400> 91

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

Ala Ile Ile Ser Tyr Asp Glu Tyr Asn Lys 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 Arg Glu Trp Val Gly Ile Arg Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 92
<211> 321
<212> ADN
<213> Secuencia Artificial

<220>
<223> Sintético: 10F10 kappa VL ADN ILT4.10K VL

<400> 92
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gggcattagc agtgctttag cctggtttca gcagaaacca 120
gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
agggtcaccg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag ttaaatagtt acccgatcac cttcggccaa 300
gggacacgac tggagattaa a 321

<210> 93
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Sintético: 10F10.IgG1.3 VH ADN ILT4.10.IgG1.3 VH

<400> 93
caggtgcagc tggaggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcaatt atatcatatg atgaatacaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagagtgg 300
gtggggatac gttactgggg ccagggaacc ctggtcaccg tctcctca 348

<210> 94
<211> 107
<212> PRT
<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.1 kappa VL

<400> 94

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

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

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

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

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

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

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

<210> 95

<211> 321

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.1 kappa VL ADN

<400> 95

gccatccagc tgaccagtc tctagctcc ctgtctgcc gctgggcca cagggtgacc 60

atcacatgca gagcctcca gggaatctct agcgccctgg cctggtacca gcagaagcca 120

ggcaaggccc ctaagctgct gatctatgat gcctcctctc tggagagcgg agtgccatcc 180

agggtcaccg gctccggctc tggcacagac ttaccctga caatcagctc cctgcagcca 240

gaggatttcg ccacatacta ttgtcagcag ttcaacagct accccatcac ctttgccag 300

ggcacacggc tggagatcaa g 321

<210> 96

<211> 107

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.3 kappa VL ILT4.11K VL

<400> 96

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

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

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

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

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

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

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

<210> 97

<211> 321

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.3 kappa VL ADN ILT4.11K VL ADN

<400> 97

gccatccagc tgaccagtc tctagctcc ctgtctgccg gcgtgggcga cagggtgacc 60

atcacatgca gagcctcca gggaatctct agcgccctgg cctggtacca gcagaagcca 120

ggcaaggccc ctaagctgct gatctatgat gcctcctctc tggagagcgg agtgccatcc 180

agggtcagcg gtcctggctc tggcacagac ttaccctga caatcagctc cctgcagcca 240

gaggatttcg ccacatacta ttgtcagcag ttcaacagct accccatcac cttggccag 300

ggcacacggc tggagatcaa g 321

<210> 98

<211> 330

<212> PRT

<213> Homo sapiens

<220>

<221> características_diversas

<222> (1)..(330)

<223> Región Constante Humano IgG1f

<400> 98

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

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 99

<211> 993

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: IgG1f Región Constante ADN

<400> 99

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60
 ggcacagcgg ccttgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
 tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca 180
 ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 240
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300
 aaatcttggt acaaaactca cacatgccca ccgtgccag cacctgaact cctgggggga 360
 ccgtcagtct tctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 420
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgaggagga gcagtacaac 540
 agcacgtacc gtgtggtcag cgtctcacc gtctgcacc aggactggct gaatggcaag 600
 gagtacaagt gcaaggctc caacaaagcc ctcccagccc ccatcgagaa aacctctcc 660
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 720
 atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840
 ctggactccg acggctcctt ctctctat agcaagctca ccgtggacaa gagcaggtgg 900
 cagcagggga acgtcttctc atgtccgtg atgcatgagg ctctgcacaa ccactacacg 960
 cagaagagcc tctccctgtc cccgggtaaa tga 993

<210> 100

<211> 329

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: IgG1.3 (o IgG1.3f) cadena pesada de una región constante
(L234A, L235E, G237A)

<400> 100

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

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

225 230 235 240
 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly
 325

<210> 101

<211> 107

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Cadena ligera ejemplar de una región constante

<400> 101

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> 102

<211> 329

<212> PRT

<213> Homo sapiens

<220>

<221> características_diversas

<222> (1)..(329)

<223> IgG1f (alotipo f de tipo silvestre) cadena pesada de región constante

<400> 102

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

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
 325

<210> 103

<211> 329

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: IgG1.1f Cadena pesada de una región constante (L234A, L235E, G237A, A330S, P331S)

<400> 103

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

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

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

130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205
 Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240
 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly
 325

<210> 104

<211> 329

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: IgG1fa.P238K (o IgG1.P238K) cadena pesada de una región constante

<400> 104

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

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

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

35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu Gly Gly Lys Ser Val Phe Leu Phe Pro Pro
 115 120 125
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly
 325

<210> 105
 <211> 990
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Sintético: IgG1.3 cadena pesada de una región constante ADN

<400> 105

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gcgctgacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg    60
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtcg    120
tggaactcag gcgccctgac cagcggcggtg cacaccttcc cggctgtcct acagtcttca    180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc    240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc    300
aaatcttggt acaaaactca cacatgcccc ccgtgcccag cacctgaagc cgaagggggc    360
ccgtcagtct tctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct    420
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg    480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgaggagga gcagtacaac    540
agcacgtacc gtgtggtcag cgtcctcacc gtctgcacc aggactggct gaatggcaag    600
gagtacaagt gcaaggctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc    660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag    720
atgaccaaga accaggtcag cctgacctgc ctggtaaag gcttctatcc cagcgacatc    780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg    840
ctggactccg acggctcctt ctctcttat agcaagctca ccgtggacaa gagcaggtgg    900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacag    960
cagaagagcc tctccctgtc cccgggtga                                     990

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<210> 106
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Sintético: Cadena ejemplar ligera de una región constante de ADN

<400> 106

cgtacggtgg ctgcaccatc tgtcttcac ttcccgccat ctgatgagca gttgaaatct 60
 ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagagggc caaagtacag 120
 tgaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180
 agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240
 aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcaciaag 300
 agcttcaaca ggggagagtg ttag 324

<210> 107
 <211> 598
 <212> PRT
 <213> Homo sapiens

<220>
 <221> características_diversas
 <222> (1)..(598)
 <223> Precurso humano ILT4, con señal de péptido

<400> 107

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

Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp
 20 25 30

Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser
 35 40 45

Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
 50 55 60

Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn
 65 70 75 80

Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr
 85 90 95

Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro
 100 105 110

Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala
 115 120 125

Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys
 130 135 140

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

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

Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp
 180 185 190

Ser His Arg Cys Tyr Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser
 195 200 205

Ser Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys
 210 215 220

Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser
 225 230 235 240

Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu
 245 250 255

Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro
 260 265 270

Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg
 275 280 285

Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser
 290 295 300

Glu Cys Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln
 305 310 315 320

Ile Arg Gly Thr Pro Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala
 325 330 335

Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His
 340 345 350

Thr Phe Leu Leu Thr Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu
 355 360 365

Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser
 370 375 380

Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu
 385 390 395 400

Asn Ser Asp Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu
 405 410 415

Val Val Ser Gly Pro Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro
 420 425 430

Ile Ser Thr Pro Ala Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
 435 440 445

Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
 450 455 460

Ile Leu Val Ala Val Val Leu Leu Leu Leu Leu Leu Leu Leu Phe
465 470 475 480

Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
485 490 495

Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
500 505 510

Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
515 520 525

Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly
530 535 540

Val Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp Val
545 550 555 560

Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr Glu
565 570 575

Pro Pro Pro Ser Gln Glu Arg Glu Pro Pro Ala Glu Pro Ser Ile Tyr
580 585 590

Ala Thr Leu Ala Ile His
595

<210> 108

<211> 577

<212> PRT

<213> Homo sapiens

<220>

<221> características_diversas

<222> (1)..(577)

<223> Desarrollo humano ILT4, sin señal de péptido

<400> 108

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1 5 10 15

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

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

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

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr

65 70 75 80
 Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
 85 90 95
 Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
 100 105 110
 Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys Glu Ser Gln Val Ala
 115 120 125
 Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu Glu His Pro Gln
 130 135 140
 Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
 145 150 155 160
 Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
 165 170 175
 Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
 180 185 190
 Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
 195 200 205
 Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
 210 215 220
 Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu
 225 230 235 240
 Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
 245 250 255
 Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln
 260 265 270
 Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro
 275 280 285
 Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
 290 295 300
 Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
 305 310 315 320
 Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
 325 330 335
 Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
 340 345 350
 Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
 355 360 365

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

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Pro
 385 390 395 400

Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro Ile Ser Thr Pro Ala
 405 410 415

Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser
 420 425 430

Gly Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu Val Ala Val
 435 440 445

Val Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His
 450 455 460

Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe
 465 470 475 480

Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr Asp Arg Gly Leu
 485 490 495

Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu Asn Leu Tyr
 500 505 510

Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr
 515 520 525

Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu
 530 535 540

His Ser Leu Thr Leu Arg Arg Lys Ala Thr Glu Pro Pro Pro Ser Gln
 545 550 555 560

Glu Arg Glu Pro Pro Ala Glu Pro Ser Ile Tyr Ala Thr Leu Ala Ile
 565 570 575

His

<210> 109

<211> 438

<212> PRT

<213> Homo sapiens

<220>

<221> características_diversas

<222> (1)..(438)

<223> Región ILT4 ECD humano

<400> 109

Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser Val Ile

1 5 10 15
 Thr Gln Gly Ser Pro Val Thr Leu Ser Cys Gln Gly Ser Leu Glu Ala
 20 25 30
 Gln Glu Tyr Arg Leu Tyr Arg Glu Lys Lys Ser Ala Ser Trp Ile Thr
 35 40 45
 Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile Pro Ser
 50 55 60
 Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr Ser Arg
 65 70 75 80
 Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met Thr Gly
 85 90 95
 Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val Val Thr
 100 105 110
 Ser Gly Gly Arg Val Thr Leu Gln Cys Glu Ser Gln Val Ala Phe Gly
 115 120 125
 Gly Phe Ile Leu Cys Lys Glu Gly Glu Glu Glu His Pro Gln Cys Leu
 130 135 140
 Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe Ser Val
 145 150 155 160
 Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr Gly Tyr
 165 170 175
 Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu Leu Glu
 180 185 190
 Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val Gln Pro
 195 200 205
 Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys Val Ser
 210 215 220
 Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu Arg Asp
 225 230 235 240
 Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser Gln Ala
 245 250 255
 Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln Tyr Arg
 260 265 270
 Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro Ser Asp
 275 280 285
 Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro Phe Ile
 290 295 300

Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val Thr Leu
305 310 315 320

Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr Lys Ala
325 330 335

Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu Tyr Pro
340 345 350

Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala His Ala
355 360 365

Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Asn Ser Asp Pro Tyr Leu Leu
370 375 380

Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Pro Ser Met
385 390 395 400

Gly Ser Ser Pro Pro Pro Thr Gly Pro Ile Ser Thr Pro Ala Gly Pro
405 410 415

Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu
420 425 430

Gly Arg His Leu Gly Val
435

<210> 110

<211> 597

<212> PRT

<213> Homo sapiens

<220>

<221> características_diversas

<222> (1)..(597)

<223> Precurso Humano ILT4, con señal de péptido, isdeoma 2

<400> 110

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

Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp
20 25 30

Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser
35 40 45

Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50 55 60

Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn

65 70 75 80
 Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr
 85 90 95
 Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro
 100 105 110
 Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala
 115 120 125
 Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys
 130 135 140
 Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu
 145 150 155 160
 Glu Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser
 165 170 175
 Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp
 180 185 190
 Ser His Arg Cys Tyr Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser
 195 200 205
 Ser Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys
 210 215 220
 Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser
 225 230 235 240
 Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu
 245 250 255
 Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro
 260 265 270
 Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg
 275 280 285
 Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser
 290 295 300
 Glu Cys Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln
 305 310 315 320
 Ile Arg Gly Thr Pro Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala
 325 330 335
 Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His
 340 345 350
 Thr Phe Leu Leu Thr Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu
 355 360 365

Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser
 370 375 380

Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Leu
 385 390 395 400

Asn Ser Asp Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu
 405 410 415

Val Val Ser Gly Pro Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro
 420 425 430

Ile Ser Thr Pro Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
 435 440 445

Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly Ile
 450 455 460

Leu Val Ala Val Val Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu
 465 470 475 480

Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg
 485 490 495

Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr
 500 505 510

Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu
 515 520 525

Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val
 530 535 540

Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr
 545 550 555 560

Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr Glu Pro
 565 570 575

Pro Pro Ser Gln Glu Arg Glu Pro Pro Ala Glu Pro Ser Ile Tyr Ala
 580 585 590

Thr Leu Ala Ile His
 595

<210> 111

<211> 576

<212> PRT

<213> Homo sapiens

<220>

<221> características_diversas

<222> (1)..(576)

<223> Desarrollo humano ILT4, isdeoma 2, sin signal de péptido

<400> 111

Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser
1 5 10 15

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

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

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

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
100 105 110

Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys Glu Ser Gln Val Ala
115 120 125

Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu Glu His Pro Gln
130 135 140

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
195 200 205

Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
210 215 220

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

Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
245 250 255

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

Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro
275 280 285

Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
290 295 300

Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
305 310 315 320

Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
325 330 335

Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
340 345 350

Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
355 360 365

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

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Pro
385 390 395 400

Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro Ile Ser Thr Pro Gly
405 410 415

Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly
420 425 430

Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu Val Ala Val Val
435 440 445

Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His Arg
450 455 460

Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln
465 470 475 480

His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr Asp Arg Gly Leu Gln
485 490 495

Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala
500 505 510

Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg
515 520 525

Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His
530 535 540

Ser Leu Thr Leu Arg Arg Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu
545 550 555 560

Arg Glu Pro Pro Ala Glu Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
565 570 575

<210> 112
 <211> 437
 <212> PRT
 <213> Homo sapiens

<220>
 <221> características_diversas
 <222> (1)..(437)
 <223> Humano ILT4 isdeoma 2, ECD

<400> 112

Gly Thr Ile Pro Lys Pro Thr Leu Trp Ala Glu Pro Asp Ser Val Ile
 1 5 10 15

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

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

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

Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr Ser Arg
 65 70 75 80

Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met Thr Gly
 85 90 95

Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val Val Thr
 100 105 110

Ser Gly Gly Arg Val Thr Leu Gln Cys Glu Ser Gln Val Ala Phe Gly
 115 120 125

Gly Phe Ile Leu Cys Lys Glu Gly Glu Glu Glu His Pro Gln Cys Leu
 130 135 140

Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe Ser Val
 145 150 155 160

Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr Gly Tyr
 165 170 175

Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu Leu Glu
 180 185 190

Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val Gln Pro
 195 200 205

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

210 215 220
 Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr Lys Glu Gly Glu Arg Asp
 225 230 235 240
 Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser Gln Ala
 245 250 255
 Asn Phe Thr Leu Gly Pro Val Ser Arg Ser Tyr Gly Gly Gln Tyr Arg
 260 265 270
 Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Cys Ser Ala Pro Ser Asp
 275 280 285
 Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro Phe Ile
 290 295 300
 Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val Thr Leu
 305 310 315 320
 Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr Lys Ala
 325 330 335
 Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu Tyr Pro
 340 345 350
 Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala His Ala
 355 360 365
 Gly Thr Tyr Arg Cys Tyr Gly Ser Leu Asn Ser Asp Pro Tyr Leu Leu
 370 375 380
 Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Pro Ser Met
 385 390 395 400
 Gly Ser Ser Pro Pro Pro Thr Gly Pro Ile Ser Thr Pro Gly Pro Glu
 405 410 415
 Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly
 420 425 430
 Arg His Leu Gly Val
 435

<210> 113

<211> 454

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.IgG1.3 HC

<400> 113

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

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

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly
 450

<210> 114

<211> 107

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.4 VL

<400> 114

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

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

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Ile
 85 90 95

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

<210> 115

 $\langle 211 \rangle$ 321

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.4 VL ADN

<400> 115

gccatccagc tgaccagag ccctagctcc ctgtctgcc gctgtggcga cagggtgacc 60

atcacatgca gagcctccca gggaatctct agcgccctgg cctggttcca gcagaagcca 120

ggcaaggccc ctaagctgct gatctacgat gcctcctctc tggagtccgg cgtgccctct 180

aggttctccg gctctggcag cggcaccgac ttaccctga caatcagctc cctgcagcca 240

gaggattttg ccacatacta ttgtcagcag ttcaactctt atcccatcac ctttgccag 300

ggcacacggc tggagatcaa g 321

<210> 116

$\langle 211 \rangle$ 214

<212> PRT

<213> Secuencia Artificial

$\langle 220 \rangle$

<223> Sintético: 10F10.4 LC

<400> 116

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala

20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 117

<211> 642

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 10F10.4 LC ADN

<400> 117

gccatccagc tgaccagag ccctagctcc ctgtctgccg gcgtgggcga cagggtgacc 60

atcacatgca gagcctcca gggaatctct agcgccctgg cctggttcca gcagaagcca 120

ggcaaggccc ctaagctgct gatctacgat gcctcctctc tggagtccgg cgtgccctct 180

aggttctccg gctctggcag cggcaccgac ttaccctga caatcagctc cctgcagcca 240

gaggattttg ccacatacta ttgtcagcag ttaactctt atcccatcac ctttgccag 300

ggcacacggc tggagatcaa gcgtacggtg gccgcccgt ccggttttat cttccctcca 360

tcggacgagc agctcaagtc cggtagcgcg agcggtgtct gcctgctgaa caattctac 420

ccgcgcgaag ctaaagtga atggaaggtc gataacgcac ttcagtccgg gaacagccag 480

gaatctgtga ccgagcagga ctccaaggat tcgacctatt ccctgtctc gactctcacc 540

ctgtcaaagg ccgactacga gaagcacaag gtctacgcct gcgaagtgac ccatcagggc 600

ttgtcctcac ccgtgactaa gagcttcaac cggggagagt gt 642

<210> 118

<211> 371

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Cino ILT4 9152 dominio extracelular, incluyendo etiqueta His-Avi

<400> 118

Gln Ala Gly Ile Leu Pro Lys Pro Met Leu Trp Ala Glu Pro Asp Arg
1 5 10 15

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

Glu Ala Arg Gly Tyr His Leu Tyr Arg Glu Arg Lys Ser Ala Ser Trp
35 40 45

Ile Thr Leu Ile Arg Pro Glu Leu Val Lys Lys Gly Gln Phe Pro Ile
50 55 60

Pro Ser Ile Thr Trp Glu Asp Ala Gly Arg Tyr Arg Cys Gln Tyr Tyr
65 70 75 80

Ser His Ser Trp Trp Ser Glu His Ser Asp Pro Leu Glu Leu Val Val
85 90 95

Thr Gly Ala Tyr Arg Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val
100 105 110

Val Ala Ser Gly Gly Asn Val Thr Leu Gln Cys Asp Ser Arg Val Ala
115 120 125

Leu Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp Glu His Ser Gln
130 135 140

Arg Leu Asn Ser Gln Pro Arg Thr Arg Gly Ser Ser Arg Ala Val Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser Tyr Arg Cys Tyr
165 170 175

Gly Tyr Glu Leu His Ser Arg Tyr Val Trp Ser Leu Pro Ser Asp Leu
180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
195 200 205

Gln Pro Gly Pro Val Val Ala Gly Gly Asp Lys Leu Thr Leu Gln Cys

210 215 220
 Gly Ser Asp Ala Gly Tyr Asp Arg Phe Ala Leu Tyr Lys Glu Gly Glu
 225 230 235 240
 Arg Asp Phe Leu Gln Arg Pro Gly Gln Gln Leu Gln Ala Gly Leu Ala
 245 250 255
 Gln Ala Asn Phe Thr Leu Asp Pro Val Arg Gly Ser His Gly Gly Gln
 260 265 270
 Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Trp Ser Ala Pro
 275 280 285
 Ser Asp Pro Leu Asp Ile Leu Ile Ser Ala Gly Pro His Ser Gly Leu
 290 295 300
 Arg Arg Glu Cys Asp Pro Ala Val Ser Val Thr Gly Met Asp Gly His
 305 310 315 320
 Phe Leu Ser Asp Gln Gly Gly Ser Ser Ser Pro Gly Gly Gly Ser Gly
 325 330 335
 Gly Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly His His
 340 345 350
 His His His His Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
 355 360 365
 Trp His Glu
 370

<210> 119
 <211> 481
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: hILT4H dominio extracelular más etiqueta HIS-Avi (usado en Ejemplo 2)

<400> 119

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

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr
65 70 75 80

Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro Leu Val Leu Val Met
 85 90 95

Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala Gln Pro Ser Pro Val
 100 105 110

Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys Glu Ser Gln Val Ala
 115 120 125

Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu Glu Glu His Pro Gln
 130 135 140

Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
145 150 155 160

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
 165 170 175

Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser Ser Pro Ser Asp Leu
 180 185 190

Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro Ser Leu Ser Val
 195 200 205

Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser Leu Thr Leu Gln Cys
 210 215 220

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

Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser
 245 250 255

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

Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser Glu Ser Ser Ala Pro
 275 280 285

Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Ile Arg Gly Thr Pro
 290 295 300

Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala Ser Gly Glu Asn Val
305 310 315 320

Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His Thr Phe Leu Leu Thr
 325 330 335

Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu Arg Ser Ile His Glu
 340 345 350

Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala
 355 360 365

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

Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val Val Ser Gly Pro
 385 390 395 400

Ser Met Gly Ser Ser Pro Pro Pro Thr Gly Pro Ile Ser Thr Pro Ala
 405 410 415

Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser Asp Pro Gln Ser
 420 425 430

Gly Leu Gly Arg His Leu Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly
 435 440 445

Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly His His His His
 450 455 460

His His Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
 465 470 475 480

Glu

<210> 120

<211> 8

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Residuos 70-77 de hILT4

<400> 120

Ile Thr Arg Ile Arg Pro Glu Leu
 1 5

<210> 121

<211> 23

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Residuos 78-100 de hILT4

<400> 121

Val Lys Asn Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr
 1 5 10 15

Gly Arg Tyr Gly Cys Gln Tyr
 20

<210> 122

<211> 31
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: Residuos 70-100 de hILT4

<400> 122

Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn Gly Gln Phe His Ile
 1 5 10 15

Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr Gly Cys Gln Tyr
 20 25 30

<210> 123
 <211> 28
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: Residuos 154 de 181 de hILT4

<400> 123

Ile Leu Cys Lys Glu Gly Glu Glu Glu His Pro Gln Cys Leu Asn Ser
 1 5 10 15

Gln Pro His Ala Arg Gly Ser Ser Arg Ala Ile Phe
 20 25

<210> 124
 <211> 10
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: Residuos 425 de 434 de hILT4

<400> 124

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

<210> 125
 <211> 5
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 9G4 (ILT4.1) VH CDR1

<400> 125

Ser Tyr Tyr Trp Asn
1 5

<210> 126

<211> 16

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VH CDR2

<400> 126

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

<210> 127

<211> 8

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VH CDR3

<400> 127

Ser Gly Trp Tyr Tyr Phe Asp Tyr
1 5

<210> 128

<211> 11

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VL CDR1

<400> 128

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

<210> 129

<211> 7

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VL CDR2

<400> 129

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 130

<211> 9

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VL CDR3

<400> 130

Gln Gln Arg Ser Tyr Trp Pro Trp Thr
1 5

<210> 131

<211> 5

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 VH CDR1

<400> 131

Ser Ser Asp Ile Asn
1 5

<210> 132

<211> 17

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 VH CDR2

<400> 132

Trp Met Asn Pro Asn Ser Gly His Thr Gly Tyr Ala Gln Lys Phe Gln
1 5 10 15

Asp

<210> 133

<211> 16

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 VH CDR3

<400> 133

Gly Gly Asn Ser Ile Asp Trp Gly Phe Ser Tyr Tyr Gly Leu Asp Val
 1 5 10 15

<210> 134

<211> 11

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 VL CDR1

<400> 134

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 135

<211> 7

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 VL CDR2

<400> 135

Asp Ala Ser Ser Leu Glu Ser
 1 5

<210> 136

<211> 9

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9C8 VL CDR3

<400> 136

Gln Gln Phe Asn Ser Tyr Pro Phe Thr
 1 5

<210> 137

<211> 5

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2 VH CDR1

<400> 137

Asn Tyr Ala Ile Ser

1 5

<210> 138

<211> 17

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2 VH CDR2

<400> 138

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

1 5 10 15

Gly

<210> 139

<211> 19

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2 VH CDR3

<400> 139

Ser Ser Ile Thr Met Ile Arg Gly Ala Tyr Leu Tyr Tyr Tyr Asp Gly

1 5 10 15

Met Asp Val

<210> 140

<211> 12

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2H2 VL CDR1

<400> 140

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala

1 5 10

<210> 141
 <211> 7
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2H2 VL CDR2

<400> 141

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 142
 <211> 8
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2H2 VL CDR3

<400> 142

Gln Gln Tyr Gly Ser Ser Tyr Thr
 1 5

<210> 143
 <211> 5
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2E5 VH CDR1

<400> 143

Asn Tyr Gly Met His
 1 5

<210> 144
 <211> 17
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 2E5 VH CDR2

<400> 144

Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr Tyr Ala Glu Ser Val Lys

1 5 10 15

Gly

<210> 145

<211> 12

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5 VH CDR3

<400> 145

Asp Pro Phe Tyr Gly Ser Gly Asn Tyr Phe Asp Tyr

1 5 10

<210> 146

<211> 11

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5 VL CDR1

<400> 146

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala

1 5 10

<210> 147

<211> 7

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5 VL CDR2

<400> 147

Asp Ala Ser Asn Arg Ala Thr

1 5

<210> 148

<211> 10

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 2E5 VL CDR3

<400> 148

Gln Gln Arg Ser Asn Trp Pro Pro Trp Thr
1 5 10

<210> 149

<211> 5

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 VH CDR1

<400> 149

Ser Tyr Val Met Ser
1 5

<210> 150

<211> 17

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 VH CDR2

<400> 150

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

Gly

<210> 151

<211> 12

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 VH CDR3

<400> 151

Asp Gln Asp Ile Ile Ala Ala Tyr Tyr Phe Val Tyr
1 5 10

<210> 152

<211> 11

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 VL CDR1

<400> 152

Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala

1 5 10

<210> 153

<211> 7

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 VL CDR2

<400> 153

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 154

<211> 9

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 24E5 VL CDR3

<400> 154

Gln Gln Tyr Asn Ser Tyr Pro Leu Thr

1 5

<210> 155

<211> 5

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 VH CDR1

<400> 155

Asn Tyr Ala Met Asn

1 5

<210> 156

<211> 17

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 VH CDR2

<400> 156

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

Gly

<210> 157

<211> 16

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 VH CDR3

<400> 157

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

<210> 158

<211> 12

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 VL CDR1

<400> 158

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

<210> 159

<211> 7

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9 VL CDR2

<400> 159

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 160

<211> 9

<212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21D9 VL CDR3

<400> 160

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
 1 5

<210> 161
 <211> 5
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5 VH CDR1

<400> 161

Asp Tyr Tyr Leu His
 1 5

<210> 162
 <211> 17
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5 VH CDR2

<400> 162

Ile Phe His Pro Ser Gly Asp Ile Thr Ser Ser Ala Gln Asn Phe Gln
 1 5 10 15

Gly

<210> 163
 <211> 15
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5 VH CDR3

<400> 163

Gly Gly Val Leu Arg Tyr Leu Asp Trp Ser His Ala Phe Asp Ile
 1 5 10 15

<210> 164
 <211> 12
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5 VL CDR1

<400> 164
 Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
 1 5 10

<210> 165
 <211> 7
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5 VL CDR2

<400> 165
 Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 166
 <211> 6
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 21A5 VL CDR3

<400> 166
 Gln Gln Tyr Gly Ser Thr
 1 5

<210> 167
 <211> 5
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10 VH CDR1

<400> 167
 Ser Tyr Ala Met His
 1 5

<210> 168
 <211> 17
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10 VH CDR2

<400> 168

Ile Ile Ser Tyr Asp Glu Tyr Asn Lys Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 169
 <211> 7
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10 VH CDR3

<400> 169

Glu Trp Val Gly Ile Arg Tyr
 1 5

<210> 170
 <211> 11
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10 VL CDR1

<400> 170

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 171
 <211> 7
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: 10F10 VL CDR2

<400> 171

Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 172
<211> 9
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético: 10F10 VL CDR3

<400> 172

Gln Gln Phe Asn Ser Tyr Pro Ile Thr
1 5

<210> 173
<211> 16
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético: Residuos127-142 de hILT4

<400> 173

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

<210> 174
<211> 32
<212> PRT
<213> Secuencia Artificial

<220>
<223> Sintético: Residuos 182-213 de hILT4

<400> 174

Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp Ser His Arg Cys Tyr
1 5 10 15

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

<210> 175
<211> 15
<212> PRT
<213> Secuencia Artificial

<220>

<223> Sintético: Residuos 378-392 de hILT4

<400> 175

Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Ala His Ala Gly
1 5 10 15

<210> 176

<211> 454

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.e,IgG1f (Igual que Fc como SEQ ID NO: 98 w/o C-término. K)

<400> 176

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 Asn Tyr
20 25 30

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

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe
100 105 110

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

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

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

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

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

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

195	200	205
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu		
210	215	220
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro		
225	230	235 240
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys		
245	250	255
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val		
260	265	270
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp		
275	280	285
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr		
290	295	300
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp		
305	310	315 320
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu		
325	330	335
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg		
340	345	350
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys		
355	360	365
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp		
370	375	380
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys		
385	390	395 400
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser		
405	410	415
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser		
420	425	430
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser		
435	440	445
Leu Ser Leu Ser Pro Gly		
450		

<210> 177

<211> 454

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.e.IgG1.1f (Fc es el mismo que SEQ ID NO: 103)

<400> 177

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 Asn Tyr

20 25 30

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

35 40 45

Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe

100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr

115 120 125

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

130 135 140

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

145 150 155 160

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

165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser

180 185 190

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

195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu

210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro

225 230 235 240

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

245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Pro Gly
 450

<210> 178

<211> 449

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 21D9.e.IgG4_S228P

<400> 178

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 Asn Tyr
 20 25 30

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

35	40	45			
Ser Val Ile Ser Val 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 Asp Tyr Tyr Tyr Asp Ser Gly Ser Tyr Tyr Asp Ser Phe Phe					
100	105	110			
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr					
115	120	125			
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser					
130	135	140			
Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu					
145	150	155	160		
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His					
	165	170	175		
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser					
180	185	190			
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys					
195	200	205			
Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu					
210	215	220			
Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu					
225	230	235	240		
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu					
	245	250	255		
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser					
	260	265	270		
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu					
	275	280	285		
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr					
290	295	300			
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn					
305	310	315	320		
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser					
	325	330	335		

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

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

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

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

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

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

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

Ser

<210> 179

<211> 324

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: hlgG4 S228P (Fc de SEQ ID NO: 178)

<400> 179

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

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

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

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

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320

Leu Ser Leu Ser

<210> 180

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VH aminoácido

<400> 180

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

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

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

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

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

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

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

Thr Val Ser Ser
 115

<210> 181

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VH ADN

<400> 181

cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc ctcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttactact ggaactggat ccggcagccc 120

ccaggggaagg gactggagtg gcttggttac atctattaca gtgggagtac caagtacaac 180

ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

aagctgagct ctgtgaccgc tgcggacacg gccgtgtatt attgtgccag cagtggctgg 300

tactactttg actattgggg ccaggggaacc ctggtcaccg tctcctca 348

<210> 182

<211> 107

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VL aminoácido

<400> 182

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

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

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

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

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

Glu Asp Phe Ala Gly Tyr Tyr Cys Gln Gln Arg Ser Tyr Trp Pro Trp
 85 90 95

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

<210> 183

<211> 321

<212> ADN

<213> Secuencia Artificial

<220>

<223> Sintético: 9G4 VL ADN

<400> 183

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagggttagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcgtccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagggtatta ctgtcagcag cgtagctact ggccgtggac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 184

<211> 98

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea germinal hIGHV3-23*01

<400> 184

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

<210> 185
 <211> 11
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: Línea Germinal J Gen IGHJ4

<400> 185

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

<210> 186
 <211> 96
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Sintético: Línea Germinal hIGKV3-20*01

<400> 186

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

<210> 187

<211> 10

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea Germinal J Gen IGKJ4

<400> 187

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

<210> 188

<211> 98

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea Germinal hIGHV1-46*01

<400> 188

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 Ser Tyr
 20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg

<210> 189

<211> 11

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea Germinal J Gen IGHJ3

<400> 189

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

<210> 190

<211> 98

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea Germinal hIGHV3-30*01

<400> 190

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys 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 Arg

<210> 191

<211> 11

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea Germinal J Gen IGHJ4

<400> 191

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

<210> 192

<211> 95

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea Germinal hIGKV1-13*02

<400> 192

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

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

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

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

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

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

<210> 193

<211> 10

<212> PRT

<213> Secuencia Artificial

<220>

<223> Sintético: Línea Germinal J Gen IGKJ5

<400> 193

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