

8-mero de IL-2 diacuerpo L19

Curva	ka (1/Ms)	kd (1/s)	K _D (M)
	2,58E+06	6,88E-04	2,67E-10
Ciclo: 22	1,56 nM		
Ciclo: 23	3,125 nM		
Ciclo: 24	6,25 nM		

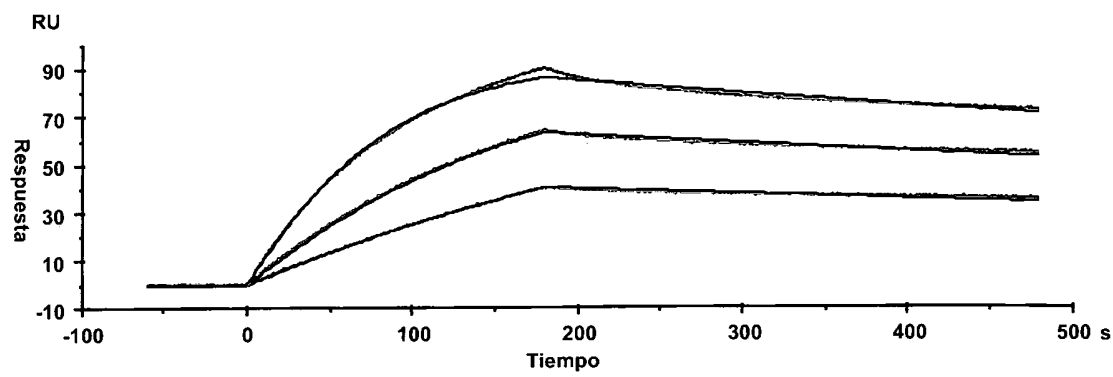


Figura 10

12-mero de IL-12 diacuerpo L19

Curva	ka (1/Ms)	kd (1/s)	K _D (M)
	2,13E+06	7,69E-04	3,62E-10
Ciclo: 32	1,56 nM		
Ciclo: 33	3,125 nM		
Ciclo: 34	6,25 nM		

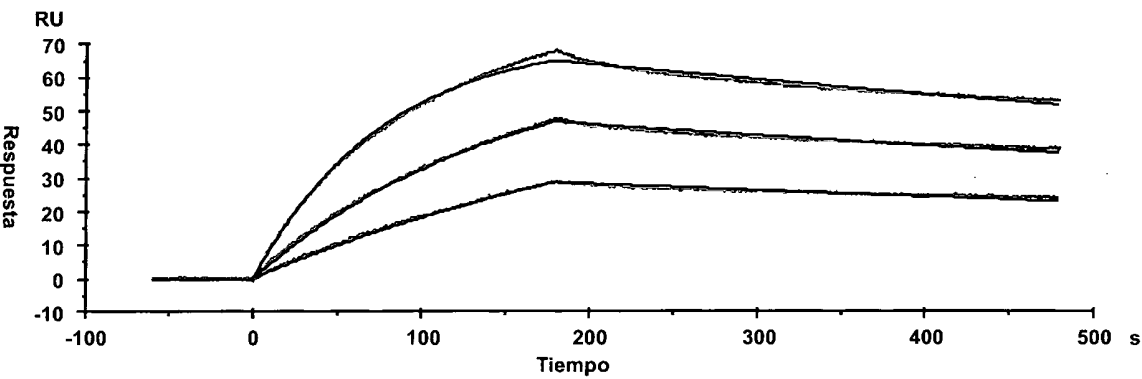


Figura 11

Dominio A de la tenascina C inmovilizada

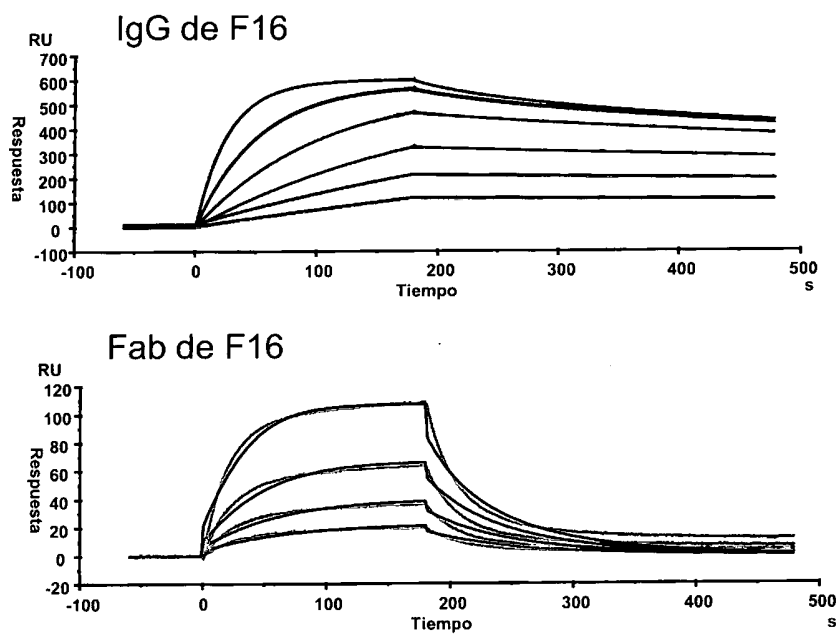
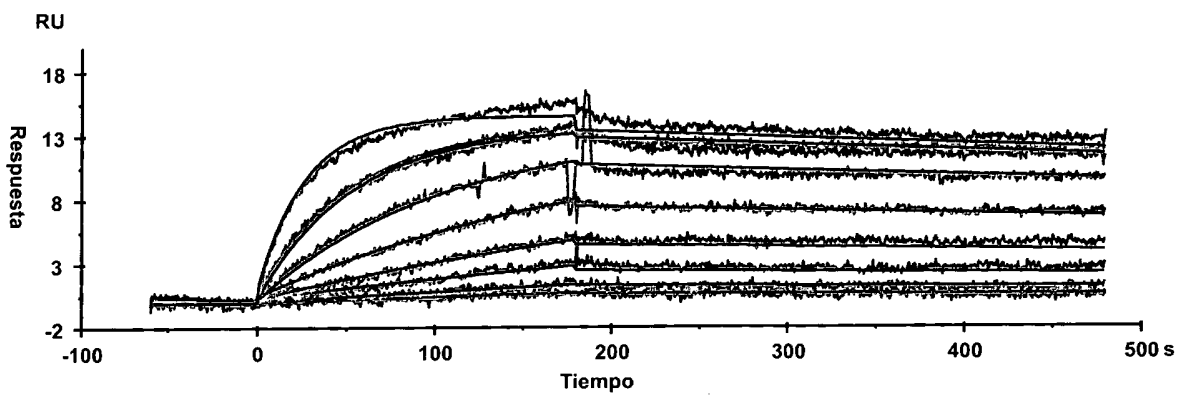


Figura 12

Receptor de IL-2 inmovilizado (β gal- γ botón)



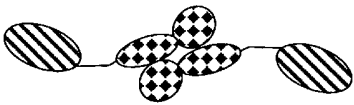
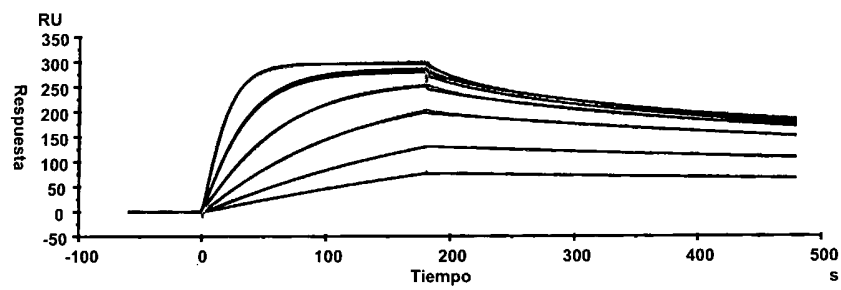
Parámetros cinéticos:

	$k_{on}(1/Ms)$	$k_{off}(1/s)$	$K_D (M)$
IL-2	7,45E+5	3,69E-4	4,95E-10

K_D publicada = ~ 1nM

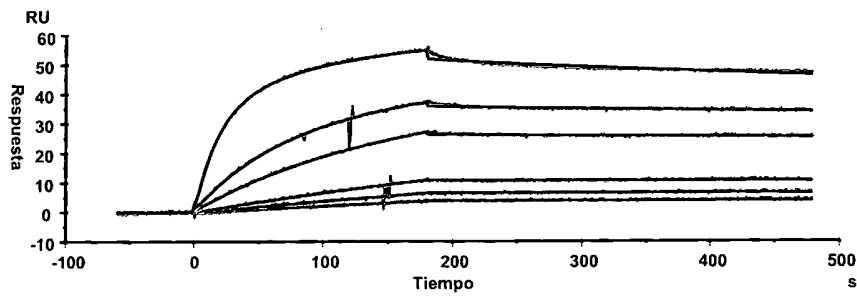
Figura 13

Dominio A1 de TNC



F16 diacuerpo IL-2

IL-2R

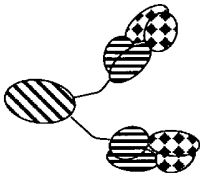
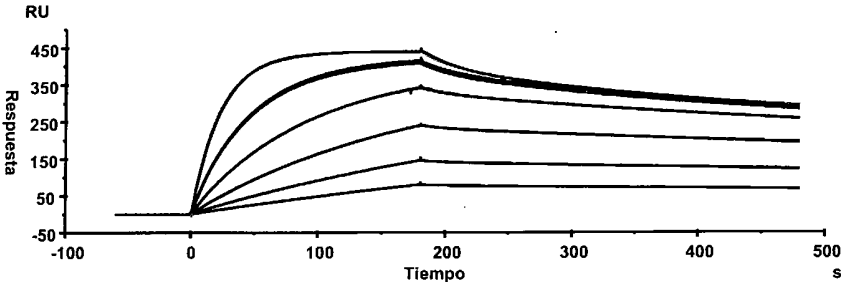


Parámetros cinéticos:

	K_D aparente (M)
TNC A1	5E-9
IL-2R	8,1E-10

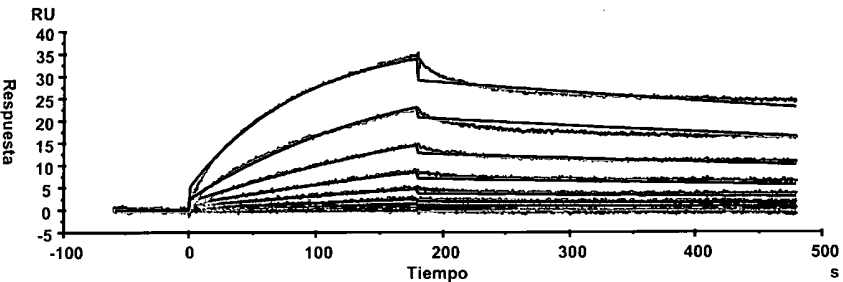
Figura 14

Dominio A1 de TNC



Fab-IL2-Fab

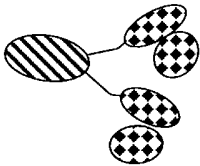
IL-2R



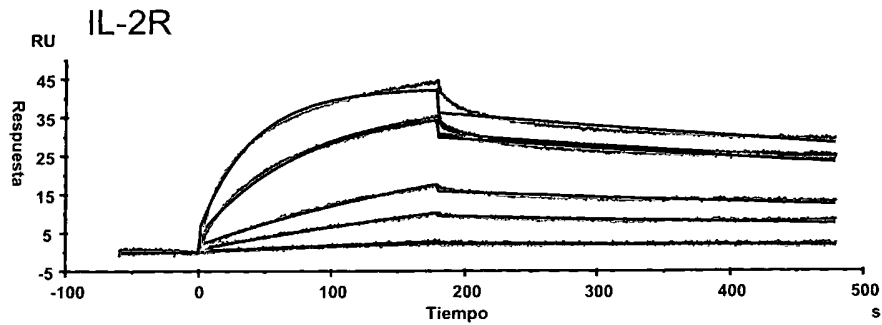
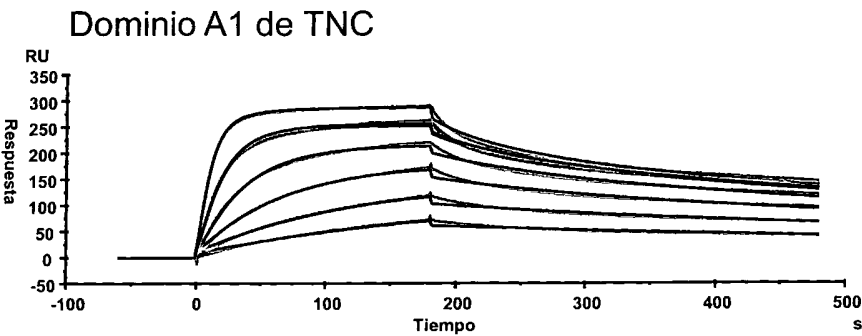
Parámetros cinéticos:

	K_D aparente (M)
TNC A1	4,8E-9
IL-2R	7,4E-9

Figura 15



scFv-IL2-scFv



Parámetros cinéticos:

	K_D aparente (M)
TNCA1	1,15E-8
IL-2R	2,5E-9

Figura 16

Resumen

formato	Dominio A1 de la tenascina C	Receptor de IL-2
	K _D aparente (M)	K _D aparente (M)
IgG de F16	2,6E-9	-
Fab de F16	5,0E-8	-
IL-2	-	4,95E-10
F16 dia IL2	5E-9	8,1E-10
Fab-IL2-Fab	4,8E-9	7,4E-9
scFv-IL2-scFv	1,15E-8	2,5E-9

Figura 17

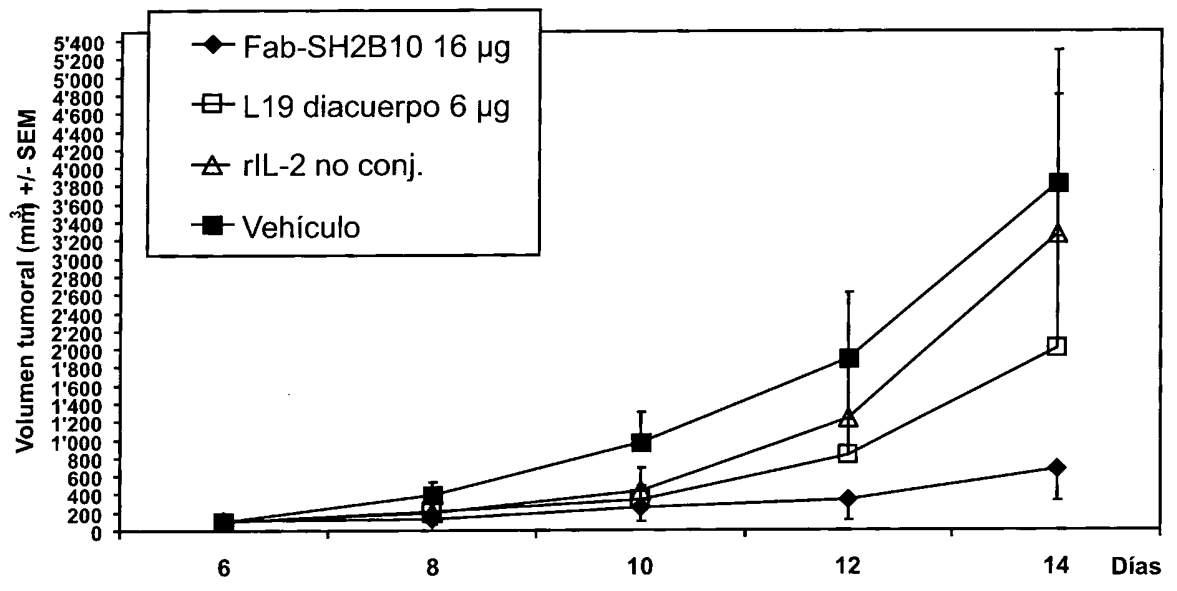


Figura 18

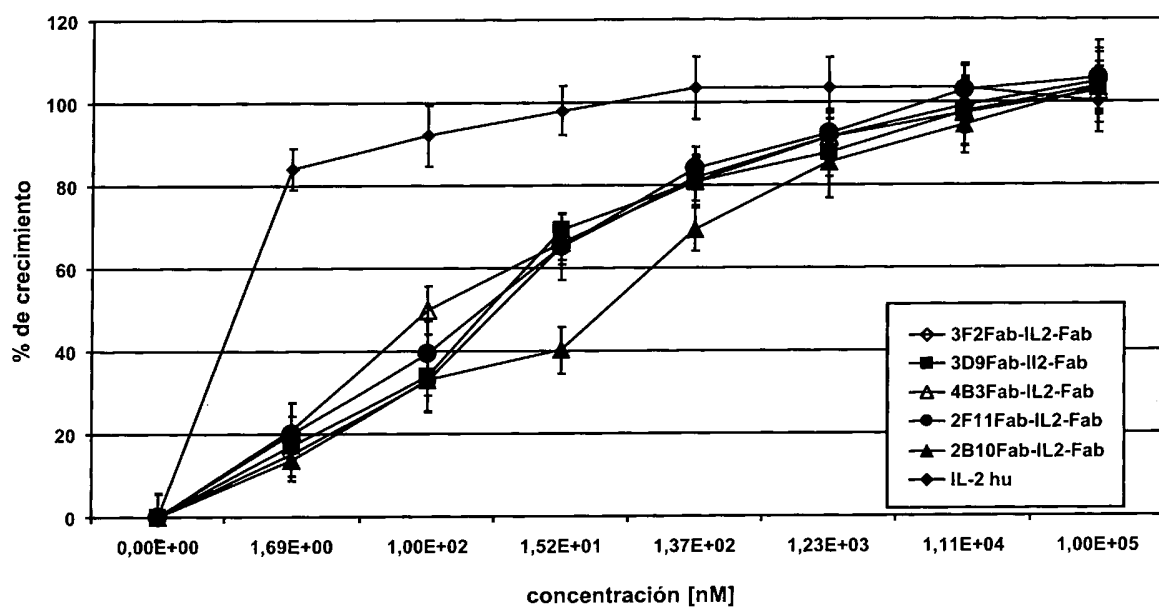


Figura 19

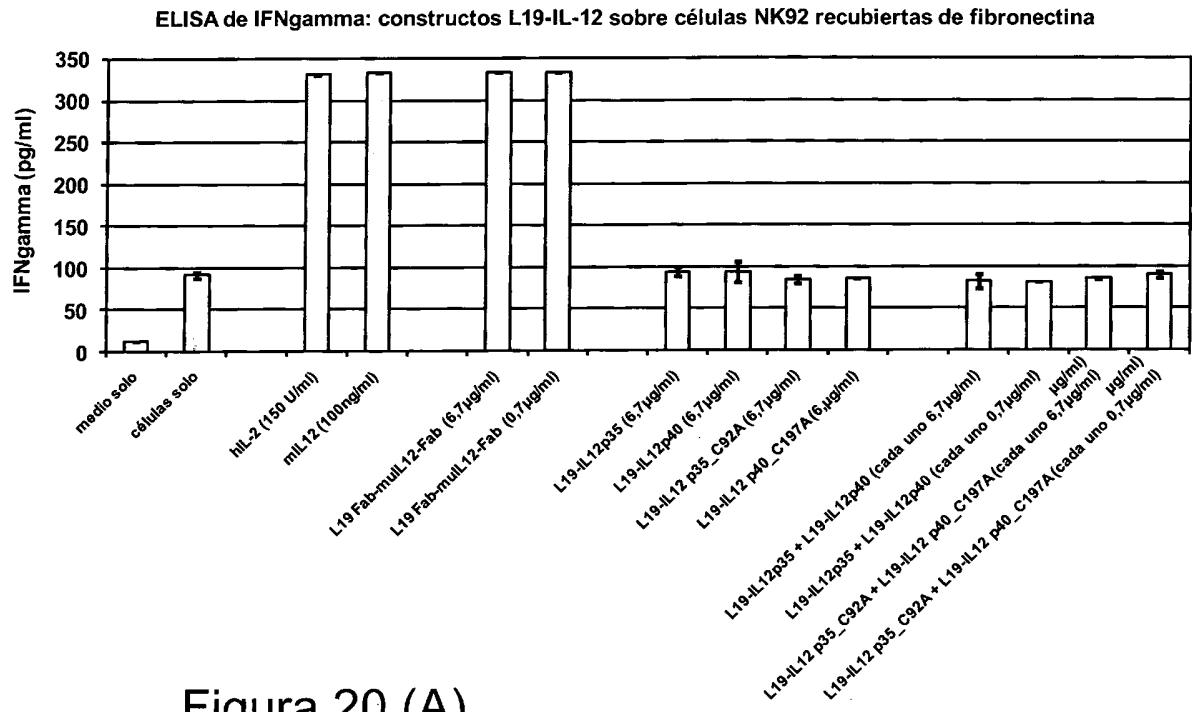


Figura 20 (A)

ELISA de IFNgamma: constructos L19 IL-12 en solución, células NK92

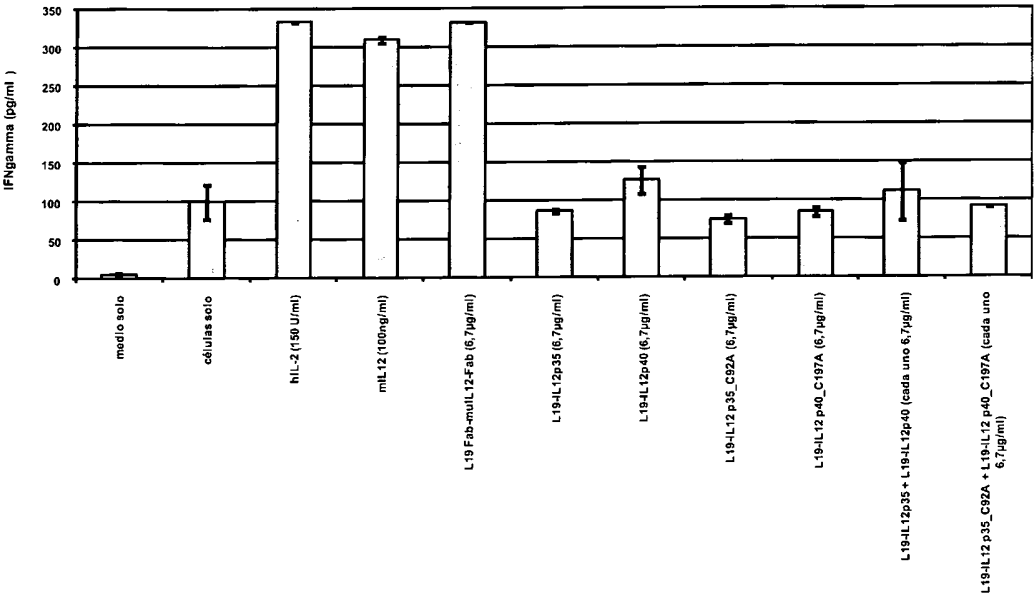


Figura 20 (B)

Figura 21

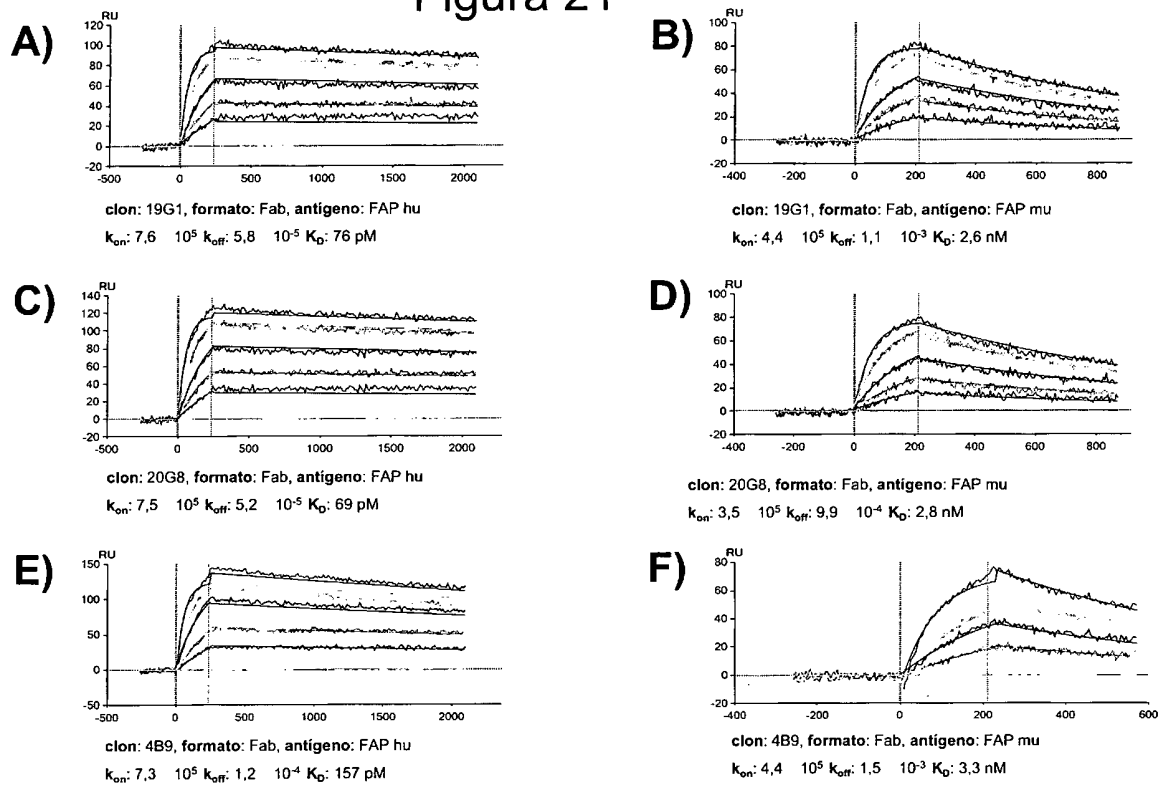
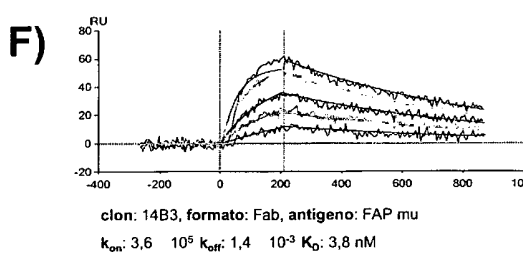
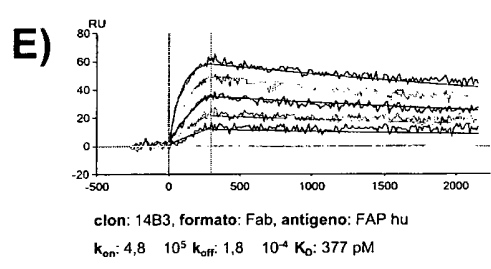
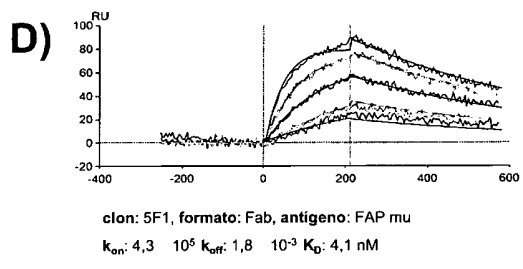
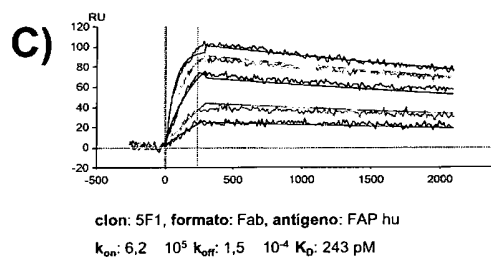
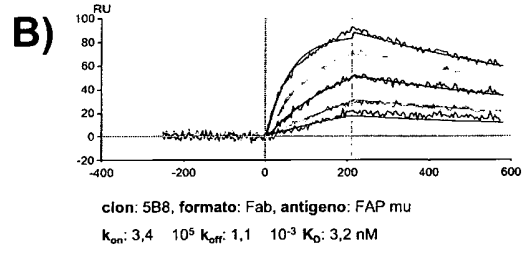
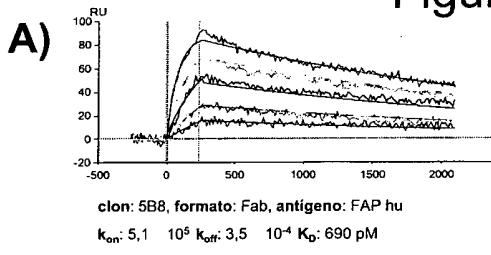


Figura 22



23 / 55

244

Figura 23

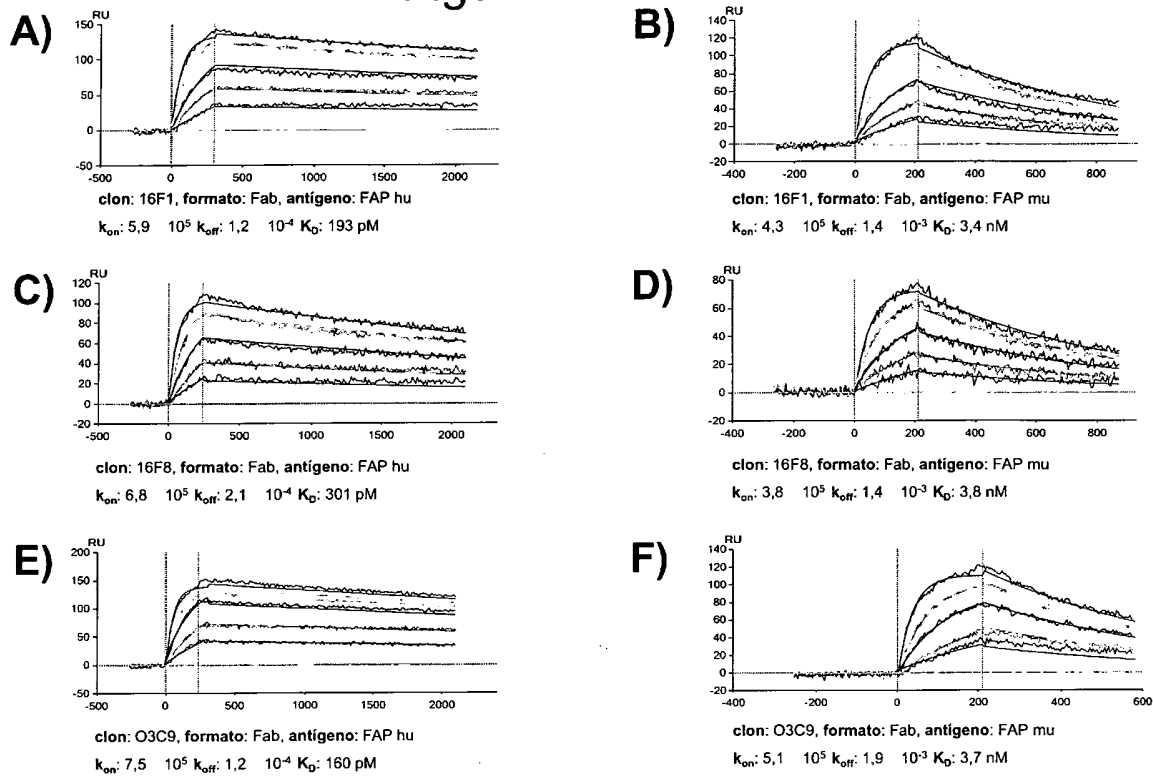


Figura 24

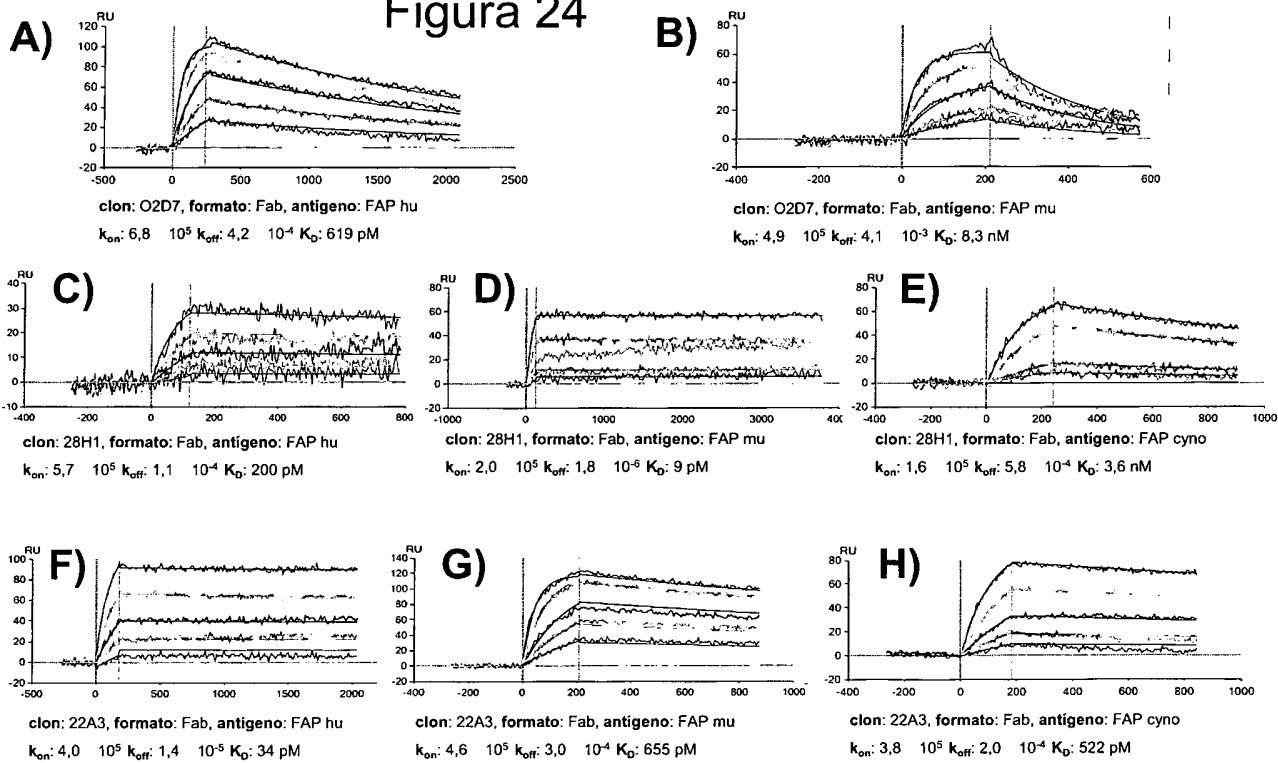


Figura 25

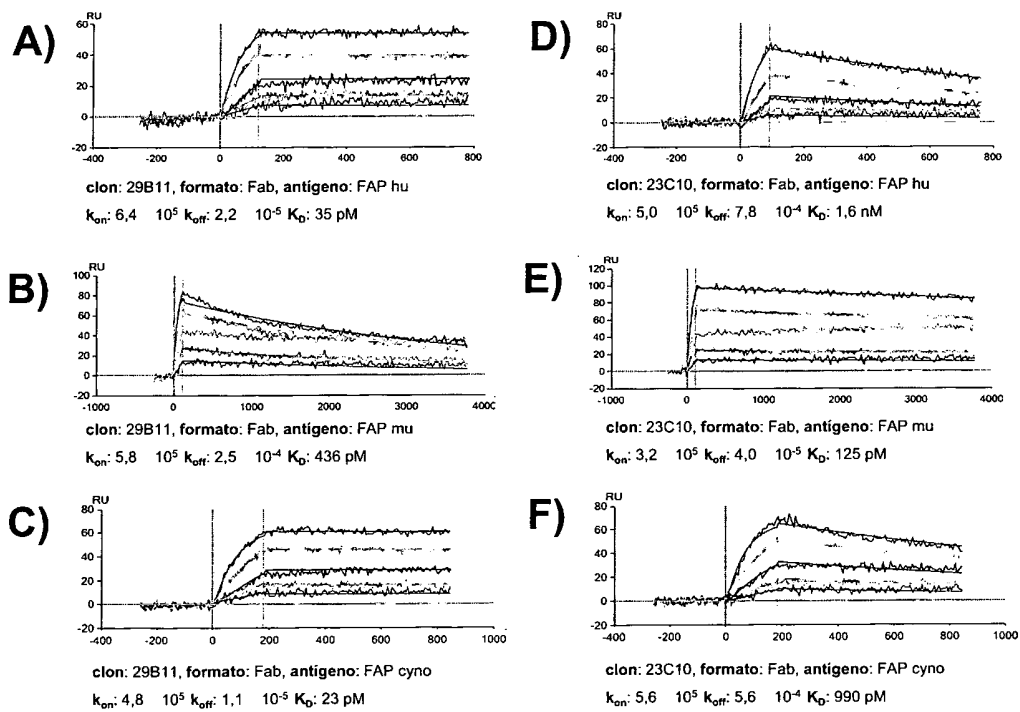
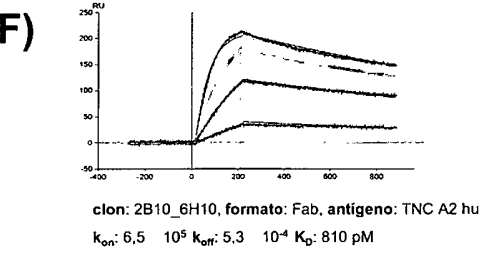
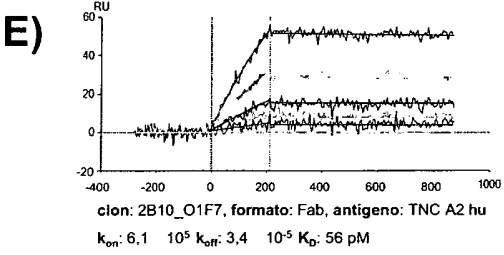
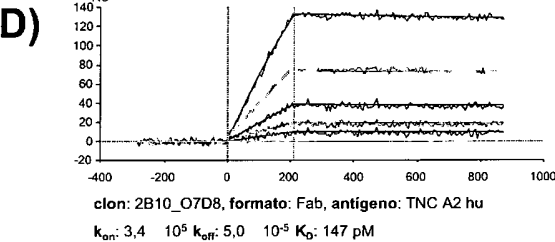
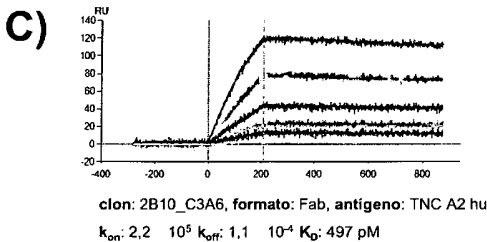
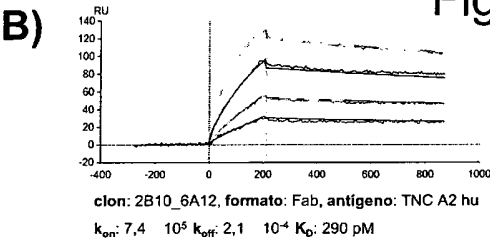
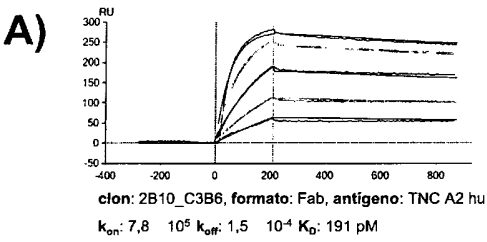


Figura 26



27/55

248

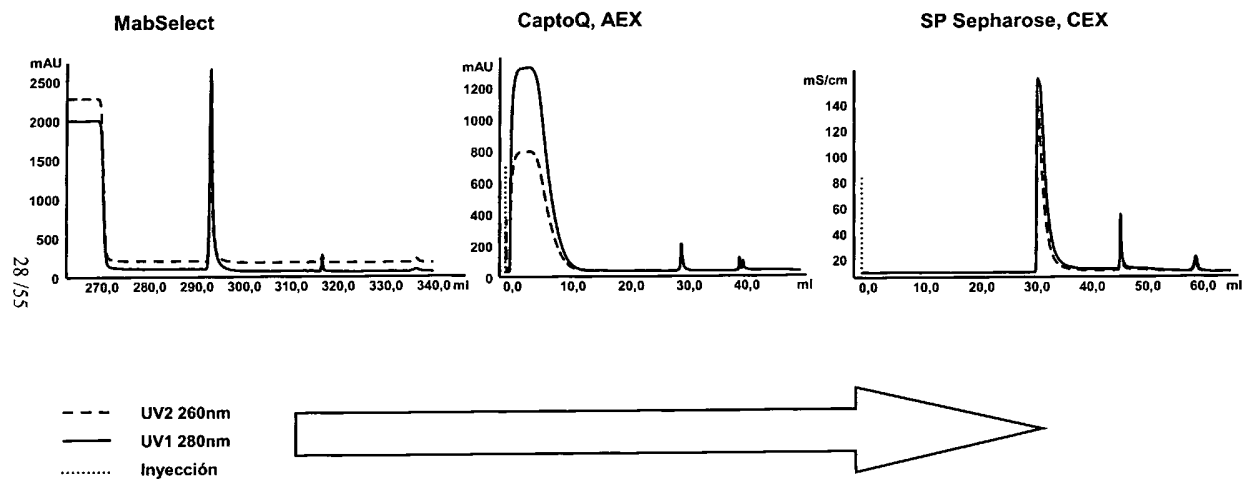


Figura 27

289

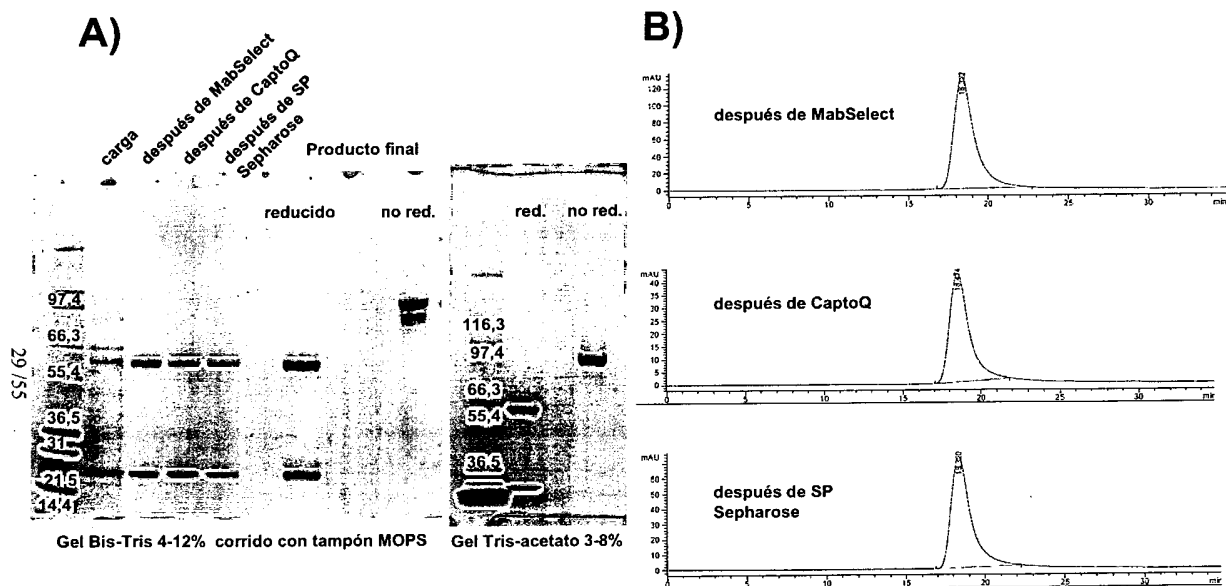


Figura 28

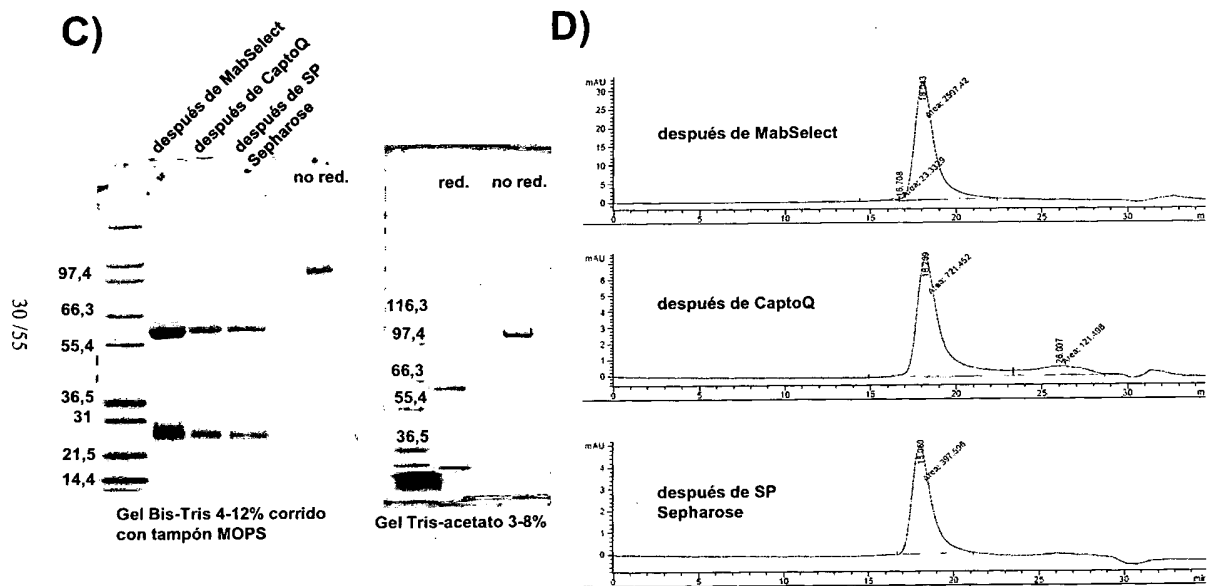


Figura 28

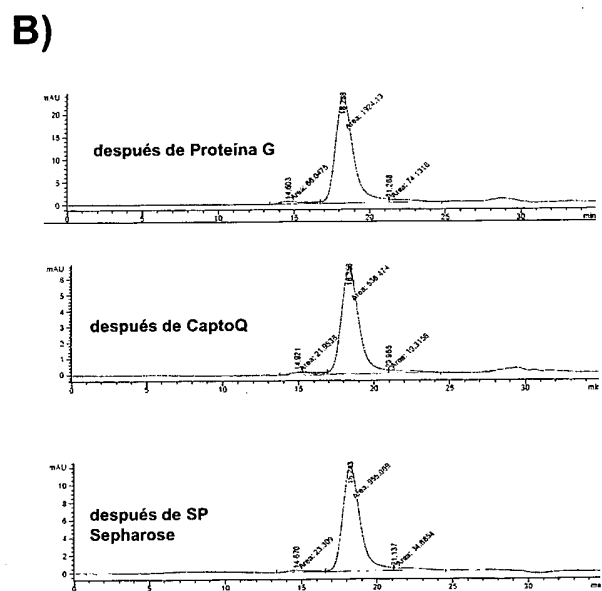
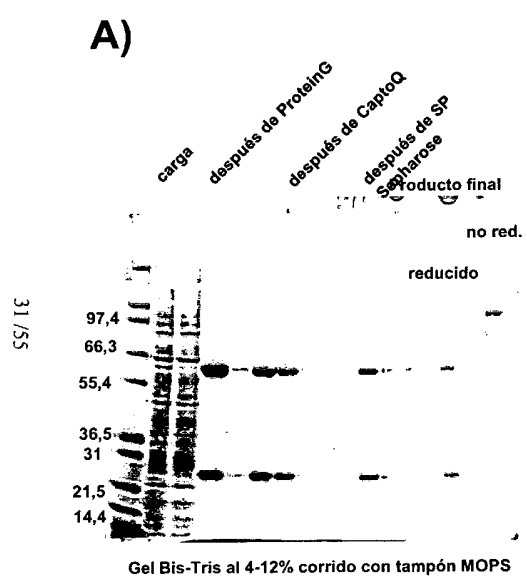


Figura 29

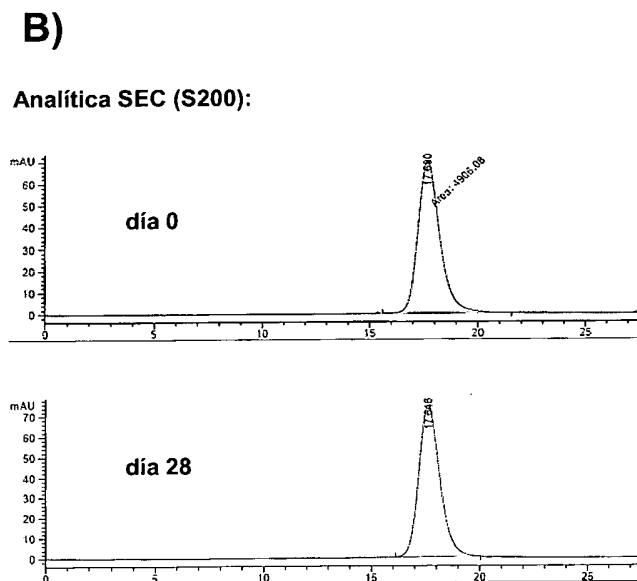
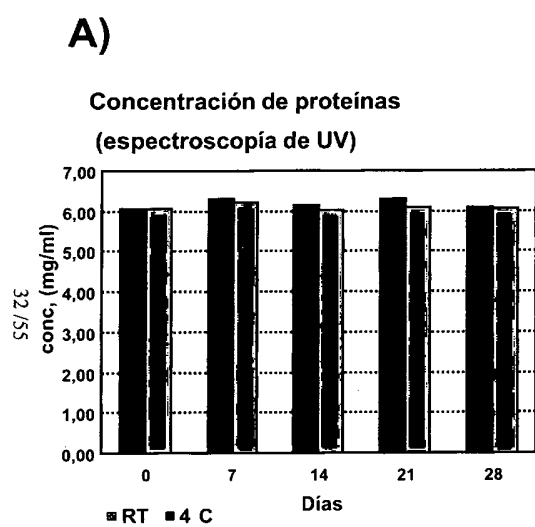
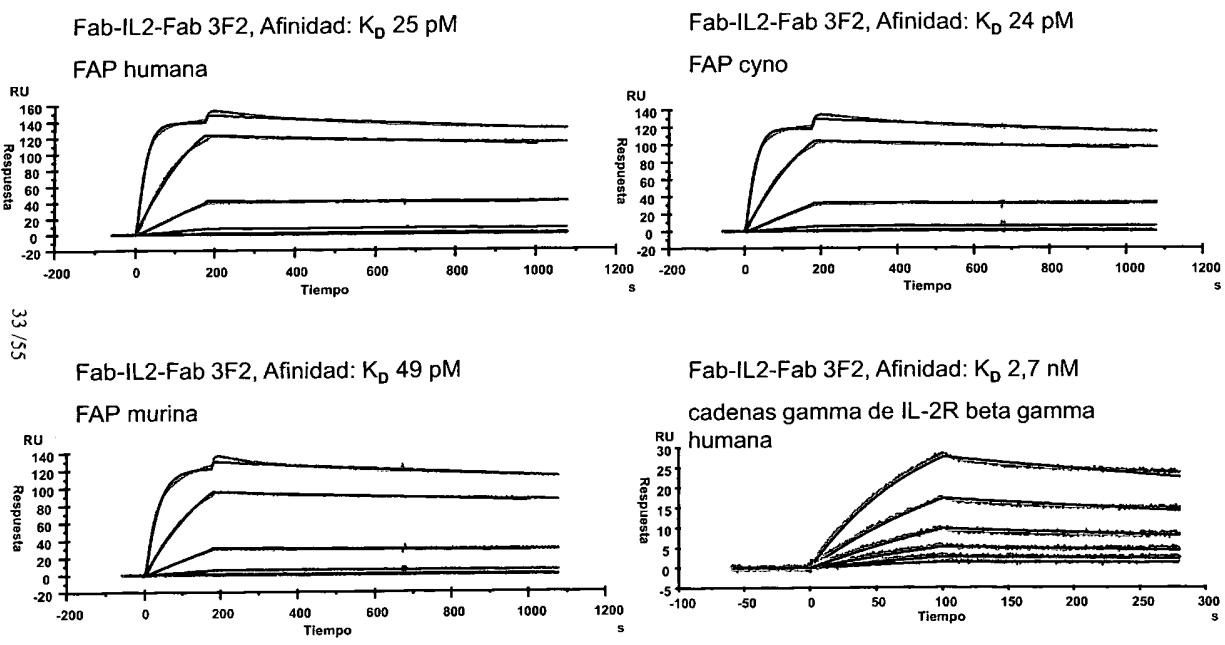


Figura 30



Fab-IL2-Fab 3F2 Anti-FAP

Figura 31

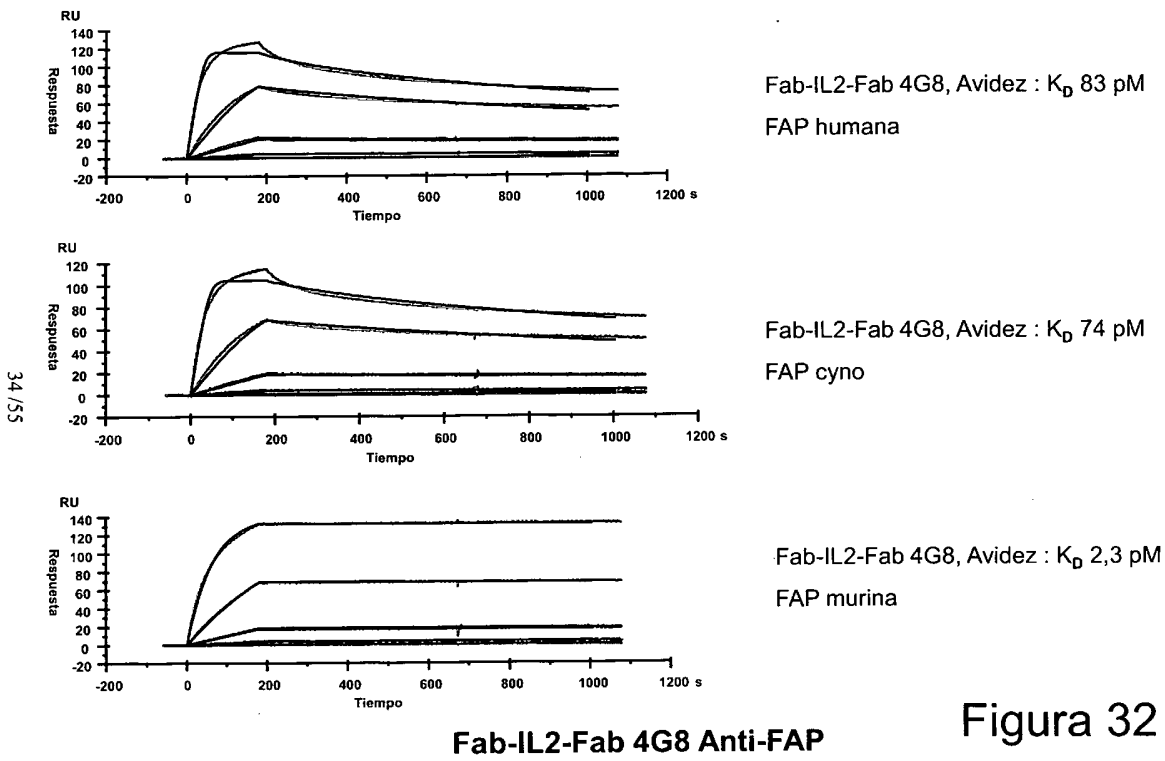
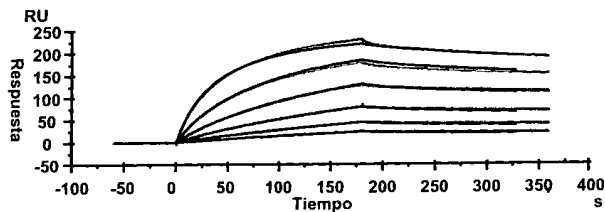
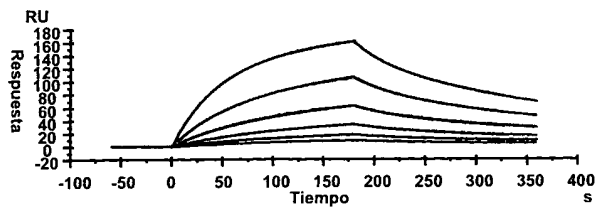


Figura 32

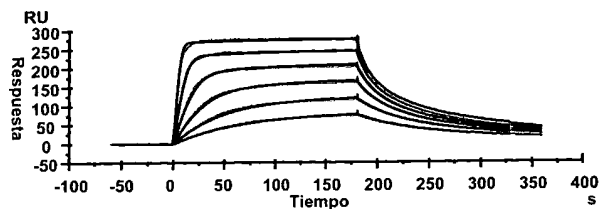
Fab-IL2-Fab 4G8, Afinidad : K_D 3,8 nM
cadenas gamma de IL-2R beta gamma humana



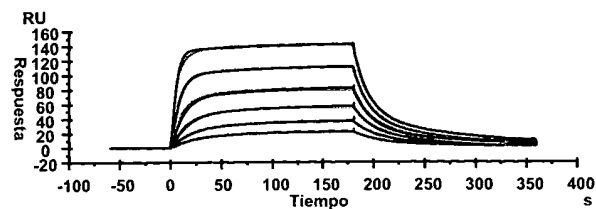
Fab-IL2-Fab 4G8, Afinidad : K_D 45,6 nM
Cadenas beta gamma de IL-2R murina



35/55
Fab-IL2-Fab 4G8, Afinidad : K_D 4,5 nM
Cadena alfa de IL-2R humana

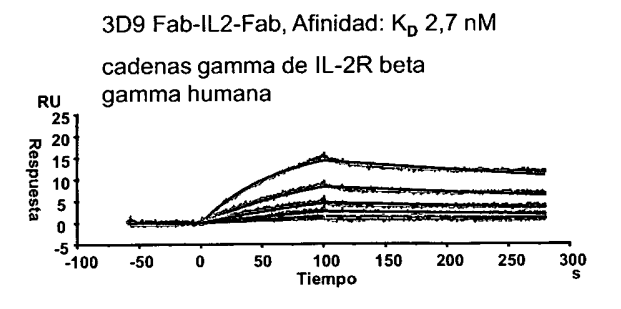
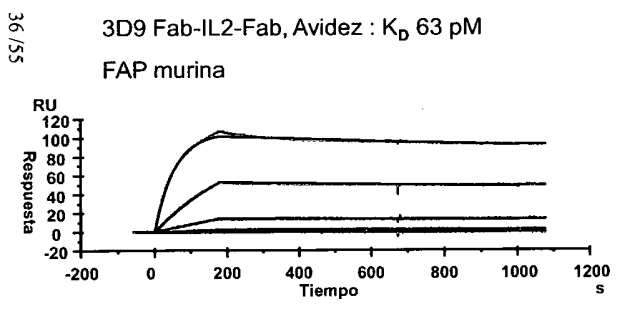
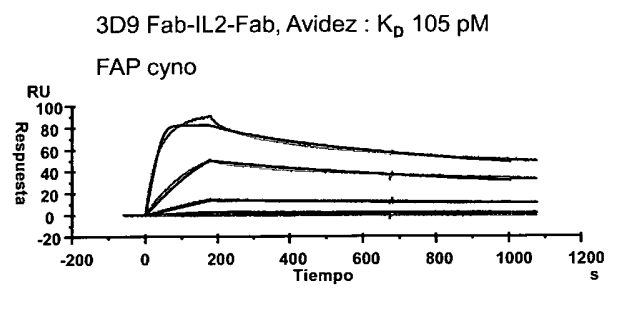
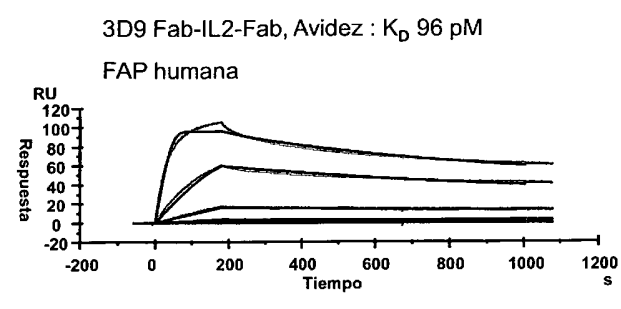


Fab-IL2-Fab 4G8, Afinidad : K_D 29 nM
Cadena alfa de IL-2R murina



Fab-IL2-Fab 4G8 anti-FAP

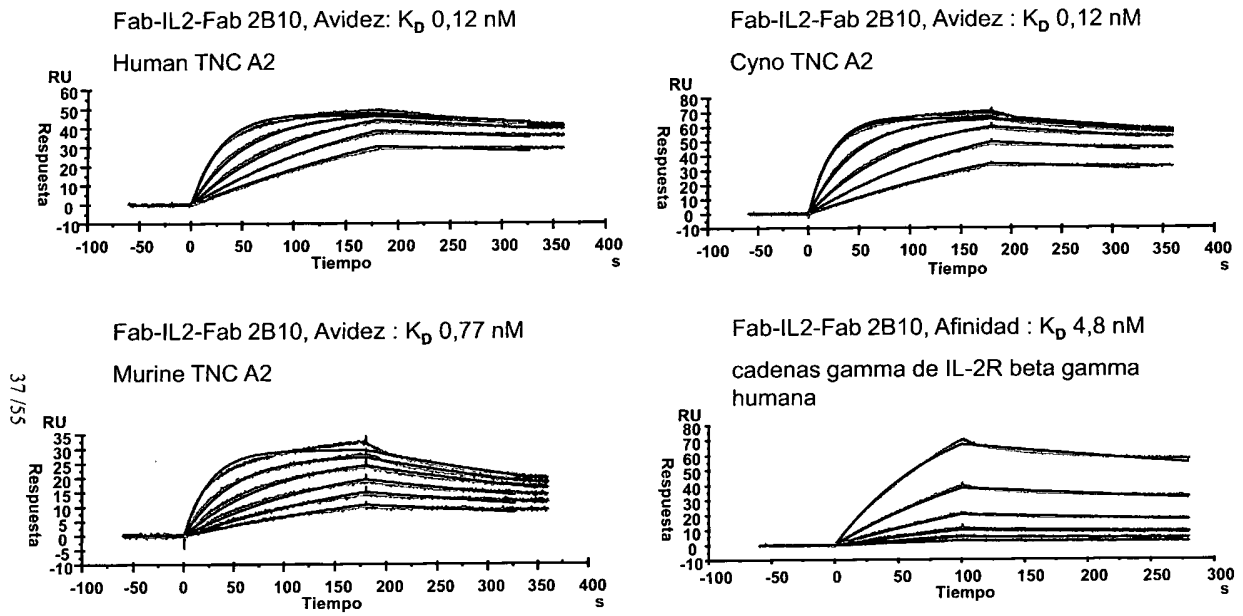
Figura 33



Fab-IL2-Fab 3D9 Anti-FAP

Figura 34

752



Fab-IL2-Fab 2B10 anti-TNC A2

Figura 35

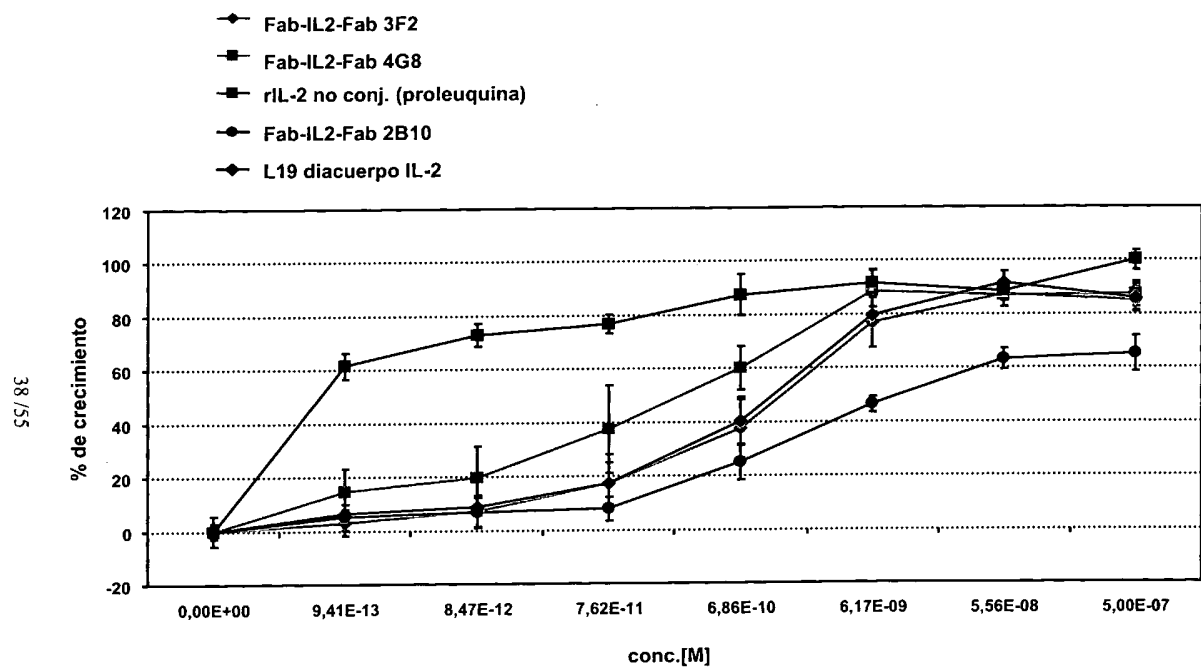
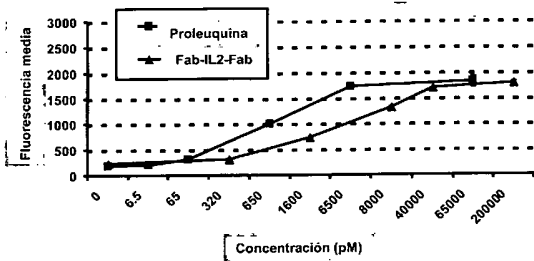
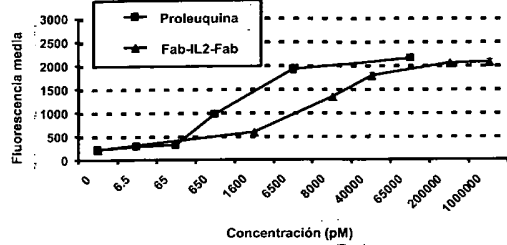


Figura 36

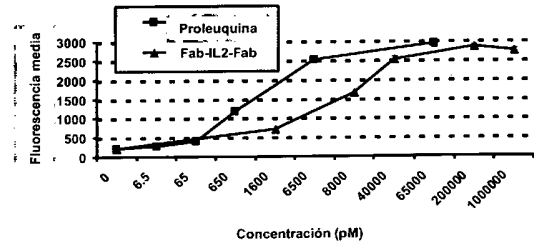
A) Ensayo PhosphoSTAT5: activación de STAT5 por Fab-IL2-Fab 4G8 vs. proleuquina en solución, células NK (CD56+)



C) Ensayo PhosphoSTAT5: activación de STAT5 por Fab-IL2-Fab 4G8 vs. proleuquina en solución. Células T citotóxicas (CD3+CD8+)



B) Ensayo PhosphoSTAT5: activación de STAT5 por Fab-IL2-Fab 4G8 vs. Proleuquina en solución. Células T ayudante (CD4+CD25-CD127+)



D) Ensayo PhosphoSTAT5: activación de STAT5 por Fab-IL2-Fab 4G8 vs. proleuquina en solución. T regs (CD4+CD25+FOXP3+)

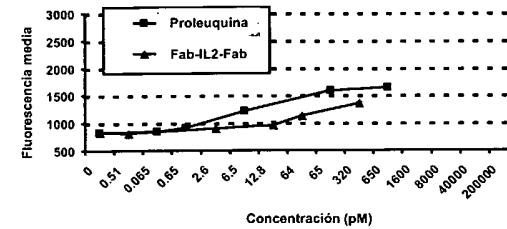


Figura 37

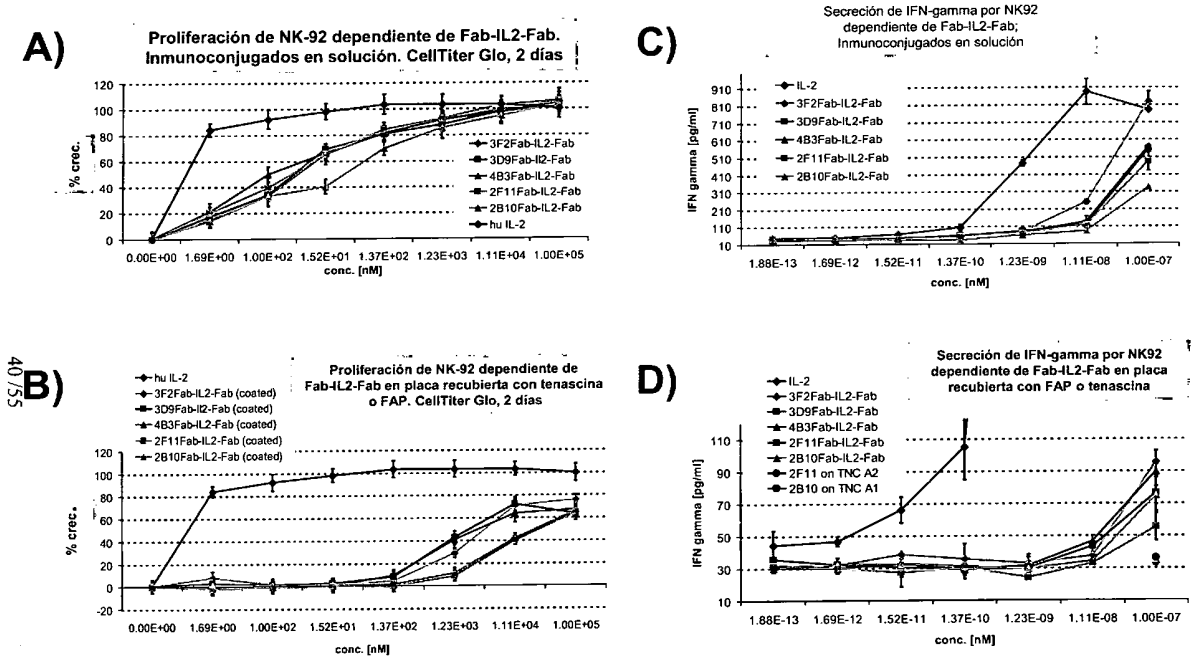


Figura 38

40/55

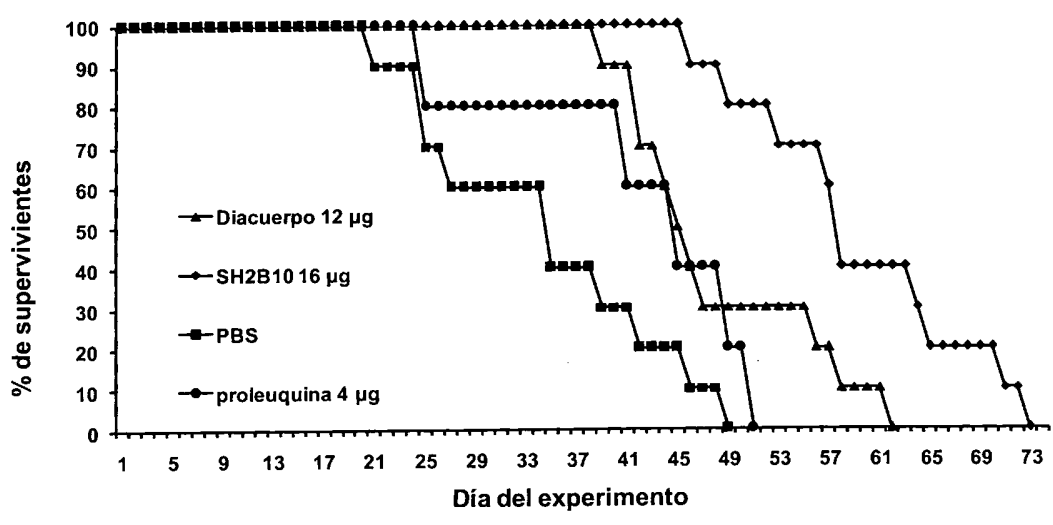


Figura 39

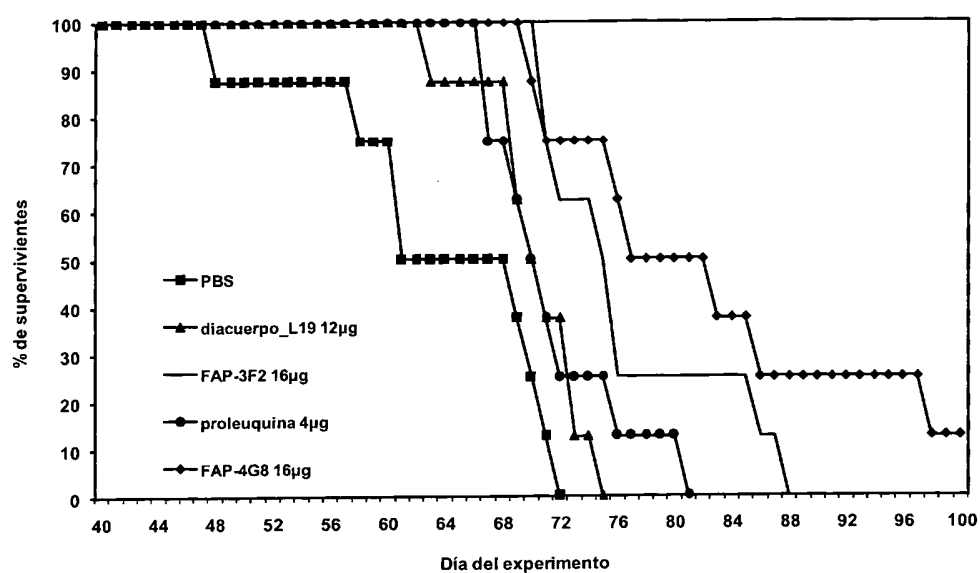


Figura 40

43/55

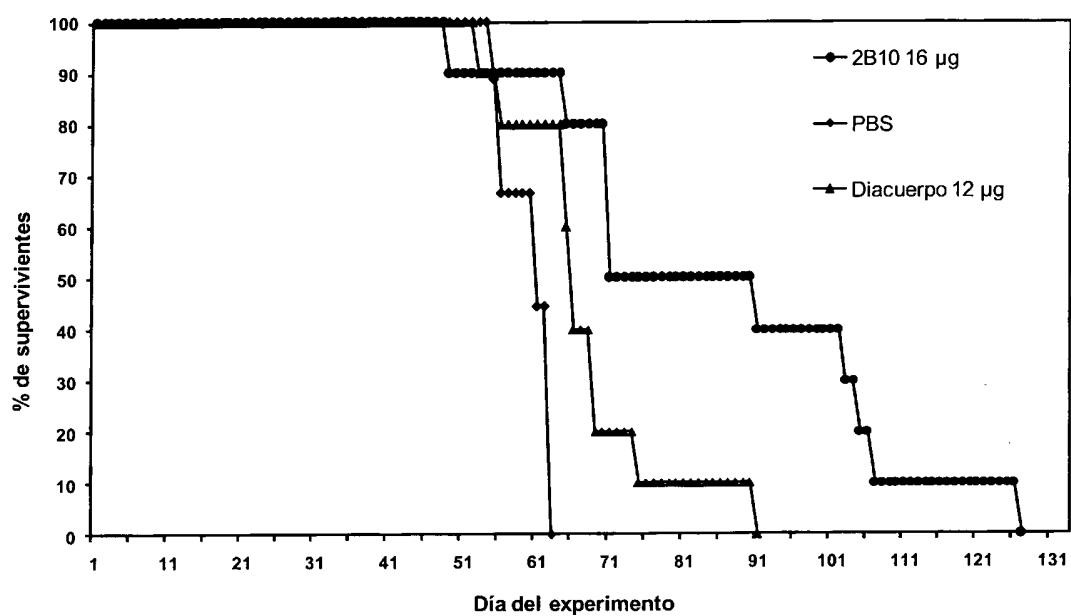


Figura 41

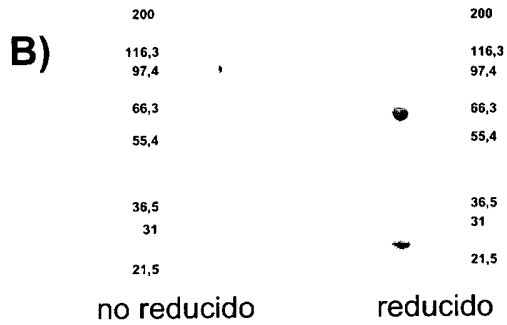
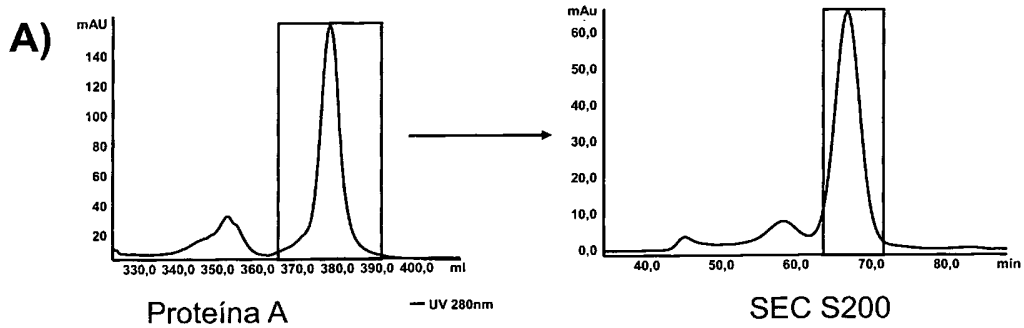


Figura 42

45/55

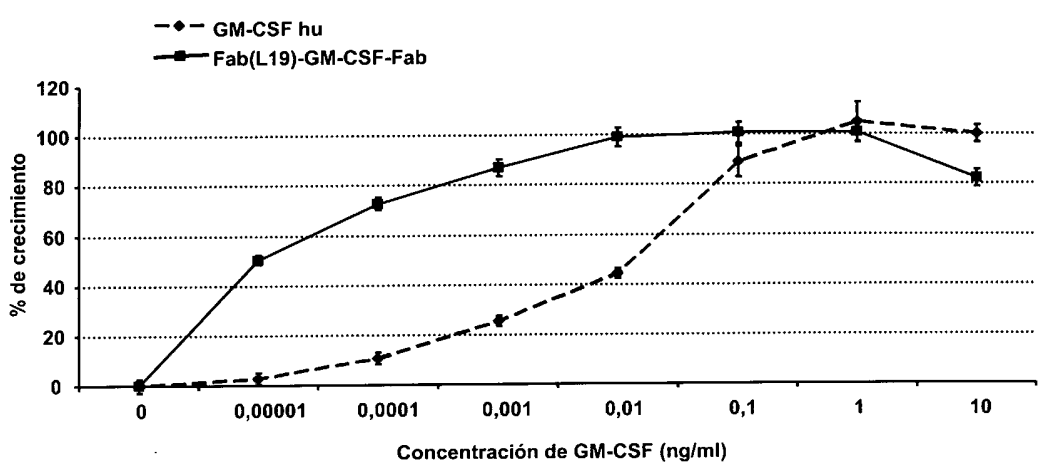


Figura 43

262

46/55

267

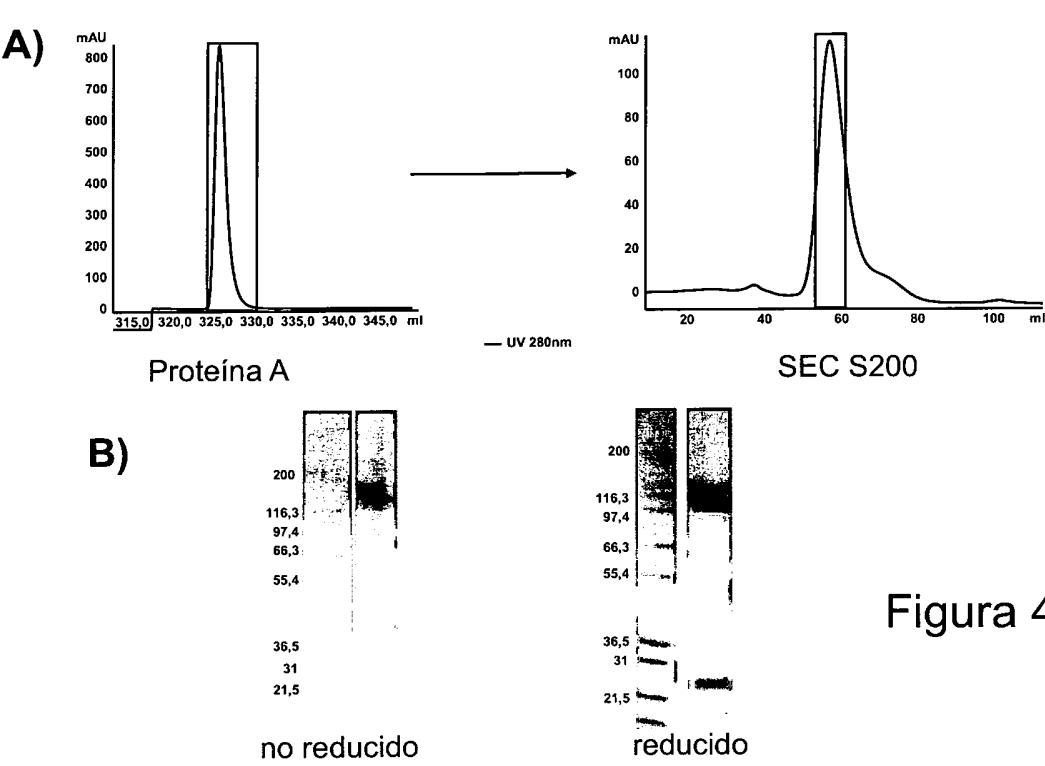
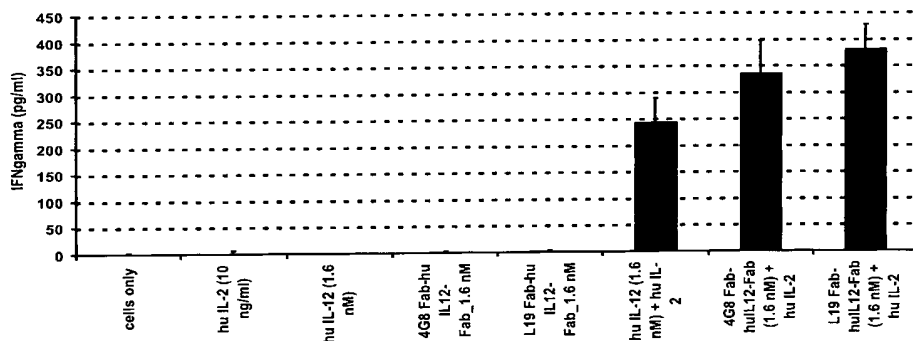


Figura 44

A)

ELISA de IFN-gamma: titulación de IL-12 hu y de constructos de IL-12 hu + mu en solución en presencia de 10 ng/ml de IL-2 hu (normalizado a números iguales de moléculas de IL-12)



B)

ELISA de IFN-gamma: titulación de constructos Fab-IL12-Fab de IL-12 hu En solución en presencia de 10 ng/ml de IL-2 hu

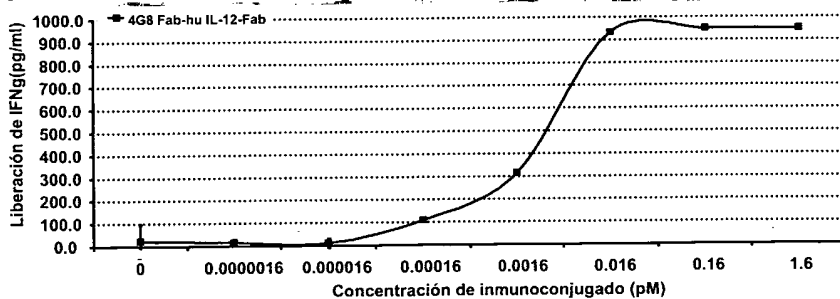


Figura 45

262

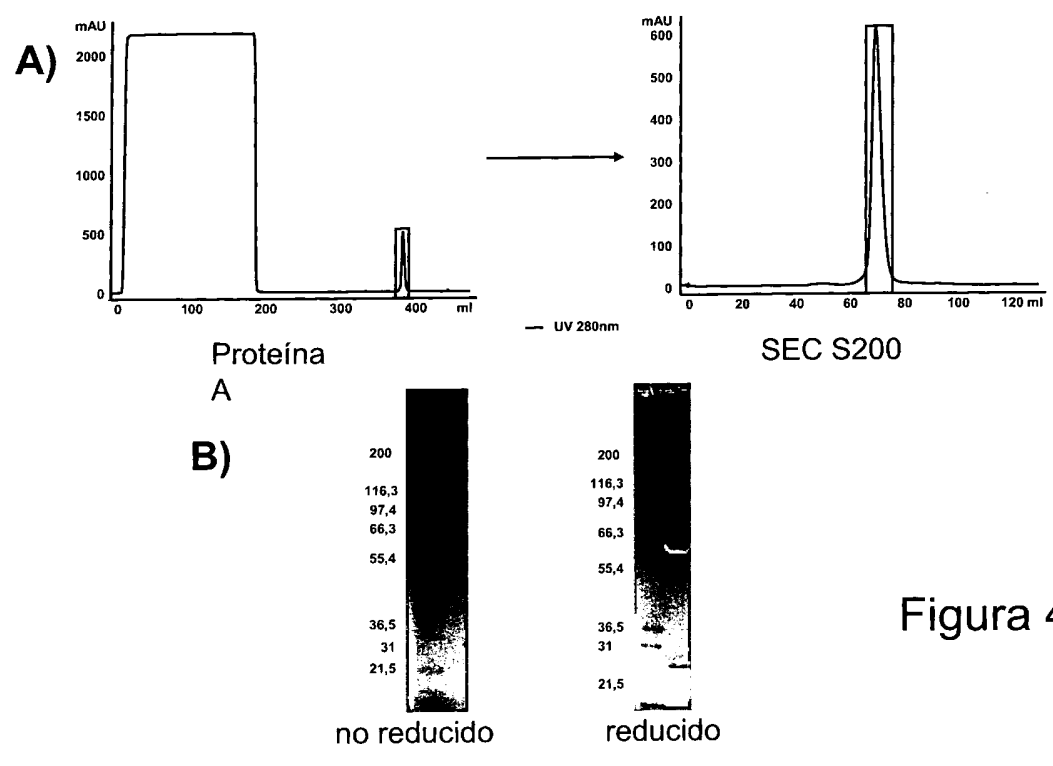


Figura 46

269

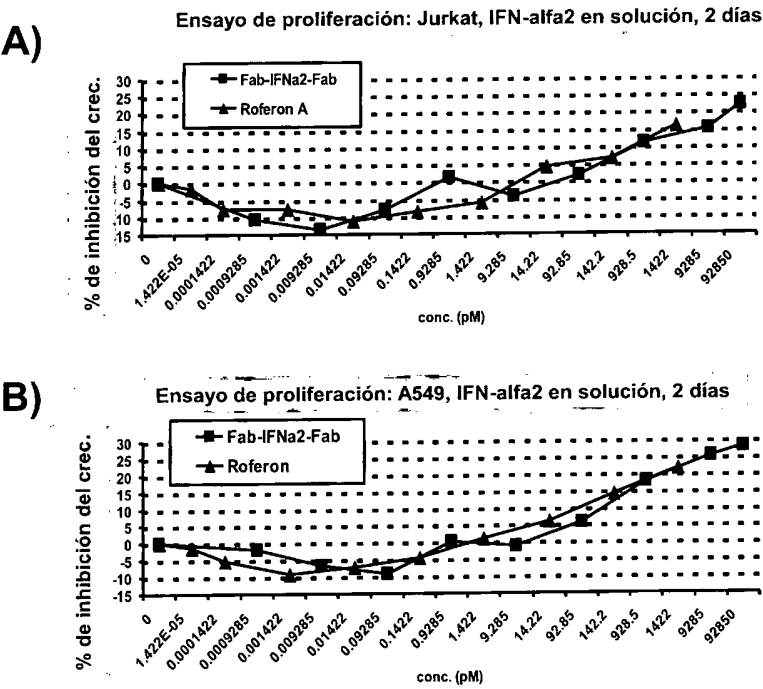
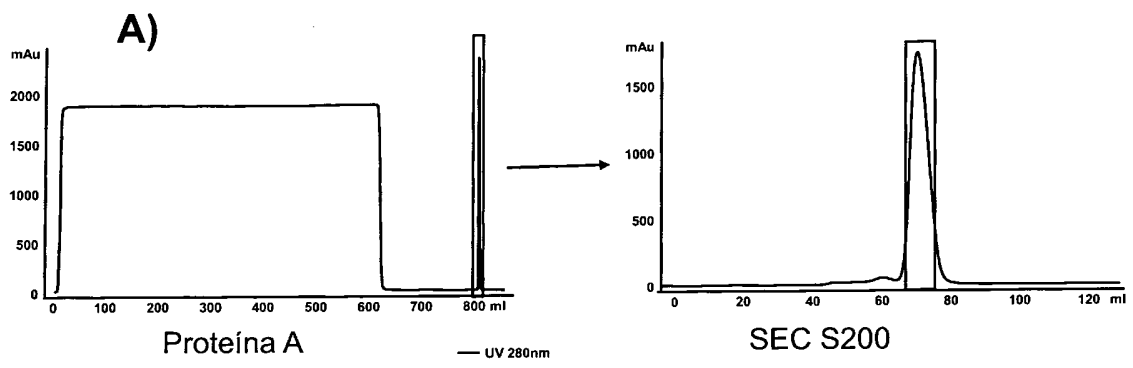


Figura 47



B)

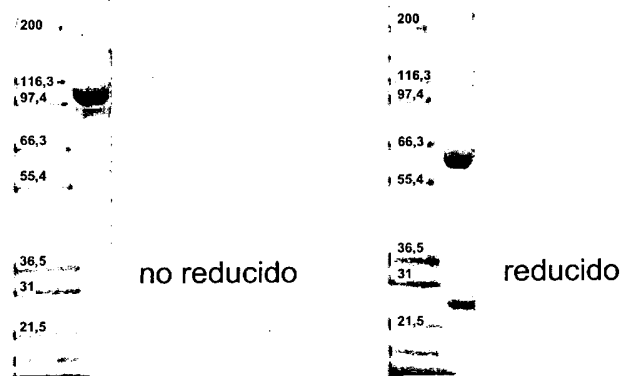
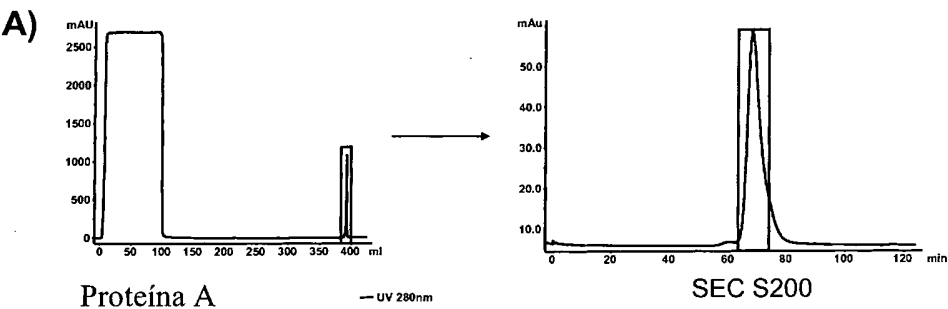
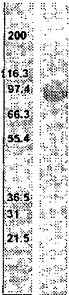


Figura 48



B)



No reducido



Reducido

Figura 49

52/55

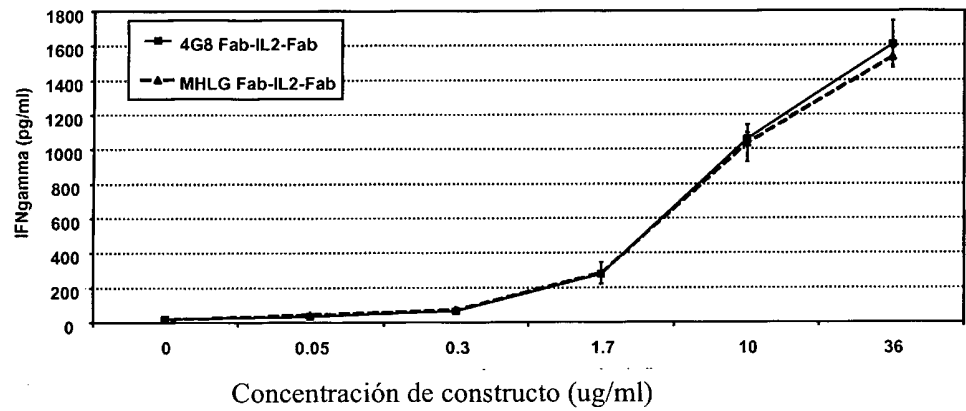


Figura 50

ELISA de IFN gamma: Constructor en solución, 24h, Células NK92

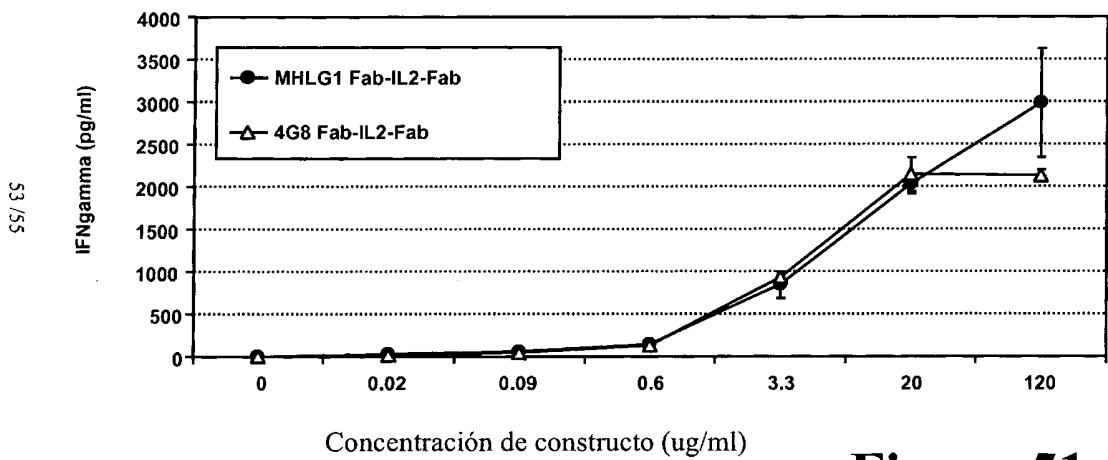


Figura 51

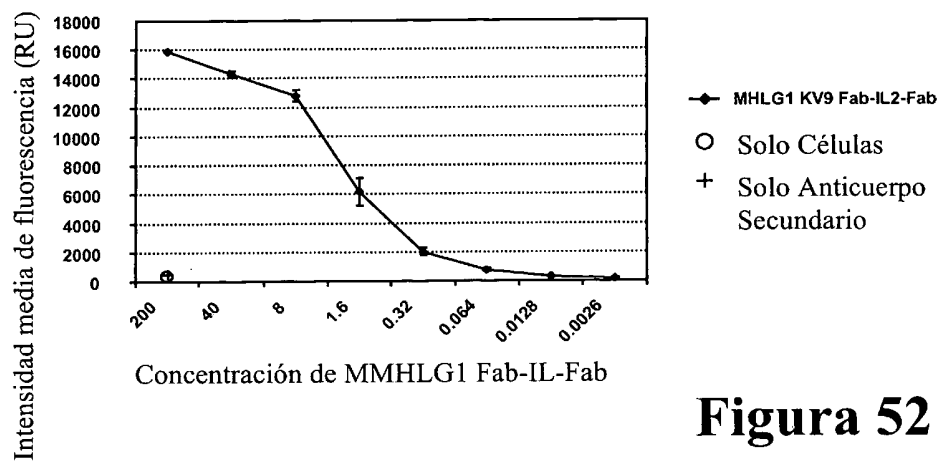


Figura 52

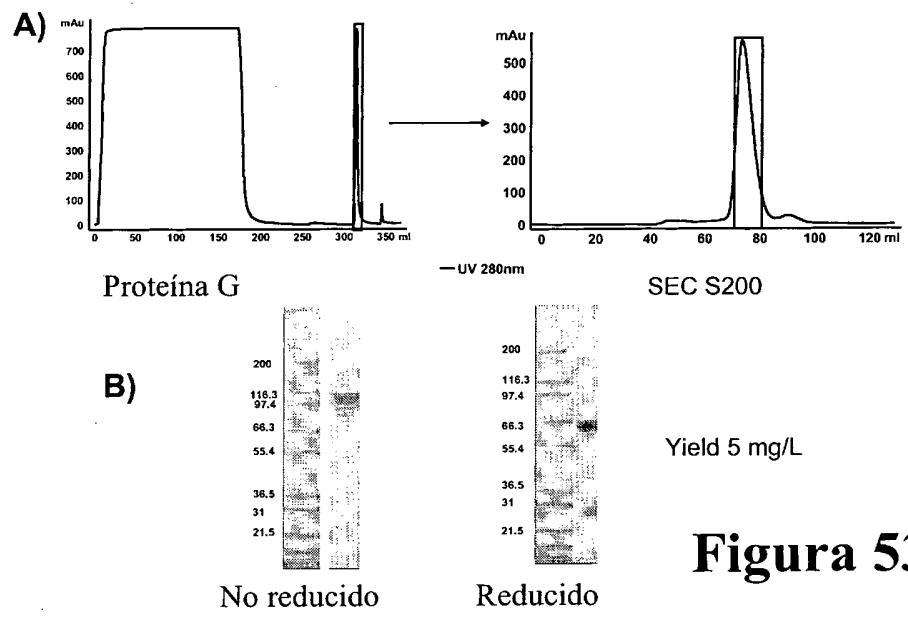


Figura 53

276

LISTADO DE SECUENCIAS

<110> Roche Glycart AG
 <120> Inmunconjugados dirigidos
 <130> 26306
 <150> US 61/234,584
 <151> 2009-08-17
 <150> EP 10162410.4
 <151> 2010-05-10
 <160> 281
 <170> PatentIn versión 3.5
 <210> 1
 <211> 1611
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> Molde para la biblioteca DP47-3
 <400> 1
 atgaaataacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60
 atggccgaaa tcgtgttaac gcagtctcca ggcaccctgt ctttgtctcc aggggaaaga 120
 gccaccctct cttgcagggc cagtcagagt gttagcagca gctacttagc ctggtaccag 180
 cagaaacctg gccaggctcc caggctctc atctatggag catccagcag ggccactggc 240
 atcccagaca ggttcagtgg cagtggatcc gggacagact tcaactctcac catcagcaga 300
 ctggagcctg aagattttgc agtgtattac tgtcagcagt atggtagctc accgtgacg 360
 ttcggccagg ggaccaaagt ggaaatcaaa cgtacgggtg ctgcaccatc tgtcttcac 420
 tccccgcat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480
 aacttctatc ccagagaggc caaagtacag tgggaagggtg ataacgccct ccaatcgggt 540
 aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600
 accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660
 catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggagccgca 720
 gaacaaaaac tcattctcaga agaggatctg aatggagccg cagactacaa ggacgacgac 780
 gacaaggggtg ccgcataata aggcgcgcca attctatttc aaggagacag tcatatgaaa 840
 tacctgtgc cgaccgtgc tgctggtctg ctgctcctcg ctgcccagcc ggcgatggcc 900
 gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 960
 tcctgtgcag cctccgatt cacctttagc agttatgcca tgagctgggt ccgccaggct 1020
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 1080

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	1140
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt	1200
ccgtattttg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaaa	1260
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	1320
ctgggctgcc tggtaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc	1380
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	1440
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	1500
gtgaatcaca agcccagcaa caccaaagtg gacaagaaag ttgagcccaa atcttgtgac	1560
gcggccgcaa gcactagtgc ccatcaccat caccatcacg ccgcggcata g	1611

<210> 2
 <211> 1617
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Molde para la biblioteca DP88-3

<400> 2	
atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc	60
atggccgata tccagatgac ccagtctcca tcctccctgt ctgcatctgt cggagaccgg	120
gtcaccatca cctgccgggc aagtcagggc attagaaatg attagggctg gtaccagcag	180
aagccagga aagccctaa ggcctgatc tatgtgcat ccagtttgca gagtggcgtc	240
ccatcaaggt tcagcggcag tggatccggg acagagttca ctctcaccat cagcagcttg	300
cagcctgaag attttgccac ctattactgc ttgcagcata atagttaccc cacgtttggc	360
cagggcacca aagtcgagat caagcgtacg gtggctgcac catctgtctt catcttcccc	420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg	600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag	660
ggcctgagct cgcctgtcac aaagagcttc aacaggggag agtgtggagc cgcagaacaa	720
aaactcatct cagaagagga tctgaatgga gccgcagact acaaggacga cgacgacaag	780
ggtgccgcat aataaggcgc gccaatctta tttaaggag acagtcatat gaaataacctg	840
ctgccgaccg ctgctgctgg tctgctgctc ctgctgccc agccggcgat ggcccagggtg	900
caattgggtgc agtctggggc tgaggtgaag aagcctgggt cctcggtgaa ggtctcctgc	960
aaggcctccg gaggcacatt cagcagctac gctataagct ggggtgcgaca ggcccctgga	1020
caagggctcg agtggatggg agggatcatc cctatctttg gtacagcaaa ctacgcacag	1080

```

aagttccagg gcagggtcac cattactgca gacaaatcca cgagcacagc ctacatggag      1140
ctgagcagcc tgagatctga ggacaccgcc gtgtattact gtgcgagact atccccaggc      1200
ggttactatg ttatggatgc ctggggccaa gggaccaccg tgaccgtctc ctcagctagc      1260
accaaaggcc catcggtctt cccctgggca cctctctcca agagcacctc tgggggcaca      1320
gcggccctgg gctgectggt caaggactac ttccccgaac cggtgacggt gtcgtggaac      1380
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc      1440
tactccctca gcagcgtggt gaccgtgccc tcagcagct tgggcaccca gacctacatc      1500
tgcaacgtga atcacaagcc cagcaacacc aaagtggaca agaaagttga gcccaaatct      1560
tgtgacgcgg ccgcaagcac tagtgcccat caccatcacc atcacgccgc ggcatag      1617

```

```

<210> 3
<211> 107
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> 2B10; VL

```

```

<400> 3

```

```

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 Arg Asn Asp
          20           25           30

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

<210> 4
<211> 321
<212> ADN
<213> Secuencia artificial

```

<220>

<223> 2B10; VL

<400> 4

```

gatatccaga tgaccacagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgctt gatctatgct gcatccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgcat aatggctctg agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                          321

```

<210> 5

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10(GS); VL

<400> 5

```

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 Arg Asn Asp
          20           25           30

```

```

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

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

```

```

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

```

<210> 6

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10(GS); VL

<400> 6
 gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcagtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgcaag aatggctctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 7
 <211> 121
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 2B10; VH

<400> 7

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

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

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

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

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 8
 <211> 363
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2B10; VH

<400> 8
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tca 363

<210> 9
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 2F11; VL

<400> 9

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 Val Pro Asp Arg Phe Ser
50 55 60

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

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

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

<210> 10
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> 2F11; VL

<400> 10
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcgtccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtta ttactgtcag cagggtcagt atactcccc caggttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 11
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 2F11(VI); VL

<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 Gly Gln Tyr Thr Pro
 85 90 95

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

<210> 12
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2F11(VI); VL

<400> 12
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtcagt atactcccc caggttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 13
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 2F11; VH

<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 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 Met Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Trp Arg Trp Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 14
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2F11; VH

<400> 14
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc agttatgcca tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac atggccgtat attactgtgc gaaatggaga 300
 tggatgatgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 15
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 2F11(MT); VH

<400> 15

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 Trp Arg Trp Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 16
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2F11(MT); VH

<400> 16

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgcca tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac accgccgtat attactgtgc gaaatggaga 300
 tggatgatgt ttgactactg gggccaagga accctgggtca cegtctcgag t 351

<210> 17
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 3F2; VL

<400> 17

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

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

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

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

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

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

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

<210> 18
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 3F2; VL

<400> 18

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt atccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 19
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 3F2(YS); VL

<400> 19

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

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

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

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

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

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

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

<210> 20
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> 3F2(YS); VL

<400> 20

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 21
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 3F2; VH

<400> 21

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 22
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 3F2; VH

<400> 22

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

286

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
 tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 23
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 3D9, VL

<400> 23

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 Gly Gln Leu Ile Pro
 85 90 95

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

<210> 24
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 3D9, VL

<400> 24

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag cagggtcagc ttattccccc tacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 25
<211> 117
<212> PRT
<213> Secuencia artificial

<220>
<223> 3D9, VH

<400> 25

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 Thr Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 26
<211> 351
<212> ADN
<213> Secuencia artificial

<220>
<223> 3D9, VH

<400> 26

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccagact 120

ccaggaagg ggctggagtg ggtctcagct attggtgtta gtactggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
 ctgggtcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 27
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 2D9(TA); VH

<400> 27

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

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 28
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2D9(TA); VH

<400> 28

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attggtgtta gtactggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
 ctgggtcctt ttgactactg gggccaagga accctgggtca cagtctcgag t 351

<210> 29
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 4G8; VL

<400> 29

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

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

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

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

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

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

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

<210> 30
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 4G8; VL

<400> 30

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtggttagc cgcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggacg gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgt ttactgtcag cagggtcagg ttattcccc tacgttcggc 300

caggggacca aagtggaaat caaa

324

<210> 31
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 4G8; VH

<400> 31

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 32
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 4G8; VH

<400> 32

gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 33
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 4B3; VL

<400> 33

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

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

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

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

<210> 34
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> 4B3; VL

<400> 34

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtc gagtgtagc agcaattact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggcgcctaca tcagggccac tggcatccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 35
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 4B3; VH

<400> 35

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 36
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 4B3; VH

<400> 36

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgtgttat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300

ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t

351

<210> 37
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 4D6; VL

<400> 37

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 Asn
 20 25 30

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

Ile Gln 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 Gly Gln Val Ile Pro
 85 90 95

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

<210> 38
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 4D6; VL

<400> 38

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcaactact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccag ggcgcctcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgt ttactgtcag cagggtcagg ttattccccc tacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 39
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 4D6; VH

<400> 39

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 40
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 4D6; VH

<400> 40

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccgatt cacctttagc agttatgcc ttagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtag 300
 ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcag t 351

<210> 41
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 2C6; VL

<400> 41

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 Gly Gln Gln Ile Pro
 85 90 95

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

<210> 42
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2C6; VL

<400> 42
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag caggctggag 240
 cctgaagatt ttgcagtgtta ttactgtcag cagggtcagc agattcccccc tacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 43
 <211> 117

<212> PRT
 <213> Secuencia artificial

<220>
 <223> 2C6; VH

<400> 43

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 44
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2C6; VH

<400> 44
 gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccggatc cacctttagc agttatgcc ttagctgggt ccgccagget 120
 ccagggaagg ggctggagtg ggtctcagct attagtggga gtgctgggta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
 tttgggaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 45

286

<211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 5H5; VL

<400> 45

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 Gly Asn Gln Ile Pro
 85 90 95

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

<210> 46
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 5H5; VL

<400> 46

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtta ttactgtcag cagggttaatc agattccccc tacgttcggt 300
 caggggacca aagtggaaat caaa 324

<210> 47
 <211> 116
 <212> PRT
 <213> Secuencia artificial

<220>

<223> 5H5; VH

<400> 47

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

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

Ser Ala Ile Ser Gly Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

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

Thr Val Ser Ser
115

<210> 48

<211> 348

<212> ADN

<213> Secuencia artificial

<220>

<223> 5H5; VH

<400> 48

gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatacca tgagctgggt ccgccggtct 120

ccaggggaagg ggctggagtg ggtctcagct attagtgggt gtggtaggac atactacgca 180

gactccgtga agggccgggt caccatctcc agagacaatt ccaagaacac gctgtatctg 240

cagatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgaa aggttggttt 300

acgccttttg actactgggg ccaaggaacc ctggtcaccg tctcgagt 348

<210> 49

<211> 108

<212> PRT

<213> Secuencia artificial

<220>

<223> 2C4; VL

<400> 49

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

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

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

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

<210> 50

<211> 324

<212> ADN

<213> Secuencia artificial

<220>

<223> 2C4; VL

<400> 50

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtc gagtgtagc agtaactact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggtgcctcca ttagggccac tggcatccca	180
gacagggtca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgt ttactgtcag cagggtaatc agattcccc tacgttcggt	300
caggggacca aagtggaaat caaa	324

<210> 51

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> 2C4; VH

<400> 51

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

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

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

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

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

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

Ala Lys Gly Trp Phe Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 52

<211> 351

<212> ADN

<213> Secuencia artificial

<220>

<223> 2C4; VH

<400> 52

gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagcggta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300

tttacgcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 53

<211> 748

<212> PRT

<213> Secuencia artificial

<220>

<223> Ectodominio de FAP humana+etiqueta poli-lys+etiqueta hist6

<400> 53

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met

485										490					495				
Ile	Leu	Pro	Pro	Gln	Phe	Asp	Arg	Ser	Lys	Lys	Tyr	Pro	Leu	Leu	Ile				
			500					505					510						
Gln	Val	Tyr	Gly	Gly	Pro	Cys	Ser	Gln	Ser	Val	Arg	Ser	Val	Phe	Ala				
		515					520					525							
Val	Asn	Trp	Ile	Ser	Tyr	Leu	Ala	Ser	Lys	Glu	Gly	Met	Val	Ile	Ala				
	530					535					540								
Leu	Val	Asp	Gly	Arg	Gly	Thr	Ala	Phe	Gln	Gly	Asp	Lys	Leu	Leu	Tyr				
545					550					555					560				
Ala	Val	Tyr	Arg	Lys	Leu	Gly	Val	Tyr	Glu	Val	Glu	Asp	Gln	Ile	Thr				
				565					570					575					
Ala	Val	Arg	Lys	Phe	Ile	Glu	Met	Gly	Phe	Ile	Asp	Glu	Lys	Arg	Ile				
			580					585					590						
Ala	Ile	Trp	Gly	Trp	Ser	Tyr	Gly	Gly	Tyr	Val	Ser	Ser	Leu	Ala	Leu				
		595					600					605							
Ala	Ser	Gly	Thr	Gly	Leu	Phe	Lys	Cys	Gly	Ile	Ala	Val	Ala	Pro	Val				
	610					615					620								
Ser	Ser	Trp	Glu	Tyr	Tyr	Ala	Ser	Val	Tyr	Thr	Glu	Arg	Phe	Met	Gly				
625					630					635					640				
Leu	Pro	Thr	Lys	Asp	Asp	Asn	Leu	Glu	His	Tyr	Lys	Asn	Ser	Thr	Val				
				645					650					655					
Met	Ala	Arg	Ala	Glu	Tyr	Phe	Arg	Asn	Val	Asp	Tyr	Leu	Leu	Ile	His				
			660					665					670						
Gly	Thr	Ala	Asp	Asp	Asn	Val	His	Phe	Gln	Asn	Ser	Ala	Gln	Ile	Ala				
		675					680					685							
Lys	Ala	Leu	Val	Asn	Ala	Gln	Val	Asp	Phe	Gln	Ala	Met	Trp	Tyr	Ser				
	690					695					700								
Asp	Gln	Asn	His	Gly	Leu	Ser	Gly	Leu	Ser	Thr	Asn	His	Leu	Tyr	Thr				
705					710					715					720				
His	Met	Thr	His	Phe	Leu	Lys	Gln	Cys	Phe	Ser	Leu	Ser	Asp	Gly	Lys				
				725					730					735					

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

<210> 54
 <211> 2244
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Ectodominio de FAP humana+etiqueta poli-lys+etiqueta hist6

<400> 54
 cgcccttcaa gagttcataa ctctgaagaa aatacaatga gagcactcac actgaaggat 60
 attttaaatg gaacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa 120
 tatcttcacg aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180
 tataaccattt tgagtaatag aaccatgaaa agtgtgaatg cttcaaatta cggcttatca 240
 cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac 300
 acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360
 cctcgtccaa ttcagtattt atgctggtcg cctgttggga gtaaattagc atatgtctat 420
 caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaaat aacatttaat 480
 ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540
 gctacaaaat atgctctctg gtggtctcct aatggaaaat ttttggcata tgcggaattt 600
 aatgatacgg atataccagt tattgcctat tcctattatg gcgatgaaca ataccctaga 660
 acaataaata ttccataccc aaaggctgga gctaagaatc ccgttggtcg gatatttatt 720
 atcgatacca cttaccctgc gtatgtaggt cccaggaag tgcctgttcc agcaatgata 780
 gcctcaagtg attattattt cagttggctc acgtgggtta ctgatgaacg agtatgtttg 840
 cagtggctaa aaagagtcca gaatgtttcg gtcctgtcta tatgtgactt cagggaagac 900
 tggcagacat gggattgtcc aaagaccag gagcatatag aagaaagcag aactggatgg 960
 gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc gtactacaaa 1020
 atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat 1080
 gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat 1140
 tcaactgtttt attctagcaa tgaatttgaa gaataccctg gaagaagaaa catctacaga 1200
 attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa 1260
 aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc 1320
 tacggcccag gcatcccat ttccaccctt catgatggac gcactgatca agaaattaa 1380
 atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag 1440
 gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct 1500

```

caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt 1560
cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg 1620
atggtcattg ccttggtgga tggtcgagga acagctttcc aaggtgacaa actcctctat 1680
gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa 1740
ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga 1800
ggatacgttt catcactggc ccttgcatct ggaactgggc ttttcaaagtg tggtatagca 1860
gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt 1920
ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca 1980
gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040
tttcaaaact cagcacagat tgctaaagct ctgggttaatg cacaagtgga tttccaggca 2100
atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc 2160
cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa 2220
aagggccacc accatcacca tcac 2244

```

<210> 55
 <211> 749
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Ectodominio de FAP murina+etiqueta poli-lys+etiqueta hist6
 <400> 55

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Asp Thr Thr Tyr Pro His His Val Gly Pro Met Glu Val Pro Val
 245 250 255

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

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

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp His Ala Trp
 290 295 300

Glu Cys Pro Lys Asn Gln Glu His Val Glu Glu Ser Arg Thr Gly Trp
 305 310 315 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr
 325 330 335

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

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

355	360	365
Trp Glu Ala Ile Tyr Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr 370 375 380		
Ser Ser Asn Glu Phe Glu Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg 385 390 395 400		
Ile Ser Ile Gly Asn Ser Pro Pro Ser Lys Lys Cys Val Thr Cys His 405 410 415		
Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys 420 425 430		
Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser 435 440 445		
Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Gln Val Leu Glu Glu 450 455 460		
Asn Lys Glu Leu Glu Asn Ser Leu Arg Asn Ile Gln Leu Pro Lys Val 465 470 475 480		
Glu Ile Lys Lys Leu Lys Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met 485 490 495		
Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile 500 505 510		
Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Lys Ser Val Phe Ala 515 520 525		
Val Asn Trp Ile Thr Tyr Leu Ala Ser Lys Glu Gly Ile Val Ile Ala 530 535 540		
Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Phe Leu His 545 550 555 560		
Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Leu Thr 565 570 575		
Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Glu Arg Ile 580 585 590		
Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu 595 600 605		

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

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

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

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

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

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

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

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

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

<210> 56
<211> 2247
<212> ADN
<213> Secuencia artificial

<220>
<223> Ectodominio de FAP murina+etiqueta poli-lys+etiqueta hist6

<400> 56
cgtccctcaa gagtttatac acctgaagga aacacaaaga gagctcttac cttgaaggat 60
attttaaagt gaacattctc atataaaaca tattttccca actggatttc agaacaagaa 120
tatcttcac aatctgagga tgataacata gtattttata atattgaaac aagagaatca 180
tatatcattt tgagtaatag caccatgaaa agtgtgaatg ctacagatta tggtttgtca 240
cctgatcggc aatttgtgta tctagaaagt gattattcaa agctctggcg atattcatac 300
acagcgacat actacatcta cgaccttcag aatggggaat ttgtaagagg atacgagctc 360
cctcgtccaa ttcagtatct atgctggctg cctgttgga gtaaattagc atatgtatat 420
caaaacaata tttatttgaa acaaagacca ggagatccac cttttcaa aacttatact 480
ggaagagaaa atagaatatt taatggaata ccagactggg tttatgaaga ggaaatgctt 540

```

gccacaaaat atgctctttg gtggtctcca gatggaaaat ttttggcata tgtagaattt 600
aatgattcag atataccaat tattgcctat tcttattatg gtgatggaca gtatcctaga 660
actataaata ttccatatcc aaaggctggg gctaagaatc cggttgttcg tgtttttatt 720
gttgacacca cctaccctca ccacgtgggc ccaatggaag tgccagttcc agaaatgata 780
gcctcaagtg actattatth cagctggctc acatgggtgt ccagtgaacg agtatgcttg 840
cagtggctaa aaagagtgca gaatgtctca gtctgtcta tatgtgattt caggggaagac 900
tggcatgcat gggaatgtcc aaagaaccag gagcatgtag aagaaagcag aacaggatgg 960
gctggtggat tctttgtttc gacaccagct tttagccagg atgccacttc ttactacaaa 1020
atatttagcg acaaggatgg ttacaaacat attcactaca tcaaagacac tgtggaaaat 1080
gctattcaaa ttacaagtgg caagtgggag gccatatata tattccgcgt aacacaggat 1140
tcaactgttt attctagcaa tgaatttgaa ggttacctg gaagaagaaa catctacaga 1200
attagcattg gaaactctcc tccgagcaag aagtgtgtaa cttgccatct aaggaaagaa 1260
aggtgccaat attacacagc aagtttcagc taaaagcca agtactatgc actcgtctgc 1320
tatggccctg gcctcccat ttccaccctc catgatggcc gcacagacca agaaatacaa 1380
gtattagaag aaaacaaaga actggaaaat tctctgagaa atatccagct gcctaaagtg 1440
gagattaaga agctcaaaga cgggggactg actttctggt acaagatgat tctgcctcct 1500
cagtttgaca gatcaaagaa gtaccctttg ctaattcaag tgtatggtgg tccttgtagc 1560
cagagtgtta agtctgtgtt tgctgttaat tggataactt atctogcaag taaggagggg 1620
atagtcattg ccctggtaga tggtcggggc actgctttcc aaggtgacaa attcctgcat 1680
gccgtgtatc gaaaactggg tgtatatgaa gttgaggacc agctcacagc tgcagaaaa 1740
ttcatagaaa tgggtttcat tgatgaagaa agaatagcca tatggggctg gtcctacgga 1800
ggttatgttt catccctggc ccttgcatct ggaactggtc ttttcaaagtg tggcatagca 1860
gtggctccag tctccagctg ggaatattac gcactatct actcagagag attcatgggc 1920
ctcccaacaa aggacgacaa tctcgaacac tataaaaatt caactgtgat ggcaagagca 1980
gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040
tttcagaact cagcacagat tgctaaagct ttggttaatg cacaagtgga tttccaggcg 2100
atgtggtact ctgaccagaa ccatggtata ttatctgggc gctcccagaa tcatttatat 2160
accacatga cgcacttctt caagcaatgc ttttctttat cagacggcaa aaagaaaaag 2220
aaaaagggcc accaccatca ccatcac 2247

```

```

<210> 57
<211> 119
<212> PRT
<213> Secuencia artificial

```

296

<220>

<223> TNC-A2 humano+etiqueta avi+etiqueta his₆

<400> 57

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

Val Gly Trp Asp Ala Leu Lys Leu Asn Trp Thr Ala Pro Glu Gly Ala
20 25 30

Tyr Glu Tyr Phe Phe Ile Gln Val Gln Glu Ala Asp Thr Val Glu Ala
35 40 45

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

Gly Leu Lys Ala Ala Thr His Tyr Thr Ile Thr Ile Arg Gly Val Thr
65 70 75 80

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

Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Gly
100 105 110

Thr His His His His His His
115

<210> 58

<211> 357

<212> ADN

<213> Secuencia artificial

<220>

<223> TNC-A2 humano+etiqueta avi+etiqueta his₆

<400> 58

gogtccaccg gggaaacccc gaacctgggc gaagtgggtg tggcggaagt gggttgggat 60

gogctgaaac tgaactggac cgcgccggaa ggcgcgtatg aatatttttt catccaggtg 120

caggaagcgg ataccgttga agcggcgcag aacctgaccg ttccgggcgg tctgcgtagc 180

accgatctgc cgggcctgaa agcggcgacc cattatacca ttaccatccg tggggtgacc 240

caggatttta gcaccacccc gctgtctgtg gaagtgtga ccgctagcgg cctgaacgac 300

atcttcgagg ctcagaaaat cgaatggcac gaaggtaccc atcaccatca ccaccac 357

<210> 59

<211> 116

<212> PRT

<213> Secuencia artificial

<220>

<223> TNC-A1 humano-etiqueta avi+etiqueta his6

<400> 59

Glu Gln Ala Pro Glu Leu Glu Asn Leu Thr Val Thr Glu Val Gly Trp
1 5 10 15

Asp Gly Leu Arg Leu Asn Trp Thr Ala Ala Asp Gln Ala Tyr Glu His
20 25 30

Phe Ile Ile Gln Val Gln Glu Ala Asn Lys Val Glu Ala Ala Arg Asn
35 40 45

Leu Thr Val Pro Gly Ser Leu Arg Ala Val Asp Ile Pro Gly Leu Lys
50 55 60

Ala Ala Thr Pro Tyr Thr Val Ser Ile Tyr Gly Val Ile Gln Gly Tyr
65 70 75 80

Arg Thr Pro Val Leu Ser Ala Glu Ala Ser Thr Ala Ser Gly Leu Asn
85 90 95

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Gly Thr His His
100 105 110

His His His His
115

<210> 60

<211> 348

<212> ADN

<213> Secuencia artificial

<220>

<223> TNC-A1 humano-etiqueta avi+etiqueta his6

<400> 60

gaacaagccc ctgagctgga aaacctcacc gtgactgagg ttggctggga tggcctcaga 60

ctcaactgga ccgcggctga ccaggcctat gagcacttta tcattcaggt gcaggaggcc 120

aacaagggtgg aggcagctcg gaacctcacc gtgcctggca gccttcgggc tgtggacata 180

ccgggctca aggcctctac gccttatata gtctccatct atgggggtgat ccagggctat 240

agaacaccag tgctctctgc tgaggcctcc acagctagcg gcctgaacga catcttcgag 300

gctcagaaaa tcgaatggca cgaaggtacc catcaccatc accaccac 348

<210> 61

<211> 124

<212> PRT
 <213> Secuencia artificial

<220>
 <223> TNC-A1 murino-etiqueta avi+etiqueta his6

<400> 61

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

Leu Thr Val Thr Glu Ala Gly Trp Asp Gly Leu Arg Leu Asn Trp Thr
 20 25 30

Ala Asp Asp Leu Ala Tyr Glu Tyr Phe Val Ile Gln Val Gln Glu Ala
 35 40 45

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

Ala Ala Asp Ile Pro Gly Leu Lys Val Ala Thr Ser Tyr Arg Val Ser
 65 70 75 80

Ile Tyr Gly Val Ala Arg Gly Tyr Arg Thr Pro Val Leu Ser Ala Glu
 85 90 95

Thr Ser Thr Ala Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
 100 105 110

Glu Trp His Glu Gly Thr His His His His His His
 115 120

<210> 62
 <211> 372
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> TNC-A1 murino-etiqueta avi+etiqueta his6

<400> 62

atttcagaat tcggatccag caccgaagaa gtgccgagcc tggaaaacct gaccgtgacc	60
gaagcgggct gggatggcct gcgtctgaac tggaccgcgg atgatctggc ctatgaatat	120
tttgtgatcc aggtgcagga agcgaacaac gttgaaaccg cgcataactt taccgtgccg	180
ggcaatctgc gtgcggcgga tattccgggc ctgaaagtgg cgaccagcta tcgtgtgagc	240
atztatggcg tggcgcgtgg ctatcgtacc ccggttctga gcgcggaaac cagcaccgct	300
agcggcctga acgacatott cgaggctcag aaaatcgaat ggcacgaagg tacccatcac	360
catcaccacc ac	372

<210> 63
 <211> 116
 <212> PRT
 <213> Secuencia artificial

<220>
 TNC-A4 humano+etiqueta avi+etiqueta his₆

<400> 63

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

Asp Gly Leu Arg Leu Asn Trp Thr Ala Ala Asp Asn Ala Tyr Glu His
 20 25 30

Phe Val Ile Gln Val Gln Glu Val Asn Lys Val Glu Ala Ala Gln Asn
 35 40 45

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

Ala Ala Thr Pro Tyr Arg Val Ser Ile Tyr Gly Val Ile Arg Gly Tyr
 65 70 75 80

Arg Thr Pro Val Leu Ser Ala Glu Ala Ser Thr Ala Ser Gly Leu Asn
 85 90 95

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Gly Thr His His
 100 105 110

His His His His
 115

<210> 64
 <211> 348
 <212> ADN
 <213> Secuencia artificial

<220>
 TNC-A4 humano+etiqueta avi+etiqueta his₆

<400> 64

gaagatctgc cgcagctggg cgatctggcc gtgagcgaag tgggctggga tggcctgcgt	60
ctgaactgga ccgcggcgga taacgcgtat gaacattttg tgattcaggt gcaggaagtg	120
aacaaagttg aagcggcgca gaacctgacc ctgccgggca gcctgcgtgc ggtggatatt	180
cggggcctgg aagcggcgac cccgtatcgt gtgagcatct atggcgtgat tcgtggctat	240
cgtaccccggt ttctgagcgc ggaagcgagc accgctagcg gcctgaacga catcttcgag	300
gctcagaaaa tcgaatggca cgaaggtacc catcaccatc accaccac	348

<210> 65
 <211> 124
 <212> PRT
 <213> Secuencia artificial

<220>
 TNC-A4 murino+etiqueta avi+etiqueta his₆

<400> 65

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

Leu Ser Val Thr Glu Val Ser Trp Asp Gly Leu Thr Leu Asn Trp Thr
 20 25 30

Thr Asp Asp Leu Ala Tyr Lys His Phe Val Val Gln Val Gln Glu Ala
 35 40 45

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

Ala Val Asp Ile Pro Gly Leu Lys Ala Asp Thr Pro Tyr Arg Val Ser
 65 70 75 80

Ile Tyr Gly Val Ile Gln Gly Tyr Arg Thr Pro Met Leu Ser Thr Asp
 85 90 95

Val Ser Thr Ala Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
 100 105 110

Glu Trp His Glu Gly Thr His His His His His
 115 120

<210> 66
 <211> 372
 <212> ADN
 <213> Secuencia artificial

<220>
 TNC-A4 murino+etiqueta avi+etiqueta his₆

<400> 66

atttcagaat tcggatccct gaccgaagat ctgccgcagc tgggcggtct gagcgtgacc 60
 gaagtgaact gggatggcct gaccctgaac tggaccaccg atgatctggc ctataaacat 120
 tttgtggtgc aggtgcagga agcgaacaac gttgaagcgg cgcagaacct gaccgttccg 180
 ggtagcctgc gtgcggtgga tattccgggc ctgaaagcgg ataccccgta tcgtgtgagc 240
 atttatggcg tgattcaggg ctatcgtacc ccgatgctgt ctaccgatgt gagcaccgct 300

agcggcctga acgacatctt cgaggctcag aaaatcgaat ggcacgaagg tacccatcac 360
catcaccacc ac 372

<210> 67
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 2D9; VL

<400> 67

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 Gly Asn Gln Ile Pro
85 90 95

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

<210> 68
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> 2D9; VL

<400> 68

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtt ttactgtcag cagggtaatc agattcccc tacgttcggt 300
caggggacca aagtggaaat caaa 324

<210> 69
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 2D9; VH

<400> 69

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

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

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

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

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

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

Ala Lys Gly Trp Phe Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 70
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 2D9; VH

<400> 70

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tctgtgacag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagcggt a gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg	300

tttacgcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t

351

<210> 71
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 4B8; VL

<400> 71

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 Gly Gln Val Ile Pro
 85 90 95

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

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

<220>
 <223> 4B8; VL

<400> 72

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccagget cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgta ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 73
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 4B8; VH

<400> 73

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 74
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 4B8; VH

<400> 74

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 75
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 7A1; VL

<400> 75

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 Gly Gln Gln Ile Pro
 85 90 95

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

<210> 76
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 7A1; VL

<400> 76

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgt ttactgtcag cagggtcagc agattcccc tacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 77
 <211> 117

<212> PRT
 <213> Secuencia artificial

<220>
 <223> 7A1; VH

<400> 77

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 78
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 7A1; VH

<400> 78
 gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
 tctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
 tttgggaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 79

<211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 13C2; VL

<400> 79

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 Gly Gln Leu Ile Pro
 85 90 95

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

<210> 80
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 13C2; VL

<400> 80
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgt ttactgtcag cagggtcagc ttattcccc tacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 81
 <211> 117
 <212> PRT
 <213> Secuencia artificial

306

<220>

<223> 13C2; VH

<400> 81

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

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

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

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

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 82

<211> 351

<212> ADN

<213> Secuencia artificial

<220>

<223> 13C2; VH

<400> 82

gaggtgcaat tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt cgcgcaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
ctgggtcctt ttgactactg gggccaagga accctgggtca cgtctcgag t 351

<210> 83

<211> 108

<212> PRT

<213> Secuencia artificial

<220>

<223> 13E8; VL

<400> 83

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 Gly Leu Asn Ile Pro
85 90 95

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

<210> 84

<211> 324

<212> ADN

<213> Secuencia artificial

<220>

<223> 13E8; VL

<400> 84

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtctga atattccctc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 85

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> 13E8; VH

<400> 85

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

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

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

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

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 86

<211> 351

<212> ADN

<213> Secuencia artificial

<220>

<223> 13E8; VH

<400> 86

gaggtgcaat tgttgaggatc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300

ttgggtccgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 87

<211> 108

<212> PRT

<213> Secuencia artificial

<220>

<223> 14C10; VL

<400> 87

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 Gly His Ile Ile Pro
 85 90 95

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

<210> 88

<211> 324

<212> ADN

<213> Secuencia artificial

<220>

<223> 14C10; VL

<400> 88

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgt ttactgtcag cagggtcata ttattcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 89

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> 14C10; VH

<400> 89

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 Ala Trp Met Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 90
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 14C10; VH

<400> 90
 gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagcttgg 300
 atggggcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 91
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 17A11; VL

<400> 91

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 Gly Leu Asn Ile Pro
 85 90 95

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

<210> 92

<211> 324

<212> ADN

<213> Secuencia artificial

<220>

<223> 17A11; VL

<400> 92

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccagggt cctcatctat ggagcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag caggggtctga atattccctc gacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 93

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> 17A11; VH

<400> 93

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 94
<211> 351
<212> ADN
<213> Secuencia artificial

<220>
<223> 17A11; VH

<400> 94
gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc ttagctgggt ccgccaggct 120
ccagggaagg ggtctggagt ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggcgc gttcaccatc tccagagaca attccaagaa cagctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300
ttgggtccgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 95
<211> 603
<212> PRT
<213> Secuencia artificial

<220>
<223> cadena pesada de Fab derivada de variante C125A de IL2-cadena pesada de Fab derivado de anticuerpo monoclonal L19

<400> 95

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 Phe
 20 25 30

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

Ser Ser Ile Ser Gly Ser Ser Gly Thr 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 Pro Phe Pro 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 Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly Gly
 210 215 220

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser Ser
 225 230 235 240

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
245 250 255

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
260 265 270

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
275 280 285

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
290 295 300

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
305 310 315 320

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
325 330 335

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
340 345 350

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu
370 375 380

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

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Ser
405 410 415

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

Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys
435 440 445

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
450 455 460

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
465 470 475 480

Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
485 490 495

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
500 505 510

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
515 520 525

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
530 535 540

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
545 550 555 560

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
565 570 575

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
580 585 590

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600

<210> 96

<211> 215

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena ligera de Fab derivada de anticuerpo monoclonal L19

<400> 96

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 Tyr 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 Thr Gly Arg Ile Pro
85 90 95

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 97
 <211> 382
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> scFv derivado de anticuerpo monoclonal L19-líinker de 8 aminoácidos
 variante C125A de IL2

<400> 97

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 Phe
 20 25 30

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

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

Thr Val Ser Ser Ser Gly Gly Ser Gly Gly Ala Ser Glu Ile Val Leu
 115 120 125

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
 130 135 140

Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp
 145 150 155 160

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Tyr Ala
 165 170 175

Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
 180 185 190

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
 195 200 205

Ala Val Tyr Tyr Cys Gln Gln Thr Gly Arg Ile Pro Pro Thr Phe Gly
 210 215 220

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

Ser Ser Ser Gly Ser Ser Ser Ser Gly Ala Pro Thr Ser Ser Ser Thr
 245 250 255

Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met
 260 265 270

Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met
 275 280 285

Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His
 290 295 300

Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
 305 310 315 320

Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
 325 330 335

Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
 340 345 350

Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn
 355 360 365

Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 370 375 380

<210> 98

<211> 377

<212> PRT

<213> Secuencia artificial

<220>

<223> proteína F16-diacuerpo-IL2

<400> 98

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 Arg Tyr
 20 25 30

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

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

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

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

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

Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu
 180 185 190

Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn
 195 200 205

Ser Ser Val Tyr Thr Met Pro Pro Val Val Phe Gly Gly Gly Thr Lys
 210 215 220

Leu Thr Val Leu Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
 225 230 235 240

Ser Ser Ser Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu
 245 250 255

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
 260 265 270

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
 275 280 285

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
 290 295 300

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

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
 325 330 335

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
 340 345 350

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
 355 360 365

Ala Gln Ser Ile Ile Ser Thr Leu Thr
 370 375

<210> 99

<211> 641

<212> PRT

<213> Secuencia artificial

<220>

<223> scFv-IL2-scFv (F16, proteína)

<400> 99

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 Arg Tyr
20 25 30

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

Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

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

Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
145 150 155 160

Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
165 170 175

Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
180 185 190

Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln
195 200 205

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Ser Val Tyr Thr Met
210 215 220

Pro Pro Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
225 230 235 240

Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ala Pro
 245 250 255
 Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu
 260 265 270
 Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro
 275 280 285
 Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala
 290 295 300
 Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu
 305 310 315 320
 Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro
 325 330 335
 Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
 340 345 350
 Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile
 355 360 365
 Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser
 370 375 380
 Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 385 390 395 400
 Gly Gly Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu
 405 410 415
 Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
 420 425 430
 Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
 435 440 445
 Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
 450 455 460
 Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln
 465 470 475 480
 Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Ser Val Tyr Thr Met
 485 490 495

Pro Pro Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
500 505 510

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Glu Val
515 520 525

Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
530 535 540

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr Gly Met
545 550 555 560

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
565 570 575

Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
580 585 590

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
595 600 605

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
610 615 620

Ala His Asn Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
625 630 635 640

Ser

<210> 100
<211> 603
<212> PRT
<213> Secuencia artificial

<220>
<223> Fab-IL2-Fab (Fl6, construction de fusión de cadena pesada-citoquina, proteína)

<400> 100

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 Arg Tyr
20 25 30

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

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

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

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

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

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

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

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

Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ala Pro Thr Ser Ser
 225 230 235 240

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
 245 250 255

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
 260 265 270

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
 275 280 285

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val

290		295		300
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu				
305		310		315 320
Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr				
		325		330 335
Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe				
		340		345 350
Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr				
		355		360 365
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu				
		370		375 380
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser				
385		390		395 400
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr Gly				
		405		410 415
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser				
		420		425 430
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys				
		435		440 445
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu				
		450		455 460
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala				
465		470		475 480
Lys Ala His Asn Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr				
		485		490 495
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro				
		500		505 510
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val				
		515		520 525
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala				
		530		535 540

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
545 550 555 560

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
565 570 575

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
580 585 590

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600

<210> 101

<211> 214

<212> PRT

<213> Secuencia artificial

<220>

<223> F16, cadena ligera, proteína

<400> 101

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly

145 150 155 160
 Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175
 Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190
 Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205
 Ala Pro Thr Glu Cys Ser
 210

 <210> 102
 <211> 466
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> proteína de fusión IL2R-beta-Fc(ojal), proteína

 <400> 102

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

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

 Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
 35 40 45

 Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
 50 55 60

 Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
 65 70 75 80

 Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln Lys Leu Thr Thr
 85 90 95

 Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
 100 105 110

 Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
 115 120 125

 Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
 130 135 140

Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
 145 150 155 160
 Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
 165 170 175
 Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
 180 185 190
 Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro
 195 200 205
 Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
 210 215 220
 Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Thr Gly Ala Gln Asp
 225 230 235 240
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 245 250 255
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 260 265 270
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 275 280 285
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 290 295 300
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 305 310 315 320
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 340 345 350
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
 355 360 365
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 370 375 380
 Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

385 390 395 400
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 405 410 415
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
 420 425 430
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 435 440 445
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 450 455 460

 Gly Lys
 465

 <210> 103
 <211> 492
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> IL2R-gamma-Fc(botón), proteína

 <400> 103
 Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1 5 10 15

 Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
 20 25 30

 Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
 35 40 45

 Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
 50 55 60

 Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
 65 70 75 80

 Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
 85 90 95

 Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
 100 105 110

 Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
 115 120 125

Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
130 135 140

Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145 150 155 160

Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
165 170 175

Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
180 185 190

Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
195 200 205

Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
210 215 220

Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225 230 235 240

Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe
245 250 255

Leu Phe Ala Leu Glu Ala Gly Ala Gln Asp Lys Thr His Thr Cys Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
290 295 300

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

370

375

380

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
 405 410 415

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 485 490

<210> 104

<211> 991

<212> PRT

<213> Secuencia artificial

<220>

<223> Fab-IL12-Fab, anticuerpo L19, scIL12 murino, proteína

<400> 104

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 Phe
 20 25 30

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

Ser Ser Ile Ser Gly Ser Ser Gly Thr 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 Pro Phe Pro 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 Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly Gly
 210 215 220

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Met Trp Glu Leu
 225 230 235 240

Glu Lys Asp Val Tyr Val Val Glu Val Asp Trp Thr Pro Asp Ala Pro
 245 250 255

Gly Glu Thr Val Asn Leu Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile
 260 265 270

Thr Trp Thr Ser Asp Gln Arg His Gly Val Ile Gly Ser Gly Lys Thr
 275 280 285

Leu Thr Ile Thr Val Lys Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys
 290 295 300

His Lys Gly Gly Glu Thr Leu Ser His Ser His Leu Leu Leu His Lys
 305 310 315 320

Lys Glu Asn Gly Ile Trp Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn
 325 330 335

Lys Thr Phe Leu Lys Cys Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr

340	345	350
Cys Ser Trp Leu Val Gln Arg Asn Met Asp Leu Lys Phe Asn Ile Lys 355 360 365		
Ser Ser Ser Ser Pro Pro Asp Ser Arg Ala Val Thr Cys Gly Met Ala 370 375 380		
Ser Leu Ser Ala Glu Lys Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys 385 390 395 400		
Tyr Ser Val Ser Cys Gln Glu Asp Val Thr Cys Pro Thr Ala Glu Glu 405 410 415		
Thr Leu Pro Ile Glu Leu Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr 420 425 430		
Glu Asn Tyr Ser Thr Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp 435 440 445		
Pro Pro Lys Asn Leu Gln Met Lys Pro Leu Lys Asn Ser Gln Val Glu 450 455 460		
Val Ser Trp Glu Tyr Pro Asp Ser Trp Ser Thr Pro Arg Ser Tyr Phe 465 470 475 480		
Ser Leu Lys Phe Phe Val Arg Ile Gln Arg Lys Lys Glu Lys Met Lys 485 490 495		
Glu Thr Glu Glu Gly Cys Asn Gln Lys Gly Ala Phe Phe Val Glu Lys 500 505 510		
Thr Ser Thr Glu Val Gln Cys Lys Gly Gly Asn Val Cys Val Gln Ala 515 520 525		
Gln Asp Arg Tyr Tyr Asn Ser Ser Cys Ser Lys Trp Ala Cys Val Pro 530 535 540		
Cys Arg Val Arg Ser Gly Gly Asp Gly Ser Gly Gly Gly Gly Ser Gly 545 550 555 560		
Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys Leu 565 570 575		
Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys Thr 580 585 590		

Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile Asp
 595 600 605

His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys Leu
 610 615 620

Pro Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu Thr
 625 630 635 640

Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser Leu
 645 650 655

Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 660 665 670

Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn His
 675 680 685

Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu Leu
 690 695 700

Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro Pro
 705 710 715 720

Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile Leu
 725 730 735

Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val Met Gly
 740 745 750

Tyr Leu Ser Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 755 760 765

Gly Gly Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 770 775 780

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 785 790 795 800

Ser Ser Phe Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 805 810 815

Glu Trp Val Ser Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala
 820 825 830

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 835 840 845

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
850 855 860

Tyr Tyr Cys Ala Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly
865 870 875 880

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
885 890 895

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
900 905 910

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
915 920 925

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
930 935 940

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
945 950 955 960

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
965 970 975

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
980 985 990

<210> 105
<211> 987
<212> PRT
<213> Secuencia artificial

<220>
<223> Fab-IL12-Fab de anticuerpo L19, scIL12 humano, proteína

<400> 105

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 Phe
20 25 30

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

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

Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro
 325 330 335
 Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg
 340 345 350
 Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser
 355 360 365
 Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly
 370 375 380
 Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr
 385 390 395 400
 Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu
 405 410 415
 Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala Val His Lys Leu Lys
 420 425 430
 Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro
 435 440 445
 Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln
 450 455 460
 Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser
 465 470 475 480
 Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg
 485 490 495
 Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile
 500 505 510
 Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr
 515 520 525
 Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro Cys Ser Gly Gly Gly
 530 535 540
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Asn Leu Pro
 545 550 555 560
 Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His Ser Gln
 565 570 575

336

Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr
 580 585 590

Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile
 595 600 605

Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu
 610 615 620

Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr
 625 630 635 640

Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met Ala Leu
 645 650 655

Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe
 660 665 670

Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe
 675 680 685

Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu
 690 695 700

Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro
 705 710 715 720

Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe
 725 730 735

Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met Ser Tyr Leu Asn Ala
 740 745 750

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu
 755 760 765

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 770 775 780

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe Ser
 785 790 795 800

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 805 810 815

Ser Ile Arg Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val Lys

820

825

830

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
835 840 845

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
850 855 860

Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
865 870 875 880

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
885 890 895

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
900 905 910

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
915 920 925

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
930 935 940

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
945 950 955 960

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
965 970 975

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
980 985

<210> 106

<211> 597

<212> PRT

<213> Secuencia artificial

<220>

<223> Fab-GMCSF-Fab, anticuerpo L19, GM-CSF humano, proteína

<400> 106

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

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

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

Ser Ser Ile Arg Gly Ser Ser Gly Thr 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 Pro Phe Pro 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 Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly Gly
210 215 220

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Arg Ser
225 230 235 240

Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
245 250 255

Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn
260 265 270

Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr
275 280 285

Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 545 550 555 560

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 565 570 575

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 580 585 590

Pro Lys Ser Cys Asp
 595

<210> 107
 <211> 636
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Fab-IFNa2-Fab, anticuerpo L19, proteína

<400> 107

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 Phe
 20 25 30

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

Ser Ser Ile Arg Gly Ser Ser Gly Thr 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 Pro Phe Pro 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 Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly Gly	210		215		220	
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Cys Asp Leu Pro Gln	225		230		235	240
Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile Leu Leu Ala Gln Met	245		250		255	
Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly	260		265		270	
Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Gln Ala	275		280		285	
Ile Ser Val Leu His Glu Met Ile Gln Gln Thr Phe Asn Leu Phe Ser	290		295		300	
Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Ser Leu Leu Glu Lys Phe	305		310		315	320
Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile	325		330		335	
Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn Val Asp Ser Ile	340		345		350	
Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Thr Glu	355		360		365	
Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met	370		375		380	
Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Arg Leu Arg Arg Lys	385		390		395	400

346

Glu Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 405 410 415

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 420 425 430

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
 435 440 445

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 450 455 460

Ser Ser Ile Arg Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val
 465 470 475 480

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 485 490 495

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 500 505 510

Ala Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 515 520 525

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 530 535 540

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 545 550 555 560

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 565 570 575

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 580 585 590

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 595 600 605

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 610 615 620

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 625 630 635

<210> 108
 <211> 1812
 <212> ADN

<213> Secuencia artificial

<220>

<223> cadena pesada de Fab derivada de variante C125A de cadena pesada de IL2-Fab derivada del anticuerpo monoclonal L19

<400> 108

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tcctgtgcag cctctggatt caccttttagc agtttttcga tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcatct atttccggtg gttcgggtac cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt	300
ccgtattttg actactgggg ccagggaacc ctggtcaccg tctcgagtgc tagcaccaag	360
ggcccatcgg tcttccccct ggcacctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tggtaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc	480
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca ccagacctc catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gataagaaag ttgagcccaa atcttgtgac	660
tccggcggag gagggagcgg cggaggtggc tccggaggtg gcggagcacc tacttcaagt	720
tctacaaaga aaacacagct acaactggag catttactgc tggatttaca gatgattttg	780
aatggaatta ataattacaa gaatcccaaa ctaccagga tgctcacatt taagttttac	840
atgcccaaga aggccacaga actgaaacat cttcagtgtc tagaagaaga actcaaacct	900
ctggaggaag tgctaaattt agctcaaagc aaaaactttc acttaagacc cagggaacta	960
atcagcaata tcaacgtaat agttctggaa ctaaagggat ctgaaacaac attcatgtgt	1020
gaatatgctg atgagacagc aaccattgta gaatttctga acagatggat tacctttgcc	1080
caaagcatca tctcaacact gacttccggc ggaggaggat ccggcggagg tggctctggc	1140
ggtggcggag aggtgcagct gttggagtct gggggaggct tggtagagcc tgggggggtcc	1200
ctgagactct cctgtgcagc ctctggattc accttttagca gtttttcgat gagctgggtc	1260
cgccaggctc cagggaaggg gctggagtgg gtctcatcta tttccggtag ttcgggtacc	1320
acatactacg cagactccgt gaagggcccg ttcaaccatc ccagagacaa ttccaagaac	1380
acgctgtatc tgcaaatgaa cagcctgaga gccgaggaca cggccgtata ttactgtgcg	1440
aaaccgtttc cgtattttga ctactggggc cagggaaccc tggtcaccgt ctcgagtgtc	1500
agcaccaagg gcccatcggg cttccccctg gcacctcct ccaagagcac ctctgggggc	1560
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	1620

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga	1680
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac	1740
atctgcaacg tgaatcacia gccagcaac accaagggtgg ataagaaagt tgagcccaaa	1800
tcttgtgact ga	1812

<210> 109
 <211> 648
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Cadena ligera de Fab derivada de anticuerpo monoclonal L19

<400> 109	
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat tatgcatcca gcagggccac tggcatocca	180
gacagggtca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag cagacgggtc gtattcctcc gacgttcggc	300
caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg	360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg	540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag	600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttag	648

<210> 110
 <211> 1149
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> scFv derivado de anticuerpo monoclonal L19-líder de 8 aminoácidos-
 variante C125A de IL2

<400> 110	
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tcctgtgcag cctctggatt caccttttagc agtttttcga tgagctgggt ccgccaggct	120
ccagggaagg ggttgagtg ggtctcatct atttcgggta gttcgggtac cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt	300
cogtattttg actactgggg ccagggaacc ctggtcaccg tctcgagtag cggcgggagc	360

```

ggcgggggcta gcgaaattgt gttgacgcag tctccaggca cctgtcttt gtctccaggg 420
gaaagagcca cctctcctg cagggccagt cagagtgtta gcagcagcta cttagcctgg 480
taccagcaga aacctggcca ggctcccagg ctctcatct attatgcac cagcagggcc 540
actggcatcc cagacagggt cagtggcagt gggctctgga cagacttcac tctcaccatc 600
agcagactgg agcctgaaga ttttgcaagt tattactgtc agcagacggg tcgtattcct 660
ccgacgttcg gccaaaggac caaggtggaa atctccgtgc tgtcttcctc atcgggtagt 720
agctcttcg gctcatcgtc ctccggagca cctacttcaa gttctacaaa gaaaacacag 780
ctacaactgg agcatttact gctggattta cagatgattt tgaatggaat taataattac 840
aagaatccca aactcaccag gatgctcaca ttttaagtttt acatgcccac gaaggccaca 900
gaactgaaac atcttcagt gctagaagaa gaactcaaac ctctggagga agtgctaaat 960
ttagctcaaa gcaaaaactt tcaactaaga ccaggggact taatcagcaa tatcaacgta 1020
atagttctgg aactaaagg atctgaaaca acattcatgt gtgaatatgc tgatgagaca 1080
gcaaccattg tagaatttct gaacagatgg attacctttg cccaaagcat catctcaaca 1140
ctgacttga 1149

```

```

<210> 111
<211> 1134
<212> ADN
<213> Secuencia artificial

```

```

<220>
<223> proteina F16-diacuerpo-IL2

```

```

<400> 111
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
tcctgtgcag cctctggatt caccttagc cggataggta tgagctgggt ccgccaggct 120
ccaggaagg ggctggagt ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagcgcac 300
aatgcttttg actactgggg ccaggaacc ctggtcaccg tgcgagtgac tagcggcgga 360
tcgtctgagc tgactcagga cctgctgtg tctgtggcct tgggacagac agtcaggatc 420
acatgccaa gacagagcct cagaagctat tatgcaagct ggtaccagca gaagccagga 480
caggccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat ccagaccga 540
ttctctggct ccagctcagg aaacacagct tccttgacca tcaactggggc tcaggcgga 600
gatgaggctg actattactg taactcctct gtttatacta tgccgccgt ggtattcggc 660
ggagggacca agctgaccgt cctaggctct tcctcatcgg gtagtagctc ttccggctca 720

```

tcgtcctccg gagcacctac ttcaagttct acaaagaaaa cacagctaca actggagcat	780
ttactgctgg atttacagat gattttgaat ggaattaata attacaagaa tcccaaactc	840
accaggatgc tcacatttaa gttttacatg cccaagaagg ccacagaact gaaacatctt	900
cagtgtctag aagaagaact caaacctctg gaggaagtgc taaatttagc tcaaagcaaa	960
aactttcact taagaccag ggacttaatc agcaatatca acgtaatagt tctggaacta	1020
aagggatctg aaacaacatt catgtgtgaa tatgctgatg agacagcaac cattgtagaa	1080
tttctgaaca gatggattac ctttgcccaa agcatcatct caaactgac ttga	1134

<210> 112

<211> 1926

<212> ADN

<213> Secuencia artificial

<220>

<223> scFv-IL2-scFv (F16, ADN)

<400> 112

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tctgtgcag cctctggatt cacctttage cggatatgta tgagctgggt ccgccaggt	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagcgc	300
aatgcttttg actactgggg ccagggaacc ctggtcaccg tgtcgagagg tggaggcgg	360
tcaggcggag gtggctctgg cggtgccgga tcgtctgagc tgactcagga ccctgctgtg	420
tctgtggcct tgggacagac agtcaggatc acatgccaa gagacagcct cagaagctat	480
tatgcaagct ggtaccagca gaagccagga caggcccctg tacttgatcat ctatggtaaa	540
aacaaccggc cctcagggat ccagaccga ttctctggct ccagctcagg aaacacagct	600
tccttgacca tcaactgggg tcaggcggaa gatgaggctg actattactg taactcctct	660
gtttatacta tgccgcccggt ggtattcggc ggagggaacca agctgaccgt cctaggctct	720
tcctcatcgg gtagtagctc ttccggctca tcgtcctccg gagcacctac ttcaagttct	780
acaaagaaaa cacagctaca actggagcat ttactgctgg atttacagat gattttgaat	840
ggaattaata attacaagaa tcccaaactc accaggatgc tcacatttaa gttttacatg	900
ccaagaagg ccacagaact gaaacatctt cagtgtctag aagaagaact caaacctctg	960
gaggaagtgc taaatttagc tcaaagcaaa aactttcact taagaccag ggacttaatc	1020
agcaatatca acgtaatagt tctggaacta aagggatctg aaacaacatt catgtgtgaa	1080
tatgctgatg agacagcaac cattgtagaa tttctgaaca gatggattac ctttgcccaa	1140
agcatcatct caaactgac ttccggcggg ggaggagagc gcggaggtg ctctggcgg	1200

ggcggatcgt ctgagctcac tcaggaccct gctgtgtctg tggccttggg acagacagtc	1260
aggatcacat gccaaaggaga cagcctcaga agctattatg caagctggta ccagcagaag	1320
ccaggacagg cccctgtact tgtcatctat ggtaaaaaaca accggccctc agggatccca	1380
gaccgattct ctggctccag ctcaggaaac acagcttcct tgaccatcac tggggctcag	1440
gcggaagatg aggctgacta ttactgtaac tcctctgttt atactatgcc gcccgtaggta	1500
ttcggcggag ggaccaagct taccgtacta ggctcaggag gcggttcagg cggaggttct	1560
ggcggcggta gcggatcggg ggtgcagctg ttggagtctg ggggaggctt ggtacagcct	1620
gggggggtccc tgagactctc ctgtgcagcc tctggattca cctttagccg gtatggtagt	1680
agctgggtcc gccaggctcc agggaagggg ctggagtggg tctcagctat tagtggtagt	1740
ggtggtagca catactacgc agactccgtg aagggccggg tcaccatctc cagagacaat	1800
tccaagaaca cgctgtatct gcaaatgaac agcctgagag ccgaggacac ggccgtatat	1860
tactgtgcga aagcgcataa tgcttttgac tactggggcc agggaaccct ggtcaccgtg	1920
tcgtga	1926

<210> 113
 <211> 1812
 <212> ADN
 <213> Secuencia artificial

<220>

<223> Fab-IL2-Fab (F16, constructo de fusión de cadena pesada-citoquina, ADN)

<400> 113	
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag cctctggatt cacctttagc cggtatggta tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagcgcac	300
aatgcttttg actactgggg ccagggaacc ctggtcaccg tgtcgagtgc tagcaccaag	360
ggcccatcgg tcttccccct ggcacctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tggtaagga ctacttcccc gaaccgggtga cgggtgcgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tggtagaccgt gccctccagc agcttgggca ccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gataagaaag ttgagcccaa atcttgtgac	660
tcttcctcat cgggtagtag ctcttccggc tcatcgctct ccggagcacc tacttcaagt	720
tctacaaaga aaacacagct acaactggag catttactgc tggatttaca gatgattttg	780

aatggaatta ataattacaa gaatcccaaa ctcaccagga tgctcacatt taagttttac	840
atgcccaaga aggccacaga actgaaacat cttcagtgtc tagaagaaga actcaaacct	900
ctggaggaag tgctaaattt agctcaaagc aaaaactttc acttaagacc cagggactta	960
atcagcaata tcaacgtaat agttctggaa cttaaaggat ctgaaacaac attcatgtgt	1020
gaatatgctg atgagacagc aaccattgta gaatttctga acagatggat tacctttgcc	1080
caaagcatca tctcaacact gacttccggc ggaggaggga gcggcggagg tggctctggc	1140
ggtggcggag aggtgcaatt gttggagtct gggggaggct tggtagagcc tgggggggcc	1200
ctgagactct cctgtgcagc ctctggattc acctttagcc ggtatggat gagctgggtc	1260
cgccaggctc caggaagg gctggagtgg gtctcagcta ttagtggtag tggtagtagc	1320
acatactacg cagactccgt gaaggccgg ttcaccatct ccagagacaa ttccaagaac	1380
acgctgtatc tgcaaatgaa cagcctgaga gccgaggaca cgccgtata ttactgtgcg	1440
aaagcgcata atgcttttga ctactggggc caggaaccc tggtcaccgt gtcgagtgt	1500
agcaccaagg gcccatcggc cttccccctg gcacctcct ccaagagcac ctctgggggc	1560
acagcggccc tgggtgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	1620
aactcaggcg cctgaccag cggcgtgcac accttcccg ctgtcctaca gtctcagga	1680
ctctactccc tcagcagcgt ggtgaccgt cctccagca gcttgggcac ccagacctac	1740
atctgcaacg tgaatcacia gccagcaac accaagggtg acaagaaagt tgagcccaaa	1800
tcttgtgact ga	1812

<210> 114
 <211> 645
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> F16, cadena ligera, ADN

<400> 114	
tcttctgagc tgactcagga cctgctgtg tctgtggcct tgggacagac agtcaggatc	60
acatgccaaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagccagga	120
caggccccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat ccagaccga	180
ttctctggct ccagctcagg aaacacagct tccttgacca tcaactgggc tcaggcggaa	240
gatgaggctg actattactg taactcctct gtttatacta tgccgcccgt ggtattcggc	300
ggagggacca agctgaccgt cctaggtcaa cccaaggctg ccccagcgt gacctgttc	360
ccccccagca gcgaggaact gcaggccaac aaggccaccc tggctctgct gatcagcgac	420
ttctacccag gcgccgtgac cgtggcctgg aaggccgaca gcagccccgt gaaggccggc	480
gtggagacca ccacccccag caagcagagc aacaacaagt acgcccag cagctacctg	540

agcctgaccc ccgagcagtg gaagagccac aggtcctaca gctgccaggt gacccacgag 600
ggcagcaccg tggagaaaac cgtggccccc accgagtga gctga 645

<210> 115
<211> 1401
<212> ADN
<213> Secuencia artificial

<220>
<223> proteína de fusión IL2R-beta-Fc(ojal), proteína de fusión, ADN

<400> 115
atggacatga gggccccgc tcagctcctg ggcctcctgc tgctctggtt cccaggtgcc 60
aggtgtgcgg tgaatggcac ttcccagttc acatgcttct acaactcgag agccaacatc 120
tcctgtgtct ggagccaaga tggggctctg caggacactt cctgccagt ccatgcctgg 180
ccggacagac ggcgggtggaa ccaaacctgt gagctgctcc cgtgagtca agcatcctgg 240
gcctgcaacc tgatcctcgg agcccagat tctcagaaac tgaccacagt tgacatcgtc 300
accctgaggg tgctgtgccg tgaggggggtg cgatggaggg tgatggccat ccaggacttc 360
aagccctttg agaaccttgc cctgatggcc cccatctccc tccaagttgt ccacgtggag 420
accacagat gcaacataag ctgggaaatc tccaagcct ccactactt tgaaagacac 480
ctggagttcg aggcccgac gctgtcccca ggccacacct gggaggaggc cccctgctg 540
actctcaagc agaagcagga atggatctgc ctggagacgc tcacccaga caccagtat 600
gagtttcagg tgcggtcaa gcctctgcaa ggcgagttca cgacctggag cccctggagc 660
cagcccttg ccttcagaac aaagcctgca gcccttgga aggacaccgg agctcaggac 720
aaaactcaca catgcccacc gtgccagca cctgaactcc tggggggacc gtcagtcttc 780
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
gtggtggtgg acgtgagcca cgaagacct gaggtcaagt tcaactggtc cgtggacggc 900
gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
aaggtctcca acaaagccct ccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080
cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac 1140
caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatgc cgtggagtgg 1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260
ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380
tcctgtctc cgggtaaattg a 1401

<210> 116
 <211> 1479
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> IL2R-gamma-Fc(botón), ADN

<400> 116
 atgttgaagc catcattacc attcacatcc ctcttattcc tgcagctgcc cctgctggga 60
 gtggggctga acaogacaat tctgacgccc aatgggaatg aagacaccac agctgatttc 120
 ttctgacca ctatgcccac tgactccctc agtggtttcca ctctgcccct cccagaggtt 180
 cagtgttttg tgttcaatgt cgagtacatg aattgcactt ggaacagcag ctctgagccc 240
 cagcctacca acctcactct gcattattgg tacaagaact cggataatga taaagtccag 300
 aagtgcagcc actatctatt ctctgaagaa atcacttctg gctgtcagtt gcaaaaaaag 360
 gagatccacc tctaccaaac atttgttggt cagctccagg acccacggga acccaggaga 420
 caggccacac agatgctaaa actgcagaat ctggtgatcc cctgggctcc agagaacctt 480
 acacttcaca aactgagtga atcccagcta gaactgaact ggaacaacag attcttgaac 540
 cactgttttg agcacttggt gcagtaccgg actgactggg accacagctg gactgaacaa 600
 tcagtggatt atagacataa gttctccttg cctagtgtgg atgggcagaa acgctacacg 660
 tttcgtgttc ggagccgctt taaccactc tgtggaagtg ctcagcattg gagtgaatgg 720
 agccacccaa tccactgggg gagcaatact tcaaaagaga atcctttcct gtttgcattg 780
 gaagccggag ctccaggaaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840
 gggggaccgt cagtcttctt cttcccccca aaacccaagg acaccctcat gatctcccg 900
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 1020
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccac cgagaaaacc 1140
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1200
 gatgagctga ccaagaacca ggtcagcctg tgggtgcctgg tcaaaggctt ctatcccagc 1260
 gacatgcccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320
 cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcacctg ggacaagagc 1380
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440
 tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 117
 <211> 2976

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL12-Fab, anticuerpo L19, scIL12 murino, ADN

<400> 117

gaggtgcagc tgttgagtc tgggggaggc ttgtacagc ctggggggtc cctgagactc	60
tctgtgcag cctctggatt cacctttagc agtttttcga tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcatct atttccggtg gttcgggtac cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt	300
ccgtattttg actactgggg ccagggaacc ctggtcaccg tctcagatgc tagcaccaag	360
ggcccatcgg tcttccccct ggcacctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tggtaagga ctacttcccc gaaccggtga cgggtgctgt gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac	600
gtgaatcaca agcccagcaa caccaaggtg gataagaaag ttgagcccaa atcttgtgac	660
tccggcggag gagggagcgg cggaggtggc tccggagggg gcggagccat gtgggagctg	720
gaaaaggacg tgtacgtggt ggaggtggac tggacccccg acgcccctgg cgagacagtg	780
aacctgacct gcgacacccc cgaagaggac gacatcacct ggaccagcga ccagcggcac	840
ggcgtgatcg gcagcggcaa gacctgacc atcacctgta aagagtttct ggacgccggc	900
cagtacacct gccacaaggg cggcgagaca ctgagccaca gccacctgct gctgcacaag	960
aaagagaacg gcatctggtc caccgagatc ctgaagaact tcaagaacaa gaccttctctg	1020
aagtgcgagg cccccaacta cagcggccgg ttacacctgca gctggctggt gcagcggaac	1080
atggacctga agttcaacat caagagcagc agcagccccc ctgacagcag ggccgtgacc	1140
tgcggcatgg ccagcctgag cgcggagaag gtgacctggt accagagggg ctacgagaag	1200
tacagcgtga gctgccagga agatgtcacc tgccccaccg ccgaggaaac cctgccccatc	1260
gagctggccc tggagcccc gcagcagaac aagtacgaga actactctac cagcttcttc	1320
atccgggaca tcatcaagcc cgaccccccc aagaacctgc agatgaagcc cctgaagaac	1380
agccaggtgg aggtgtcctg ggagtaccct gacagctggt ccacccccag aagctacttc	1440
agcctgaagt tcttcgtgag aatccagcgg aagaaagaaa agatgaaaga gacagaggaa	1500
ggctgcaacc agaagggcgc cttcttcgtc gagaaaacca gcaccgaggt gcagtgcag	1560
ggcggcaacg tgtgcgtgca ggcccaggac cgggtactaca acagcagctg cagcaagtgg	1620
gcctgcgtgc cctgcagagt gcggtctggc ggcgacggct ctggcggcgg aggaagcggc	1680

```

ggagggggca gcagagtgat ccccgtaggc ggccctgccc ggtgcctgag ccagagccgg 1740
aacctgctga aaaccaccga cgacatggtg aaaaccgcca gagagaagct gaagcactac 1800
agctgcacag ccgaggacat cgaccacgag gacatcaccg gggaccagac cagcaccctg 1860
aaaacctgcc tgcccctgga actgcacaaa aacgagagct gcctggccac ccgggagaca 1920
agcagacca cccggggcag ctgcctgcct cccagaaaaa cctccctgat gatgacctg 1980
tgctggggca gcatctacga ggacctgaag atgtaccaga ccgagttcca ggccatcaac 2040
gccgccctgc agaaccacaa tcaccagcag atcatcctgg acaagggcag gctggctgcc 2100
atcgacgagc tgatgcagag cctgaaccac aacggcgaaa ccctgcggca gaaaccccc 2160
gtgggcgagg ccgacccta ccgggtgaag atgaagctgt gcatcctgct gcacgccttc 2220
agcaccggg tggtgacct caaccgggtg atgggctacc tgcctctgc cgggggagg 2280
ggatccggcg gaggtggctc tggcggtggc ggagaggtgc agctgttga gtctggggga 2340
ggcttggtac agcctggggg gtccctgaga ctctcctgtg cagcctctgg attcaccttt 2400
agcagtttt cgatgagctg ggtccgccag gctccaggga aggggctgga gtgggtctca 2460
tctatttccg gtagttcggg taccacatac tacgcagact ccgtgaaggg ccggttcacc 2520
atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagccgag 2580
gacacggccg tatattactg tgcgaaaccg tttccgtatt ttgactactg gggccaggga 2640
accctggtca ccgtctcgag tgctagcacc aaggggccat ccgtcttccc cctggcacc 2700
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 2760
ccggaaccgg tgacgggtgtc gtggaactca ggcgcctga ccagcggcgt gcacaccttc 2820
ccggctgtcc tacagtctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 2880
agcagcttgg gcaccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 2940
gtggataaga aagttgagcc caaatcttgt gactga 2976

```

<210> 118

<211> 2964

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL12-Fab, anticuerpo L19, scIL12 humano, ADN

<400> 118

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agtttttcga tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcatct attagaggta gttcgggtac cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt 300

```

ccgtatitttg actactgggg ccagggaacc ctggtcaccg tctcgagtgc tagcaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gataagaaag ttgagcccaa atcttgtgac	660
tccggcggag gagggagcgg cggaggtggc tccggagggg gcggaatctg ggagctgaag	720
aaagacgtgt acgtggtgga gctggactgg tatcccagcg cccctggcga gatggtggtg	780
ctgacctgcg acacccccga agaggacggc atcacctgga ccctggacca gagcagcgag	840
gtgctgggca gcggcaagac cctgaccatc caggtgaaag agttcggcga cgccggccag	900
tacacctgcc acaagggcgg cgaagtgtgtg tcccacagcc tgctgtgtgt gcacaagaaa	960
gaggatggca tctggtccac cgacatcctg aaggaccaga aagagcccaa gaacaagacc	1020
ttcctgcggt gcgaggccaa gaactacagc ggccggttca cctgttggtg gctgaccacc	1080
atcagcaccg acctgacctt cagcgtgaag agcagccggg gcagcagcga ccctcagggc	1140
gtgacctgcg gagccgccac cctgagcgcc gagagagtgc ggggcgacaa caaagagtac	1200
gagtacagcg tcgagtgccg ggaagatagc gcctgccctg ccgccgagga aagcctgccc	1260
atcgaggtga tgggtggacgc cgtgcacaag ctgaagtacg agaactacac cagcagcttt	1320
ttcatccggg acatcatcaa gcccgacccc cccaagaacc tgcagctgaa gccctgaag	1380
aacagccggc aggtggaggt gtcttgggag taccctgaca cctgggtccac cccccacagc	1440
tacttcagcc tgacattctg tgtgcaggtg cagggcaaga gcaagcggga gaagaaagac	1500
cgggtgttca ccgacaagac cagcgccacc gtgatctgcc ggaagaacgc cagcatcagc	1560
gtgcggggccc aggaccggtc ctacagcagc tcttgggtcc agtgggccag cgtgccttgc	1620
agcggcggag ggggctctgg cggcgaggga tctgggggag ggggcagccg gaacctgccc	1680
gtggccaccc ccgaccccg catgttcccc tgcttgcacc acagccagaa cctgctgcgg	1740
gccgtgagca acatgctgca gaaggcccg cagaccctgg aattctaccc ctgcaccagc	1800
gaggaaatcg accacgagga catcaccaag gataagacca gcaccgtgga ggcctgcctg	1860
cccctggaac tgaccaagaa cgagagctgc ctgaacagcc gggagacaag cttcatcacc	1920
aacggcagct gcctggccag cagaaagacc agcttcatga tggccctgtg cctgagcagc	1980
atctacgagg acctgaagat gtaccaggtg gagttcaaga ccatgaacgc caagctgctg	2040
atggacccca agcggcagat cttcctggat cagaacatgc tggccgtgat cgacgagctg	2100
atgcaggccc tgaacttcaa cagcgagaca gtgccccaga agtccagcct ggaagagccc	2160

gactttctaca agaccaagat caagctgtgc atcctgctgc acgccttcag aatccggggcc	2220
gtgaccatcg accgggtgat gagctacctg aacgccagcg gagggggggg atccggcgga	2280
gggtggctctg gcgggtggcg agaggtgcag ctggtggagt ctgggggagg cttggtacag	2340
cctgggggggt cctgagact ctctgtgca gcctctggat tcacctttag cagtttttcg	2400
atgagctggg tccgccaggc tccagggaag gggctggagt gggctctcatc tattagaggt	2460
agttcgggta ccacatacta cgcagactcc gtgaagggcc ggttcaccat ctccagagac	2520
aattccaaga acacgtgtg tctgcaaatg aacagcctga gagccgagga cacggccgta	2580
tattactgtg cgaaacogtt tccgtatttt gactactggg gccagggaac cctggtcacc	2640
gtctcgagtg ctagcaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc	2700
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg	2760
acgggtgtcgt ggaactcagg cgcctgacc agcggcgtgc acaccttccc ggctgtccta	2820
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc	2880
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggataagaaa	2940
gttgagccca aatcttgtga ctga	2964

<210> 119
 <211> 1794
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Fab-GMCSF-Fab, anticuerpo L19, GM-CSF humano, ADN

<400> 119	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag cctctggatt caccttttagc agtttttcga tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcatct attagaggta gttcgggtac cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt	300
ccgtatttttg actactgggg ccagggaacc ctggtcaccg tctcgagtgc tagcaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcttac agtcctcagg actctactcc	540
ctcagcagcg tgggtaccgt gccctccagc agcttgggca cccagacctc catctgcaac	600
gtgaatcaca agcccagcaa caccaagggt gataagaaag ttgagcccaa atcttgtgac	660
tccggcggag gagggagcgg cggaggtggc tccggaggtg gcggagcacc cggccgctcg	720
cccagcccca gcacgcagcc ctgggagcat gtgaatgcca tccaggaggc cggcgtctc	780

356

ctgaacctga gtagagacac tgctgctgag atgaatgaaa cagtagaagt catctcagaa	840
atgtttgacc tccaggagcc gacctgccta cagacccgcc tggagctgta caagcagggc	900
ctgcggggca gcctcaccaa gctcaagggc cccttgacca tgatggccag ccactacaag	960
cagcactgcc ctccaacccc ggaaacttcc tgtgcaaccc agattatcac ctttgaaagt	1020
ttcaaagaga acctgaagga ctttctgctt gtcattcccct ttgactgctg ggagccagtc	1080
caggagtccg gcggaggagg atccggcgga ggtggctctg gcggtggcgg agaggtgcag	1140
ctgttgagat ctgggggagg cttggtacag cctgggggggt ccctgagact ctctgtgca	1200
gcctctggat tcacctttag cagtttttcg atgagctggg tccgccaggc tccagggaag	1260
gggctggagt ggggtctcatc tattagaggt agttcgggta ccacatacta cgcagactcc	1320
gtgaagggcc ggttcacat ctccagagac aattccaaga acacgctgta tctgcaaagt	1380
aacagcctga gagccgagga cacggccgta tattactgtg cgaaaccgtt tccgtatitt	1440
gactactggg gccagggaa cctggtcacc gtctcgagtg ctagcaccaa gggcccatcg	1500
gttttcccc tggcacctc ctccaagagc acctctgggg gcacagcggc cctgggctgc	1560
ctgggtcaagg actacttccc cgaaccgggtg acggtgtcgt ggaactcagg cgccctgacc	1620
agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc	1680
gtgggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac	1740
aagcccagca acaccaaggt ggataagaaa gttgagccca aatcttgtga ctga	1794

<210> 120
 <211> 1911
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Fab-IFNa2-Fab, anticuerpo L19, ADN

<400> 120	
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tctgtgcag cctctggatt caccttttagc agtttttcga tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcatct attagaggta gttcgggtac cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt	300
ccgtattttg actactgggg ccagggaacc ctggtcaccg tctcgagtgc tagcaccaag	360
ggcccatcgg ttttccccct ggcaacctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgtcgtg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540

```

ctcagcagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac      600
gtgaatcaca agcccagcaa caccaagggtg gataagaaag ttgagcccaa atcttgtgac      660
tccggcggag gagggagcgg cggaggtggc tccggagggg gcggatgcga cctgccccag      720
accacagcc tgggcaacag acgggccctg atcctgctgg cccagatgcg gcggatcagc      780
cccttcagct gcctgaagga ccggcacgac ttcggcttcc cccaggaaga gttcgacggc      840
aaccagttcc agaaggccca ggccatcagc gtgctgcacg agatgatcca gcagaccttc      900
aacctgttca gcaccaagga cagcagcgcc gcctgggacg agagcctgct ggaaaagttc      960
tacaccgagc tgtaccagca gctgaacgac ctggaagcct gcgtgatcca ggaagtgggc     1020
gtcgaggaaa ccccccctgat gaacgtggac agcatcctgg ccgtgaagaa gtacttcag      1080
cggatcacc cgtacctgac cgagaagaag tatagccct gcgcctggga ggtggtgcgg      1140
gccgagatca tgcggagctt cagcctgagc accaacctgc aggaacggct gcggcgaaa      1200
gagagcggcg gagggggatc cggcggaggt ggctctggcg gtggcggaga ggtgcagctg      1260
ttggagtctg ggggaggctt ggtacagcct ggggggtccc tgagactctc ctgtgcagcc      1320
tctggattca ccttttagcag tttttcgatg agctgggtcc gccaggctcc agggaagggg      1380
ctggagtggg tctcatctat tagaggtagt tcgggtacca catactacgc agactccgtg      1440
aagggccggt tcaccatctc cagagacaat tccaagaaca cgctgtatct gcaaatgaac      1500
agcctgagag ccgaggacac ggccgtatat tactgtgcga aaccgtttcc gtattttgac      1560
tactggggcc agggaaccct ggtcaccgtc tcgagtgcga gcaccaaggg cccatcggtc      1620
ttccccctgg caccctctc caagagcacc tctgggggca cagcggccct gggctgcctg      1680
gtcaaggact acttccccga accggtgacg gtgtcgtgga actcaggcgc cctgaccagc      1740
ggcgtgcaca ccttcccggc tgtcctacag tctcaggac tctactccct cagcagcgtg      1800
gtgaccgtgc cctccagcag cttgggcacc cagacctaca tctgcaacgt gaatcacaag      1860
cccagcaaca ccaagggtgga taagaaagt gagcccaaat cttgtgactg a              1911

```

```

<210> 121
<211> 108
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> 19G1; VL

```

```

<400> 121

```

```

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

```

```

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

```

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

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

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

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

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

<210> 122
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 19G1; VL

<400> 122
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtggt atccgggaca gacttactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtt ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 123
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 19G1; VH

<400> 123

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

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

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

35 40 45
 Ser Ala Ile Ile Ser Ser Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

<210> 124
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 19G1; VH

<400> 124
 gaggtgcaat tgttgagatc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcga tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagcg attattagta gtggtggtct cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 125
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 20G8; VL

<400> 125

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

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

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

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

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

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

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

<210> 126
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 20G8; VL

<400> 126
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtggtacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtt ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 127
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 20G8; VH

<400> 127

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 128
<211> 351
<212> ADN
<213> Secuencia artificial

<220>
<223> 20G8; VH

<400> 128
gaggtgcaat tgttgaggatc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcaa tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attattggga gtggtagtcg tacatactac 180
gcagactcgc tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 129
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 4B9; VL

<400> 129

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

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

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

400

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

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

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

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

<210> 130
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> 4B9; VL

<400> 130
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccagget cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 131
<211> 117
<212> PRT
<213> Secuencia artificial

<220>
<223> 4B9; VH

<400> 131

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

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

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

Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

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

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

Val Thr Val Ser Ser
115

<210> 132
<211> 351
<212> ADN
<213> Secuencia artificial

<220>
<223> 4B9; VH

<400> 132
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
tctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120
ccagggaagg ggcctggagt ggtctcagct attattgcta gtggtgctag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtc cgtctcgtc c 351

<210> 133
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 5B8; VL

<400> 133

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

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

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

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

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

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

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

<210> 134
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 5B8; VL

<400> 134
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtggtacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 135
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 5B8; VH

<400> 135

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 Trp Gly Gly Gly Arg Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

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

Val Thr Val Ser Ser
115

<210> 136
<211> 351
<212> ADN
<213> Secuencia artificial

<220>
<223> 5B8; VH

<400> 136
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct atttggggtg gtggtcgtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtc cgtctcgtc c 351

<210> 137
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 5F1; VL

<400> 137

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

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

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

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

366

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

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

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

<210> 138
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> 5F1; VL

<400> 138
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 139
<211> 117
<212> PRT
<213> Secuencia artificial

<220>
<223> 5F1; VH

<400> 139

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65

70

75

80

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

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

Val Thr Val Ser Ser
 115

<210> 140
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 5F1; VH

<400> 140
 gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccagget 120
 ccagggaagg ggctggagtg ggtctcagct attattagta gtggggctag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 tttggtggtt ttaactactg gggccaagga accctgggtca cgtctcgtc c 351

<210> 141
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 14B3; VL

<400> 141

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

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

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

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

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

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

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

<210> 142
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> 14B3; VL

<400> 142
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtc gagtggtacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccagggt cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtta ttactgtcag caggggtatta tgcttccccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 143
<211> 117
<212> PRT
<213> Secuencia artificial

<220>
<223> 14B3; VH

<400> 143

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 144
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 14B3; VH

<400> 144
 gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctcoggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attttggcta gtggtgcgat cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 145
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 16F1; VL

<400> 145

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

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

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

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

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

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

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

<210> 146
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 16F1; VL

<400> 146
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc caggttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 147
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 16F1; VH

<400> 147

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

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

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

85

90

95

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

Val Thr Val Ser Ser
 115

<210> 148
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 16F1; VH

<400> 148
 gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcaggt attattggta gtggtggtat cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 tttggtggtt ttaactactg gggccaagga accctggtca ccgtctcgtc c 351

<210> 149
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 16F8; VL

<400> 149

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

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

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

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

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

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

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

<210> 150
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 16F8; VL

<400> 150
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtggtacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgta ttactgtcag caggggtatta tgcttcccc caggttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 151
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 16F8; VH

<400> 151

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 Leu 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

376

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

Val Thr Val Ser Ser
 115

<210> 152
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 16F8; VH

<400> 152
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attcttggtg gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 tttggtggtt ttaactactg gggccaagga accctgggtc c cgtctcgtc c 351

<210> 153
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> O3C9; VL

<400> 153

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

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

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

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

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

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

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

<210> 154
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> O3C9; VL

<400> 154
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 155
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> O3C9; VH

<400> 155

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

100

105

110

Val Thr Val Ser Ser
115

<210> 156
<211> 351
<212> ADN
<213> Secuencia artificial

<220>
<223> O3C9; VH

<400> 156
gaggtgcaat tggtggagtc tgggggagge ttggtacagc ctgggggggc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttttgcca tgagctgggt ccgtcagtct 120
ccaggggaagg ggctggagtg ggtctcagct attattggta gtggtagtaa cacatactac 180
gcagactccg tgaagggccg gttcaccate tccagagaca attccaagaa cacgtctgat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
tttgggtggt ttaactactg gggccaagga accctggtca ccgtctcgtc c 351

<210> 157
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> O2D7; VL

<400> 157

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

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

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

Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Thr 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 Ala Ile Met Leu Pro
85 90 95

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

<210> 158
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> O2D7; VL

<400> 158
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccagget cctcatcaat gtgggctccc gtagggccac tggcacccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag caggctatta tgcttctctc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 159
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> O2D7; VH

<400> 159

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 160
<211> 351
<212> ADN
<213> Secuencia artificial

<220>
<223> O2D7; VH

<400> 160
gagggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccagget 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttgggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 161
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> 28H1; VL

<400> 161

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

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

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

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

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

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

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

<210> 162
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 28H1; VL

<400> 162
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttagc cgcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 163
 <211> 116
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 28H1; VH

<400> 163

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

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

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

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

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

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

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

Thr Val Ser Ser

115

<210> 164
 <211> 348
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 28H1; VH

<400> 164
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agtcatgcta tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct atttgggcta gtggggagca atactacgca 180
 gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
 cagatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgaa aggggtggctg 300
 ggtaattttg actactgggg ccaaggaacc ctggtcaccg tctcgagt 348

<210> 165
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 22A3; VL

<400> 165

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

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

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

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

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

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

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

<210> 166
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 22A3; VL

<400> 166
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 167
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 22A3; VH

<400> 167

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 168
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 22A3; VH

<400> 168
 gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attattggta gtggtagtat cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtagg 300
 tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 169
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 29B11; VL

<400> 169

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

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

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

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

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

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

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

<210> 170
 <211> 324

<212> ADN
 <213> Secuencia artificial

<220>
 <223> 29B11; VL

<400> 170
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtta ttactgtcag caggggtatta tgcttcccc caggttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 171
 <211> 117
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 29B11; VH

<400> 171

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 172

386

<211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> 29B11; VH

<400> 172
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attattggta gtggtggtat cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300
 tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 173
 <211> 108
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 23C10; VL

<400> 173

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

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

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

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

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

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

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

<210> 174
 <211> 324
 <212> ADN
 <213> Secuencia artificial

<220>

<223> 23C10; VL

<400> 174

```

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcttgca gggccagtc gagtgtagc cgcagctact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca      180
gacagggtca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtga ttactgtcag cagggtcagg ttattcccc tacgttcggc      300
caggggacca aagtggaaat caaa                                           324

```

<210> 175

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> 23C10; VH

<400> 175

```

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

```

```

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

```

```

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

```

```

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

```

```

Val Thr Val Ser Ser
          115

```

<210> 176

<211> 351

<212> ADN

<213> Secuencia artificial

<220>

<223> 23C10; VH

<400> 176

```
gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc      60
tcctgtgcag cctccggatt cacctttagc agttctgcca tgagctgggt ccgccaggct      120
ccagggaagg ggctggagtg ggtctcagct attagtacta atggtaatta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtag      300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t              351
```

<210> 177

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_C3B6; VL

<400> 177

```
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 Arg Asn Asp
          20           25           30
```

```
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
          65           70           75           80
```

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

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

<210> 178

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_C3B6; VL

<400> 178

```

gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatget gcatccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcagtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgca g aatggctctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                           321

```

<210> 179

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_C3B6; VH

<400> 179

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
              100              105              110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
              115              120

```

<210> 180

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_C3B6; VH

<400> 180

```

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggagct atcatcccga tccttggtat cgcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 181

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_6A12; VL

<400> 181

```

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 Arg Asn Asp
          20           25           30

```

```

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

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

```

```

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

```

<210> 182

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_6A12; VL

<400> 182

```

gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtagca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcagtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgcat aatgggtctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                              321

```

<210> 183

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_6A12; VH

<400> 183

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
          100              105              110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
          115              120

```

<210> 184

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_6A12; VH

<400> 184

```

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcttgcaagg cctccggagg cacattcagc agctatgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggagtg atcatcccta tccttggtac cgcaaactac      180
gcacagaagt tocagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 185

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_C3A6; VL

<400> 185

```

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 Arg Asn Val
          20           25           30

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

<210> 186

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_C3A6; VL

<400> 186

```

gacatccaga tgaccagtc tccttcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatgat tcgtccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttcaactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgcag aatggctctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                          321

```

<210> 187

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_C3A6; VH

<400> 187

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
              100              105              110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
              115              120

```

<210> 188

<211> 363

<212> ADN

<213> Secuencia artificial

396

<220>

<223> 2B10_C3A6; VH

<400> 188

```

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 189

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_wt; VL

<400> 189

```

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 Arg Asn Val
          20           25           30

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

<210> 190

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_wt; VL

<400> 190

```

gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca ggggattcgt aatgttttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgacg aatggctctg agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                          321

```

<210> 191

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_wt; VH

<400> 191

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100              105              110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
115              120

```

<210> 192

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_wt; VH

<400> 192

```

cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 193

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_VD; VL

<400> 193

```

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 Arg Asn Asp
          20           25           30

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

<210> 194

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_VD; VL

<400> 194

```

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca ggggattcgt aatgatttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttcaactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgca g aatggctctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                           321

```

<210> 195

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_VD; VH

<400> 195

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
          100          105          110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
          115          120

```

<210> 196

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_D1A2_VD; VH

<400> 196

```

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 197

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_O7D8; VL

<400> 197

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

<210> 198

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_O7D8; VL

<400> 198

```

gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gagcattcgt aatgttttag gctggtagca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatgat gtgtccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttcaactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgcag aatggctctgc agcccgcgac gtttgccag      300
ggcaccaaag tcgagatcaa g                                              321

```

<210> 199

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_O7D8; VH

<400> 199

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
          100              105              110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
          115              120

```

<210> 200

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_O7D8; VH

<400> 200

```

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 201

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_O1F7; VL

<400> 201

```

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 Arg Asn Val
          20           25           30

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

<210> 202

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_O1F7; VL

<400> 202

```

gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatgat gcgtccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcctgcag aatggctctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                          321

```

<210> 203

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_O1F7; VH

<400> 203

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
          100              105              110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
          115              120

```

<210> 204

<211> 363

<212> ADN

<213> Secuencia artificial

406

<220>

<223> 2B10_O1F7; VH

<400> 204

```

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 205

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_6H10; VL

<400> 205

```

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 Arg Asn Val
20           25           30

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

<210> 206

<211> 321

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_6H10; VL

<400> 206

```

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgcct gatccaggct gctaccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgagc aatggctctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                          321

```

<210> 207

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> 2B10_6H10; VH

<400> 207

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
              100              105              110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser
              115              120

```

<210> 208

<211> 363

<212> ADN

<213> Secuencia artificial

<220>

<223> 2B10_6H10; VH

<400> 208

```

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc      60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

```

<210> 209

<211> 605

<212> PRT

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 3F2 (constructo de fusión cadena pesada-citoquina)

<400> 209

```

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

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

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

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

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

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

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

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

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

```

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser
225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
260 265 270

Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
290 295 300

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

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

385 390 395 400

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
405 410 415

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
			500					505					510		

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

```
<210> 210
<211> 1818
<212> ADN
<213> Secuencia artificial
```

<220>
<223> Fab-IL2-Fab 3F2 (constructo de fusión cadena pesada-citoquina)

<400> 210
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtc ccgtctcgag tgctagcacc 360
aagggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac 540
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt 660
gactccggcg gaggaggag cggcggaggt ggctccggag gtggcggagc acctacttca 720
agttctacaa agaaaacaca gctacaactg gagcatttac tgctggattt acagatgatt 780
ttgaatggaa ttaataatta caagaatccc aaactcacca ggatgctcac atttaagttt 840
tacatgccca agaaggccac agaactgaaa catcttcagt gtctagaaga agaactcaaa 900
cctctggagg aagtgtctaaa tttagctcaa agcaaaaact ttcacttaag acccagggac 960
ttaatcagca atatcaacgt aatagttctg gaactaaagg gatctgaaac aacattcatg 1020
tgtgaatatg ctgatgagac agcaaccatt gtagaatttc tgaacagatg gattaccttt 1080
gcccaaagca tcactcctaac actgacttcc ggcggaggag gatccggcgg aggtggctct 1140
ggcggtgggc gagaggtgca attggtggag tctgggggag gcttgggtaca gcctgggggg 1200
tccttgagac tctcctgtgc agcctccgga ttcaccttta gcagttatgc catgagctgg 1260
gtccgccagg ctccaggga ggggctggag tgggtctcag ctattagtgg tagtggtggt 1320
agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag 1380
aacacgctgt atctgcagat gaacagcctg agagccgagg acacggccgt atattactgt 1440
gcgaaagggg ggtttggtgg ttttaactac tggggccaag gaacctggt caccgtctcg 1500
agtgtagca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct 1560
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 1620
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt octacagtcc 1680
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag 1800
cccaaattct gtgactga 1818

<210> 211
 <211> 605
 <212> PRT
 <213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 4G8 (constructo de fusión cadena pesada-citoquina)

<400> 211

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly
 210 215 220
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser
 225 230 235 240
 Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 245 250 255
 Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 260 265 270
 Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
 275 280 285
 Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 290 295 300
 Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 305 310 315 320
 Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 325 330 335
 Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 340 345 350
 Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 355 360 365
 Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 385 390 395 400
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 405 410 415
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 420 425 430
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 435 440 445
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 212

<211> 1818

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 4G8 (constructo de fusión cadena pesada-citoquina)

<400> 212

gaggtgcaat tgttgagtc tgggggaggc ttgtacagc ctgggggggc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtag	300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc	360
aaggggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggetgtcc tacagtcttc aggactctac	540

416

```

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      600
aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt      660
gactccggcg gaggagggag cggcggaggt ggctccggag gtggcggagc acctacttca      720
agttctacaa agaaaacaca gctacaactg gagcatttac tgctggattt acagatgatt      780
ttgaatggaa ttaataatta caagaatccc aaactcacca ggatgctcac atttaagttt      840
tacatgcccc agaaggccac agaactgaaa catcttcagt gtctagaaga agaactcaaa      900
cctctggagg aagtgctaaa tttagctcaa agcaaaaact ttcacttaag acccagggac      960
ttaatcagca atatcaacgt aatagttctg gaactaaagg gatctgaaac aacattcatg     1020
tgtgaatatg ctgatgagac agcaaccatt gtagaatttc tgaacagatg gattaccttt     1080
gccccaaagca tcatctcaac actgacttcc ggcggaggag gatccggcgg aggtggctct     1140
ggcgggtggcg gagaggtgca attgttggag tctgggggag gcttggtaga gcctgggggg     1200
tccctgagac tctcctgtgc agcctccgga ttcaccttta gcagttatgc catgagctgg     1260
gtccgccagg ctccagggaa ggggctggag tgggtctcag ctattagtgg tagtgggtgt     1320
agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag     1380
aacacgctgt atctgcagat gaacagcctg agagccgagg acacggccgt atattactgt     1440
gcgaaagggg ggctgggtaa ttttgactac tggggccaag gaaccctggt caccgtctcg     1500
agtgctagca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct     1560
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg     1620
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc     1680
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccacg     1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag     1800
cccaaattct gtgactga                                     1818

```

```

<210> 213
<211> 605
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> Fab-IL2-Fab 3D9 (constructo de fusión cadena pesada-citoquina)
<400> 213

```

```

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 Thr Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser
 225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 260 265 270

Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
 275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
290 295 300

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
405 410 415

Ala Met Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
420 425 430

Ser Ala Ile Gly Val Ser Thr Gly Ser Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser

530

535

540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 214

<211> 1818

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 3D9 (constructo de fusión cadena pesada-citoquina)

<400> 214

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tctctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccagact	120
ccaggggaagg ggctggagtg ggtctcagct attggtgtta gtactggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg	300
ctgggtcctt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc	360
aagggcccat cggctctccc cctggcaccc tccccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa ggactacttc ccgaaccgg tgacgggtgc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc cggctgtcc tacagtcctc aggactctac	540
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt	660
gactccggcg gaggaggag cggcggaggt ggctccggag gtggcggagc acctacttca	720
agttctacaa agaaaacaca gctacaactg gagcatttac tgctggattt acagatgatt	780
ttgaatggaa ttaataatta caagaatccc aaactcacca ggatgctcac atttaagttt	840
tacatgccca agaaggccac agaactgaaa catcttcagt gtctagaaga agaactcaaa	900
cctctggagg aagtgctaaa tttagctcaa agcaaaaact ttcacttaag acccaggac	960
ttaatcagca atatcaacgt aatagttctg gaactaaagg gatctgaaac aacattcatg	1020
tgtgaatatg ctgatgagac agcaaccatt gtagaatttc tgaacagatg gattaccttt	1080

gccc aaagca tc atctcaac actgacttcc ggcggaggag gatccggcgg aggtggctct 1140
ggcgggtggcg gagagggtgca attgttggag tctggggggag gcttggtaca gcctgggggg 1200
tccctgagac tctcctgtgc agcctccgga ttcaccttta gcagttatgc tatgagctgg 1260
gtccgccaga ctccagggaa ggggctggag tgggtctcag ctattggtgt tagtactggt 1320
agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag 1380
aacacgctgt atctgcagat gaacagcctg agagccgagg acacggccgt atattactgt 1440
gcgaaagggt ggctgggtcc ttttgactac tggggccaag gaaccctggt caccgtctcg 1500
agtgtagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gaggacctct 1560
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 1620
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 1680
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag 1800
cccaaattctt gtgactga 1818

<210> 215
<211> 605
<212> PRT
<213> Secuencia artificial

<220>
<223> Fab-IL2-Fab 2F11 (constructo de fusión cadena pesada-citoquina)
<400> 215

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

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

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 355 360 365
 Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 385 390 395 400
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 405 410 415
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 420 425 430
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 435 440 445
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 450 455 460
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 465 470 475 480
 Ala Lys Trp Arg Trp Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 485 490 495
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 500 505 510
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 515 520 525
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 530 535 540
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 545 550 555 560
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 565 570 575
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 580 585 590
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 595 600 605

<210> 216
 <211> 1818
 <212> ADN
 <213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 2F11 (constructo de fusión cadena pesada-citoquina)

<400> 216

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac accgcogtat attactgtgc gaaatggaga	300
tggatgatgt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc	360
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtctc aggactctac	540
tcctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt	660
gactccggcg gaggaggag cggcggaggt ggctccggag gtggcggagc acctacttca	720
agttctacaa agaaaacaca gctacaactg gagcatttac tgctggattt acagatgatt	780
ttgaatggaa ttaataatta caagaatccc aaactcacca ggatgctcac atttaagttt	840
tacatgccc aagaaggccac agaactgaaa catcttcagt gtctagaaga agaactcaaa	900
cctctggagg aagtgtctaaa tttagctcaa agcaaaaact ttcacttaag acccaggagc	960
ttaatcagca atatcaacgt aatagttctg gaactaaagg gatctgaaac aacattcatg	1020
tgtgaatatg ctgatgagac agcaaccatt gtagaatttc tgaacagatg gattaccttt	1080
gccc aaagca tcattctaac actgacttcc ggcgaggag gatccggcg aggtggctct	1140
ggcggtggcg gagaggtgca attgttgag tctgggggag gcttggtaca gcctgggggg	1200
tccctgagac tctcctgtgc agcctccgga ttcaccttta gcagttatgc catgagctgg	1260
gtccgccagg ctccaggga ggggctggag tgggtctcag ctattagtgg tagtgggtgt	1320
agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag	1380
aacacgctgt atctgcagat gaacagcctg agagccgagg acaccgccgt atattactgt	1440
gcgaaatgga gatggatgat gtttgactac tggggccaag gaaccctgggt caccgtctcg	1500
agtgctagca ccaagggccc atcggtcttc ccctggcac cctcctccaa gagcacctct	1560
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg	1620

426

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 1680
 tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag 1740
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag 1800
 cccaaatctt gtgactga 1818

<210> 217
 <211> 605
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Fab-IL2-Fab 4B3 (constructo de fusión cadena pesada-citoquina)

<400> 217

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser
 225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 260 265 270

Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
 275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 290 295 300

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 405 410 415

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 218

<211> 1818

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 4B3 (constructo de fusión cadena pesada-citoquina)

<400> 218

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttage agttatgcc ttagctgggt ccgccaggct 120

ccaggaagg ggctggagt ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

```

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc ccggaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcttc aggactctac 540
tcctctagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt 660
gactccggcg gaggagggag cggcgagggt ggctccggag gtggcggagc acctacttca 720
agttctacaa agaaaacaca gctacaactg gagcatttac tgctggattt acagatgatt 780
ttgaatggaa ttaataatta caagaatccc aaactcacca ggatgctcac atttaagttt 840
tacatgcccc agaaggccac agaactgaaa catcttcagt gtctagaaga agaactcaaa 900
cctctggagg aagtgctaaa tttagctcaa agcaaaaact ttcacttaag acccagggac 960
ttaatcagca atatcaacgt aatagttctg gaactaaagg gatctgaaac aacattcatg 1020
tgtgaatatg ctgatgagac agcaaccatt gtagaatttc tgaacagatg gattaccttt 1080
gccccaaagca tcattctaac actgacttcc ggcgaggag gatccggcgg aggtggctct 1140
ggcggtgggc gagaggtgca attgttgagg tctgggggag gcttggtaca gcctgggggg 1200
tccttgagac tctctgtgc agcctccgga ttcaccttta gcagttatgc catgagctgg 1260
gtccgccagg ctccagggaa ggggctggag tgggtctcag ctattagtgg tagtggtggt 1320
agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag 1380
aacacgctgt atctgcagat gaacagcctg agagccgagg acacggccgt atattactgt 1440
gcgaaagggg ggctgggtaa ttttgactac tggggccaag gaaccctggt caccgtctcg 1500
agtgctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 1560
gggggcacag cgccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 1620
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1680
tcaggactct actcctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag 1800
cccaaattct gtgactga 1818

```

<210> 219

<211> 993

<212> PRT

<213> Secuencia artificial

<220>

<223> Fab-IL12-Fab 4G8 (IL-12 murina; constructo de fusión cadena pesada-citoquina)

<400> 219

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Met Trp Glu
 225 230 235 240

Leu Glu Lys Asp Val Tyr Val Val Glu Val Asp Trp Thr Pro Asp Ala
 245 250 255
 Pro Gly Glu Thr Val Asn Leu Thr Cys Asp Thr Pro Glu Glu Asp Asp
 260 265 270
 Ile Thr Trp Thr Ser Asp Gln Arg His Gly Val Ile Gly Ser Gly Lys
 275 280 285
 Thr Leu Thr Ile Thr Val Lys Glu Phe Leu Asp Ala Gly Gln Tyr Thr
 290 295 300
 Cys His Lys Gly Gly Glu Thr Leu Ser His Ser His Leu Leu Leu His
 305 310 315 320
 Lys Lys Glu Asn Gly Ile Trp Ser Thr Glu Ile Leu Lys Asn Phe Lys
 325 330 335
 Asn Lys Thr Phe Leu Lys Cys Glu Ala Pro Asn Tyr Ser Gly Arg Phe
 340 345 350
 Thr Cys Ser Trp Leu Val Gln Arg Asn Met Asp Leu Lys Phe Asn Ile
 355 360 365
 Lys Ser Ser Ser Ser Pro Pro Asp Ser Arg Ala Val Thr Cys Gly Met
 370 375 380
 Ala Ser Leu Ser Ala Glu Lys Val Thr Leu Asp Gln Arg Asp Tyr Glu
 385 390 395 400
 Lys Tyr Ser Val Ser Cys Gln Glu Asp Val Thr Cys Pro Thr Ala Glu
 405 410 415
 Glu Thr Leu Pro Ile Glu Leu Ala Leu Glu Ala Arg Gln Gln Asn Lys
 420 425 430
 Tyr Glu Asn Tyr Ser Thr Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro
 435 440 445
 Asp Pro Pro Lys Asn Leu Gln Met Lys Pro Leu Lys Asn Ser Gln Val
 450 455 460
 Glu Val Ser Trp Glu Tyr Pro Asp Ser Trp Ser Thr Pro Arg Ser Tyr
 465 470 475 480
 Phe Ser Leu Lys Phe Phe Val Arg Ile Gln Arg Lys Lys Glu Lys Met
 485 490 495

Lys Glu Thr Glu Glu Gly Cys Asn Gln Lys Gly Ala Phe Phe Val Glu
500 505 510

Lys Thr Ser Thr Glu Val Gln Cys Lys Gly Gly Asn Val Cys Val Gln
515 520 525

Ala Gln Asp Arg Tyr Tyr Asn Ser Ser Cys Ser Lys Trp Ala Cys Val
530 535 540

Pro Cys Arg Val Arg Ser Gly Gly Asp Gly Ser Gly Gly Gly Gly Ser
545 550 555 560

Gly Gly Gly Gly Ser Arg Val Ile Pro Val Ser Gly Pro Ala Arg Cys
565 570 575

Leu Ser Gln Ser Arg Asn Leu Leu Lys Thr Thr Asp Asp Met Val Lys
580 585 590

Thr Ala Arg Glu Lys Leu Lys His Tyr Ser Cys Thr Ala Glu Asp Ile
595 600 605

Asp His Glu Asp Ile Thr Arg Asp Gln Thr Ser Thr Leu Lys Thr Cys
610 615 620

Leu Pro Leu Glu Leu His Lys Asn Glu Ser Cys Leu Ala Thr Arg Glu
625 630 635 640

Thr Ser Ser Thr Thr Arg Gly Ser Cys Leu Pro Pro Gln Lys Thr Ser
645 650 655

Leu Met Met Thr Leu Cys Leu Gly Ser Ile Tyr Glu Asp Leu Lys Met
660 665 670

Tyr Gln Thr Glu Phe Gln Ala Ile Asn Ala Ala Leu Gln Asn His Asn
675 680 685

His Gln Gln Ile Ile Leu Asp Lys Gly Met Leu Val Ala Ile Asp Glu
690 695 700

Leu Met Gln Ser Leu Asn His Asn Gly Glu Thr Leu Arg Gln Lys Pro
705 710 715 720

Pro Val Gly Glu Ala Asp Pro Tyr Arg Val Lys Met Lys Leu Cys Ile
725 730 735

Leu Leu His Ala Phe Ser Thr Arg Val Val Thr Ile Asn Arg Val Met

740										745					750				
Gly	Tyr	Leu	Ser	Ser	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser				
		755							760					765					
Gly	Gly	Gly	Gly	Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val				
	770						775					780							
Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr				
	785					790					795					800			
Phe	Ser	Ser	Tyr	Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly				
				805						810					815				
Leu	Glu	Trp	Val	Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr				
			820						825					830					
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys				
		835						840					845						
Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala				
		850					855					860							
Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Trp	Leu	Gly	Asn	Phe	Asp	Tyr	Trp	Gly				
	865					870					875				880				
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser				
				885						890					895				
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala				
			900						905					910					
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val				
		915						920					925						
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala				
		930					935					940							
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val				
	945					950					955				960				
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His				
				965						970					975				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys				
			980						985					990					

Asp

<210> 220
 <211> 2982
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Fab-IL12-Fab 4G8 (IL-12 murina; constructo de fusión cadena pesada-citoquina)
 construct)

<400> 220
 gaggtgcaat tgctggaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
 agctgcgccg ccagcggcctt caccttcagc agctacgcca tgtcttgggt ccgccaggcc 120
 cctggaaagg gcctggaatg ggtgtccgcc atcagcggca gcggcggcag cacctactac 180
 gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
 ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc caagggctgg 300
 ctgggcaact tcgactactg gggccagggc actctggtca cagtgtctag cgctagcacc 360
 aagggcccat cggctcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 420
 gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480
 ggcgcctga ccagcggcgt gcacaccttc ccggtgtgct tacagtcttc aggactctac 540
 tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 600
 aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt 660
 gactccggcg gaggagggag cggcggaggt ggctccggag ggggcggagc catgtgggag 720
 ctggaaaagg acgtgtacgt ggtggaggtg gactggaccc ccgacgccc tggcgagaca 780
 gtgaacctga cctgcgacac ccccgaagag gacgacatca cctggaccag cgaccagcgg 840
 cacggcgtga tcggcagcgg caagaccctg accatcaccg tgaaagagtt tctggacgcc 900
 ggccagtaca cctgccacaa gggcggcgag aactgagcc acagccacct gctgctgcac 960
 aagaaagaga acggcatctg gtccaccgag atcctgaaga acttcaagaa caagaccttc 1020
 ctgaagtgcg agggccccc aaacagcggc cggttcacct gcagctggct ggtgcagcgg 1080
 aacatggacc tgaagttcaa catcaagagc agcagcagcc cccctgacag cagggccgtg 1140
 acctgcggca tggccagcct gagcggcgag aaggtgaccc tggaccagag ggactacgag 1200
 aagtacagcg tgagctgcca ggaagatgtc acctgcccc cgcggagga aaccctgccc 1260
 atcgagctgg ccctggaagc ccggcagcag aacaagtacg agaactactc taccagcttc 1320
 ttcacccggg acatcatcaa gcccagcccc cccaagaacc tgcagatgaa gcccctgaag 1380
 aacagccagg tggaggtgtc ctgggagtag cctgacagct ggtccacccc cagaagctac 1440

```

ttcagcctga agttcttcgt gagaatccag cggaagaaag aaaagatgaa agagacagag 1500
gaaggctgca accagaaggg cgccttcttc gtcgagaaaa ccagcaccga ggtgcagtgc 1560
aagggcgga acgtgtgcgt gcaggcccag gaccggtact acaacagcag ctgcagcaag 1620
tgggcctgcg tgccctgcag agtgcggtct ggcggcgacg gctctggcgg cggaggaagc 1680
ggcggagggg gcagcagagt gatccccgtg agcggccctg cccggtgctt gagccagagc 1740
cggaacctgc tgaaaaccac cgacgacatg gtgaaaaccg ccagagagaa gctgaagcac 1800
tacagctgca cagccgagga catcgaccac gaggacatca cccgggacca gaccagcacc 1860
ctgaaaacct gcctgcccct ggaactgcac aaaaacgaga gctgcctggc caccgggag 1920
acaagcagca ccacccgggg cagctgcctg cctcccaga aaacctccct gatgatgacc 1980
ctgtgcctgg gcagcatcta cgaggacctg aagatgtacc agaccgagtt ccaggccatc 2040
aacgccgccc tgcagaacca caatcaccag cagatcatcc tggacaaggg catgctggtc 2100
gccatcgacg agctgatgca gagcctgaac cacaacggcg aaacctgcg gcagaaaccc 2160
cccgctggcg aggccgaccc ctaccgggtg aagatgaagc tgtgcatcct gctgcacgcc 2220
ttcagcacc cgggtggtgac catcaaccgg gtgatgggct acctgtcctc tgccggggga 2280
gggggatccg gcggaggtgg ctctggcggg ggcgagagg tgcaattgct ggaaagcggc 2340
ggaggactgg tgcagcctgg cggcagcctg agactgagct gcgcgccag cggcttcacc 2400
ttcagcagct acgcatgtc ttgggtccgc caggccccctg gaaagggcct ggaatgggtg 2460
tccgccatca gcggcagcgg cggcagcacc tactacgcg acagcgtgaa gggccggttc 2520
accatcagcc gggacaacag caagaacacc ctgtacctgc agatgaacag cctgagagcc 2580
gaggacaccg ccgtgtacta ctgcgccaag ggctggctgg gcaacttcga ctactggggc 2640
cagggcactc tggtcacagt gtctagcgt agcaccaagg gcccatcggt ctccccctg 2700
gcacctcctt ccaagagcac ctctgggggc acagcgccc tgggctgcct ggtcaaggac 2760
tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac 2820
accttccccg ctgtcctaca gtctcagga ctctactccc tcagcagcgt ggtgaccgtg 2880
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcaca gccagcaac 2940
accaaggtgg ataagaaagt tgagcccaa tcttgtgact ga 2982

```

<210> 221

<211> 603

<212> PRT

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 28H1 (constructo de fusión cadena pesada-citoquina)

<400> 221

436

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

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
 260 265 270

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
 275 280 285

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
 290 295 300

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
 305 310 315 320

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
 325 330 335

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
 340 345 350

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu
 370 375 380

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

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Ala
 405 410 415

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

Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys Gly
 435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
 465 470 475 480

Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 485 490 495

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 500 505 510

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 515 520 525

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 530 535 540

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 545 550 555 560

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 565 570 575

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 580 585 590

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 595 600

<210> 222

<211> 1812

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 2BH1 (constructo de fusión cadena pesada-citoquina)

<400> 222

gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg	60
tctgcgcgcg cctccggctt caccttctec tcccagcca tgtcctgggt ccgacaggct	120
cctggcaaag gcctggaatg ggtgtccgcc atctgggctt ccggcgagca gtactacgcc	180
gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg	240
cagatgaact cctgcgggc cgaggacacc gccgtgtact actgtgcaa gggctggctg	300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag	360
ggaccctcgc tgttccccct ggcctccctc agcaagtcta cctctggcgg caccgcgct	420
ctgggctgcc tggtaagga ctacttccc gagcccgta ccgtgtcctg gaactctggc	480
gccctgacca gcggcgtcca cacctttcca gccgtgctgc agtcctccgg cctgtactcc	540
ctgtcctccg tcgtgaccgt gccctccagc tctctgggca ccagacctc catctgcaac	600
gtgaaccaca agccctccaa caccaagggt gacaagaagg tggaacccaa gtccctgcgac	660
agtgggtgggg gaggatctgg tggcggagggt tctggcggag gtggcgctcc tacatcctcc	720
agcaccaaga aaaccagct ccagctggaa catctcctgc tggatctgca gatgatcctg	780
aacggcatca acaactacaa gaaccccaag ctgacccgga tgctgacctt caagttctac	840

```

atgccaaga aggccaccga gctgaaacat ctgcagtgcc tggaagagga actgaagcct      900
ctggaagagg tgctgaacct ggcccagtc aagaacttcc acctgaggcc tcgggacctg      960
atctccaaca tcaacgtgat cgtgctggaa ctgaagggtc ccgagacaac cttcatgtgc     1020
gagtacgccg acgagacagc taccatcgtg gaatttctga accggtggat caccttcgcc     1080
cagtccatca tctccacctt gacctccggt ggtggcggat ccgggggagg gggttctggc     1140
ggaggcggag aagtgcagct gctggaatcc ggcgagggcc tggcgcagcc tggcggatct     1200
ctgagactgt cctgcgccgc ctccggcttc accttctcct cccacgccat gtcctgggtc     1260
cgacaggctc caggcaaggg cctggaatgg gtgtccgcca tctgggcctc cggcgagcag     1320
tactacgccg actctgtgaa gggcgggttc accatctccc gggacaactc caagaacacc     1380
ctgtacctgc agatgaactc cctgcggggc gaggacaccg ccgtgtacta ctgtgccaag     1440
ggctggctgg gcaacttcga ctactggggc cagggcaccc tggtcaccgt gtcctccgcc     1500
tctaccaagg gcccctccgt gttccctctg gcccctcca gcaagtctac ctctggcggc     1560
accgcgcctc tgggctgcct ggtcaaggac tacttccccg agcccgtagc cgtgtcctgg     1620
aactctggcg ccttgaccag cggcgtgcac acctttccag ccgtgctgca gtcctccggc     1680
ctgtactccc tgctctccgt cgtgaccgtg cctccagct ctctgggcac ccagacctac     1740
atctgcaacg tgaaccacaa gcctccaac accaagggtg acaagaagg ggaaccaag      1800
tctgcgact ga                                     1812

```

```

<210> 223
<211> 605
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> Fab-IL2-Fab 29B11 (constructo de fusión cadena pesada-citoquina)

```

```

<400> 223

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

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

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser
225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
260 265 270

Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
290 295 300

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu

	325		330		335
Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu	340		345		350
Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu	355		360		365
Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	370		375		380
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	385		390		395
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	405		410		415
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	420		425		430
Ser Ala Ile Ile Gly Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val	435		440		445
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	450		455		460
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	465		470		475
Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu	485		490		495
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu	500		505		510
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys	515		520		525
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser	530		535		540
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser	545		550		555
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser	565		570		575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 595 600 605

<210> 224
 <211> 1818
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Fab-IL2-Fab 29B11 (constructo de fusión cadena pesada-citoquina)

<400> 224
 gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
 tcttgccgcg cctccggctt caccttctcc tctacgcca tgtcctgggt ccgacaggct 120
 cctggcaaag gcttggaatg ggtgtccgcc atcatcggct ccggcggcat cacctactac 180
 gccgactctg tgaagggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240
 ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtgc caagggctgg 300
 ttccgaggct tcaactactg gggacagggc accctgggtca ccgtgtccag cgctagcacc 360
 aagggaccct ccgtgttccc cctggccccc tccagcaagt ctacctctgg cggcaccgcc 420
 gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgaccgtgtc ctggaactct 480
 ggcgcctga ccagcggcgt ccacaccttt ccagccgtgc tgacgtctc cggcctgtac 540
 tccctgtcct ccgtcgtgac cgtgccctcc agctctctgg gcacccagac ctacatctgc 600
 aacgtgaacc acaagccctc caacaccaag gtggacaaga aggtggaacc caagtcctgc 660
 gacagtgggtg ggggaggatc tgggtggcgga ggttctggcg gaggtggcgc tctacatcc 720
 tccagcacca agaaaaccca gctccagctg gaacatctcc tgctggatct gcagatgatc 780
 ctgaacggca tcaacaacta caagaacccc aagctgaccc ggatgctgac cttcaagttc 840
 tacatgcccc agaaggccac cgagctgaaa catctgcagt gcctggaaga ggaactgaag 900
 cctctggaag aggtgctgaa cctggcccag tccaagaact tccacctgag gcctcgggac 960
 ctgatctcca acatcaacgt gatcgtgctg gaactgaagg gctccgagac aaccttcatg 1020
 tgcgagtacg ccgacgagac agctaccatc gtggaatttc tgaaccggtg gatcaccttc 1080
 gccagtcaca tcatctccac cctgacctcc ggtggtggcg gatccggggg agggggttct 1140
 ggcggaggcg gagaagtgca gctgctggaa tccggcggag gcctggtgca gcctggcgga 1200
 tctctgagac tgtcctgcgc cgcctccggc ttcaccttct cctcctatgc catgtcctgg 1260
 gtccgacagg ctccaggcaa gggcctggaa tgggtgtccg ccatcatcgg ctccggcggc 1320
 atcacctact acgccgactc tgtgaagggc cggttcacca tctcccggga caactccaag 1380

```

aacaccctgt acctgcagat gaactccctg cgggccgagg acaccgccgt gtactactgt      1440
gccaaagggct ggttcggagg cttcaactac tggggccagg gcaccctggg caccgtgtcc      1500
tccgcctcta ccaagggccc ctccgtgttc cctctggccc cctccagcaa gtctacctct      1560
ggcggcaccg ccgctctggg ctgcctgggc aaggactact tccccgagcc cgtgaccgtg      1620
tcctggaact ctggcgccct gaccagcggc gtgcacacct ttccagccgt gctgcagtcc      1680
tccggcctgt actccctgtc ctccgtcgtg accgtgccct ccagctctct gggcaccacg      1740
acctacatct gcaacgtgaa ccacaagccc tccaacacca aggtggacaa gaaggtggaa      1800
cccaagtcct gcgactga                                     1818

```

```

<210> 225
<211> 605
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> Fab-IL2-Fab 19G1 (constructo de fusión cadena pesada-citoquina)

```

```

<400> 225

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly
 210 215 220
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Pro Thr Ser
 225 230 235 240
 Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 245 250 255
 Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 260 265 270
 Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
 275 280 285
 Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 290 295 300
 Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 305 310 315 320
 Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 325 330 335
 Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 340 345 350
 Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 355 360 365
 Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 385 390 395 400

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 405 410 415

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

Ser Ala Ile Ile Ser Ser Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 465 470 475 480

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 595 600 605

<210> 226

<211> 1818

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 19G1 (constructo de fusión cadena pesada-citoquina)

<400> 226

gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg

tcttgcgccg ccagcggcctt caccttcagc agctacgcca tgagctgggt ccgccaggcc	120
cctggcaagg gactggaatg ggtgtccgcc atcatcagct ctggcggcct gacctactac	180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctggcca cagtgtccag cgctagcacc	360
aagggaccca gcgtgttccc cctggccccc agcagcaaga gcacatctgg cggaacagcc	420
gccctgggct gcctgggtcaa agactacttc cccgagcccg tgaccgtgtc ctggaacagc	480
ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgacagagcag cggcctgtac	540
agcctgagca gcgtgggtcac cgtgcctagc tctagcctgg gcacccagac ctacatctgc	600
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggaacc caagagctgc	660
gactccggcg gagggcgatc tggcgggtga ggctccggag gcggaggcgc tctactagc	720
agctccacca agaaaaccca gctccagctg gaacatctgc tgctggatct gcagatgatc	780
ctgaacggca tcaacaacta caagaacccc aagctgacct ggatgctgac cttcaagttc	840
tacatgcccc agaaggccac cgaactgaaa catctgcagt gcctggaaga ggaactgaag	900
cctctggaag aggtgctgaa cctggcccag agcaagaact tccacctgag gcccaggac	960
ctgatcagca acatcaacgt gatcgtgctg gaactgaagg gcagcgagac aaccttcagt	1020
tgcgagtacg ccgacgagac agccaccatc gtggaatttc tgaaccggtg gatcaccttc	1080
gccagagca tcatcagcac cctgacaagc ggaggcggcg gatccggcgg aggcggatct	1140
ggcggaggag gcgagggtcca gctgctcgaa agcggcggag gactggtgca gcctggcggc	1200
agcctgagac tgtcttgccg cgcagcggc ttcacctca gcagctacgc catgagctgg	1260
gtccgccagg cccctggcaa gggactggaa tgggtgtccg ccatcatcag ctctggcggc	1320
ctgacctact acgccgacag cgtgaagggc cggttcacca tcagccggga caacagcaag	1380
aacaccctgt acctgcagat gaacagcctg cgggccgagg acaccgccgt gtactactgc	1440
gccaaaggat ggttcggcgg cttcaactac tggggacagg gcacctggt cacagtgtcc	1500
agcgcagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcacatct	1560
ggcggaacag ccgccctggg ctgcctggtc aaagactact tccccagacc cgtgaccgtg	1620
tcttgaaca gcggagccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc	1680
agcggcctgt acagcctgag cagcgtggtc accgtgccta gctctagcct gggcaccag	1740
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa	1800
cccaagagct gcgactga	1818

<211> 605
 <212> PRT
 <213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 20G8 (constructo de fusión cadena pesada-citoquina)

<400> 227

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser
 225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 260 265 270

Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
 275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 290 295 300

Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 405 410 415

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

Ser Ala Ile Ile Gly Ser Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
 435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 450 455 460

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

465 470 475 480

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 228
<211> 1818
<212> ADN
<213> Secuencia artificial

<220>
<223> Fab-IL2-Fab 20G8 (constructo de fusión cadena pesada-citoquina)

<400> 228
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120
cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcagccg gacctactac 180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc 360
aagggaccca gcgtgttccc cctggccccc agcagcaaga gcacatctgg cggaacagcc 420
gccctggget gcctgttcaa agactacttc cccgagcccg tgaccgtgtc ctggaacagc 480
ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac 540
agcctgagca gcgtggtcac cgtgcctagc tctagcctgg gcacccagac ctacatctgc 600

446

```

aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggaacc caagagctgc      660
gactccggcg gaggcggatc tggcgggtgga ggctccggag gcggaggcgc tcctactagc      720
agctccacca agaaaaccca gctccagctg gaacatctgc tgctggatct gcagatgatc      780
ctgaacggca tcaacaacta caagaacccc aagctgaccc ggatgctgac cttcaagttc      840
tacatgccca agaaggccac cgaactgaaa catctgcagt gcctggaaga ggaactgaag      900
cctctggaag aggtgctgaa cctggcccag agcaagaact tccacctgag gccagggac      960
ctgatcagca acatcaacgt gatcgtgctg gaactgaagg gcagcgagac aaccttcagt     1020
tgcgagtacg ccgacgagac agccaccatc gtggaatttc tgaaccggtg gatcaccttc     1080
gccagagca tcatcagcac cctgacaagc ggaggcggcg gatccggcgg aggcggatct     1140
ggcggaggag gcgaggtcca gctgctcgaa agcggcggag gactggtgca gcctggcggc     1200
agcctgagac tgtcttgccg cgccagcggc ttcaccttca gcagctacgc catgagctgg     1260
gtccgccagg cccttgcaa gggactgaa tgggtgtccg ccatcatcgg ctctggcagc     1320
cggacctact acgccgacag cgtgaagggc cggttcacca tcagccggga caacagcaag     1380
aacacctgt acctgcagat gaacagcctg cgggccgagg acaccgccgt gtactactgc     1440
gccaagggat ggttcggcgg cttcaactac tggggacagg gcacctggt cacagtgtcc     1500
agcgcagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcacatct     1560
ggcggaaacg ccgcctggg ctgcctggtc aaagactact tccccagacc cgtgaccgtg     1620
tcctggaaca gcggagccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc     1680
agcggcctgt acagcctgag cagcgtggtc accgtgccta gctctagcct gggcaccag     1740
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa     1800
cccaagagct gcgactga                                     1818

```

```

<210> 229
<211> 215
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> cadena ligera de 3F2

```

```

<400> 229

```

```

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

```

```

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

```

```

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

```

35

40

45

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

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

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

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

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

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

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

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 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> 230
 <211> 648
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> cadena ligera de 3F2

<400> 230
 gagatcgtgc tgaccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60
 ctgtctctga gagctccca gtccgtgacc tcctctacc tcgctggta tcagcagaag 120
 cccggccagg cccctcggct gctgatcaac gtgggcagtc ggagagccac cggcatcct 180
 gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240

```

cccgaggact tcgccgtgta ctactgccag cagggcatca tgctgcccc cacctttggc 300
cagggcacca aggtggaaat caagcgtacg gtggccgctc cctccgtgtt catcttccca 360
ccctccgacg agcagctgaa gtccggcacc gcctccgtcg tgtgcctgct gaacaacttc 420
tacccccgcg aggccaaggt gcagtggaag gtggacaacg ccctgcagtc cggcaactcc 480
caggaatccg tcaccgagca ggactccaag gacagcacct actccctgtc ctccaccctg 540
accctgtcca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag 600
ggcctgtcca gccccgtgac caagtccttc aaccggggcg agtgctga 648

```

<210> 231
 <211> 215
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> cadena ligera de 4G8

<400> 231

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

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

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

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

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

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

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

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 Gly Gln Leu Ile Pro
 85 90 95

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 234

<211> 648

<212> ADN

<213> Secuencia artificial

<220>

<223> cadena ligera de 3D9

<400> 234

```

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcttgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgtt ttactgtcag cagggtcagc ttattcccc tacgttcggc      300
caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg      360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc      480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctcg      540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag      600
ggcctgagct cgcctgtcac aaagagcttc aacaggggag agtggttag      648

```

```

<210> 235
<211> 215
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> cadena ligera de 2F11

```

```

<400> 235

```

```

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 Gly Gln Tyr Thr Pro
          85           90           95

```

```

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

```

```

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

```

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 236
 <211> 648
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> cadena ligera de 2F11

<400> 236
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtgtagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgt ttactgtcag cagggtcagt ataactcccc cacgttcggc 300
 caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
 ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtag 648

<210> 237
 <211> 215
 <212> PRT
 <213> Secuencia artificial

<220>

<223> cadena ligera de 4B3

<400> 237

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

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

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

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 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> 238

<211> 648

<212> ADN
 <213> Secuencia artificial

<220>
 <223> cadena ligera de 4B3

<400> 238
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtc gagtggttagc agcaattact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggcgcctaca tcagggccac tggcatccca 180
 gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtt ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
 caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatcccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
 ggctgagct cgcccgtcac aaagagcttc aacaggggag agtgtag 648

<210> 239
 <211> 613
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Fab-IL2-Fab 2B10 (constructo de fusión cadena pesada-citoquina)

<400> 239

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

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

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

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

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

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

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

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

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

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

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

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
245 250 255

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
260 265 270

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
275 280 285

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
290 295 300

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
305 310 315 320

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
325 330 335

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
340 345 350

456

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
 355 360 365

Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 385 390 395 400

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

Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly
 420 425 430

Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr
 435 440 445

Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 450 455 460

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 465 470 475 480

Val Tyr Tyr Cys Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe
 485 490 495

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 500 505 510

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 515 520 525

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 530 535 540

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 545 550 555 560

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 565 570 575

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 580 585 590

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

595

600

605

Pro Lys Ser Cys Asp
610

<210> 240

<211> 1842

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab 2B10 (constructo de fusión cadena pesada-citoquina)

<400> 240

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac	300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc	360
tcagctagca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag	660
cccaaactct gtgactccgg cggaggaggg agcggcggag gtggctccgg aggtggcgga	720
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat	780
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc	840
acattttaagt ttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa	900
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttacttta	960
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa	1020
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga	1080
tggattacct ttgcccagg catcatctca aactgactt cggcggagg aggatccggc	1140
ggaggtggct ctggcgtgg cggacaggtg caattggtgc agtctggggc tgaggtgaag	1200
aagcctgggt cctcggtgaa ggtctcctgc aaggcctccg gaggcacatt cagcagctac	1260
gctataagct ggggtgcgaca ggcccctgga caagggtctg agtggatggg agggatcatc	1320
cctatctttg gtacagcaaa ctacgcacag aagttccagg gcagggtcac cattactgca	1380
gacaaatcca cgagcacagc ctacatggag ctgagcagcc tgagatctga ggacaccgcc	1440

gtgtattact gtgcgagact gtaacggttac gcttactacg gtgcttttga ctactggggc 1500
 caagggacca ccgtgaccgt ctctcagct agcaccaagg gcccatcggt ctccccctg 1560
 gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac 1620
 tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg cctgaccag cggcgtgcac 1680
 accttccccg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg 1740
 ccctccagca gcttggggcac ccagacctac atctgcaacg tgaatcaca gccagcaac 1800
 accaaggtgg ataagaaagt tgagcccaaa tcttgtgact ga 1842

<210> 241

<211> 613

<212> PRT

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab C3B6 (constructo de fusión cadena pesada-citoquina)

<400> 241

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

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

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

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

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

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

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

145		150		155		160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala						
	165		170			175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val						
	180		185			190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His						
	195		200			205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys						
	210		215			220
Asp Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly						
	225		230			240
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His						
	245		250			255
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys						
	260		265			270
Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys						
	275		280			285
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys						
	290		295			300
Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu						
	305		310			320
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu						
	325		330			335
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala						
	340		345			350
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile						
	355		360			365
Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser						
	370		375			380
Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys						
	385		390			400

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

Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly
 420 425 430

Leu Glu Trp Met Gly Ala Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr
 435 440 445

Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 450 455 460

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 465 470 475 480

Val Tyr Tyr Cys Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe
 485 490 495

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 500 505 510

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 515 520 525

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 530 535 540

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 545 550 555 560

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 565 570 575

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 580 585 590

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 595 600 605

Pro Lys Ser Cys Asp
 610

<210> 242

<211> 1842

<212> ADN

<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab C3B6 (constructo de fusión cadena pesada-citoquina)

<400> 242

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggagct atcatcccga tccttggtat cgcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac	300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc	360
tcagctagca ccaagggccc atcgggtcttc ccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccacg	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag	660
cccaaactct gtgactccgg cggaggaggg agcggcggag gtggctccgg aggtggcgga	720
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat	780
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc	840
acattttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa	900
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttactta	960
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa	1020
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga	1080
tggattacct ttgccc aaag catcatctca aactgactt ccggcggagg aggatccggc	1140
ggaggtggct ctggcgggtg cggacagggt caattgggtc agtctggggc tgaggtgaag	1200
aagcctgggt cctcggtgaa ggtctcctgc aaggcctccg gaggcacatt cagcagctac	1260
gctataagct gggtgcgaca ggccctgga caagggtcag agtggatggg agctatcatc	1320
ccgatccttg gtatcgcaaa ctacgcacag aagttccagg gcagggtcac cattactgca	1380
gacaaatcca cgagcacagc ctacatggag ctgagcagcc tgagatctga ggacaccgcc	1440
gtgtattact gtgcgagact gtacggttac gcttactacg gtgcttttga ctactggggc	1500
caagggacca ccgtgaccgt ctctcagct agcaccaagg gcccatcggg cttccccctg	1560
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac	1620
tacttccccg aaccgggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac	1680
accttccccg ctgtcctaca gtctcagga ctctactccc tcagcagcgt ggtgaccgtg	1740
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacao gccagcaac	1800
accaaggtgg ataagaaagt tgagcccaaa tcttgtgact ga	1842

<210> 243
 <211> 613
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Fab-IL2-Fab 6A12 (constructo de fusión cadena pesada-citoquina)

<400> 243

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

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

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

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

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

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

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

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

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

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

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

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

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
 245 250 255

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
 260 265 270

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
 275 280 285

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
 290 295 300

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
 305 310 315 320

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
 325 330 335

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 340 345 350

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
 355 360 365

Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 385 390 395 400

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

Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly
 420 425 430

Leu Glu Trp Met Gly Val Ile Ile Pro Ile Leu Gly Thr Ala Asn Tyr
 435 440 445

Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 450 455 460

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
465 470 475 480

Val Tyr Tyr Cys Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe
485 490 495

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
500 505 510

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
515 520 525

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
530 535 540

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
545 550 555 560

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
565 570 575

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
580 585 590

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
595 600 605

Pro Lys Ser Cys Asp
610

<210> 244
<211> 1842
<212> ADN
<213> Secuencia artificial

<220>
<223> Fab-IL2-Fab 6A12 (constructo de fusión cadena pesada-citoquina)

<400> 244
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctatgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggagtg atcatccta tccttggtac cgcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360

466

```

tcagctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcaccacag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag 660
cccaaactct gtgactccgg cggaggaggg agcggcggag gtggctccgg aggtggcgga 720
gcacctactt caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 780
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 840
acatttaagt ttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 900
gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 960
agaccacagg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 1020
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 1080
tggattacct ttgccc aaag catcatctca acactgactt cggcgaggag aggatccggc 1140
ggaggtggct ctggcggtgg cggacagggtg caattgggtgc agtctggggc tgaggtgaag 1200
aagcctgggt cctcgggtgaa ggtctcctgc aaggcctccg gaggcacatt cagcagctat 1260
gctataagct gggtgcgaca ggccctgga caagggtcgc agtggatggg agtgatcatc 1320
cctatccttg gtaccgcaaa ctacgcacag aagttccagg gcagggtcac cattactgca 1380
gacaaatcca cgagcacagc ctacatggag ctgagcagcc tgagatctga ggacaccgcc 1440
gtgtattact gtgcgagact gtacggttac gttactacg gtgcttttga ctactggggc 1500
caagggacca ccgtgaccgt ctctcagct agcaccaagg gccatcgggt cttccccctg 1560
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac 1620
tacttccccg aacoggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac 1680
accttccccg ctgtcctaca gtctcagga ctctactccc tcagcagcgt ggtgaccgtg 1740
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacao gccagcaac 1800
accaaggtgg ataagaaagt tgagccaaa tcttgtgact ga 1842

```

```

<210> 245
<211> 214
<212> PRT
<213> Secuencia artificial

```

```

<220>
<223> cadena ligera de 2B10

```

```

<400> 245

```

```

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 Arg Asn Asp
 20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg 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 Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asn Gly Leu Gln Pro Ala
 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> 246
 <211> 645
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> cadena ligera de 2B10

<400> 246

gatataccaga tgacccagtc tccatctctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgctt gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcagtggatc cgggacagag ttcaactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgagc aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtttag 645

<210> 247
 <211> 214
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> cadena ligera de D1A2

<400> 247

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 Arg Asn Asp
 20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asn Gly Leu Gln Pro Ala
 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> 248
<211> 645
<212> ADN
<213> Secuencia artificial

<220>
<223> cadena ligera de D1A2

<400> 248
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
atcacctgcc gggcaagtca ggggattcgt aatgatttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgct gatctatgat gcttacagct tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgagc aatggctctgc agcccgagac gtttgccag 300
ggcaccaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 249
<211> 214
<212> PRT
<213> Secuencia artificial

<220>

<223> cadena ligera de O7D8

<400> 249

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asn Gly Leu Gln Pro Ala
 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> 250

<211> 645

<212> ADN
 <213> Secuencia artificial

<220>
 <223> cadena ligera de O7D8

<400> 250
 gatatccaga tgaccagtc tccatctctc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gagcattcgt aatgttttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgctt gatctatgat gtgtccagtt tgcagagtgg cgteccatca 180
 aggttcagcg gcggtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgcat aatggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 ccagagaggg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtttag 645

<210> 251
 <211> 615
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Fab-IL2-Fab MHLG1 (constructo de fusión cadena pesada-citoquina)

<400> 251

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly Arg Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

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

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

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

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

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

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

Cys Asp Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 225 230 235 240

Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
 245 250 255

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
 260 265 270

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
 275 280 285

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
 290 295 300

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
 305 310 315 320

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
 325 330 335

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
 340 345 350

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
 355 360 365

Ile Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 385 390 395 400

Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 405 410 415

Thr Phe Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys
 420 425 430

Gly Leu Glu Trp Val Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly
 435 440 445

Arg Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 450 455 460

Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu
 465 470 475 480

Asp Thr Ala Val Tyr Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His
 485 490 495

Tyr Phe Asp His Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
 500 505 510

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
 515 520 525

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 530 535 540

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 545 550 555 560

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 565 570 575

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
 580 585 590

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys

595

600

605

Val Glu Pro Lys Ser Cys Asp
610 615

<210> 252
<211> 1848
<212> ADN
<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab MHLG1 (constructo de fusión cadena pesada-citoquina)

<400> 252

gaagtgcagc tgggtggagtc tggaggaggc ttggtcaagc ctggcgggctc cctgcggctc	60
tctctgtcag cctccggatt cacatttagc aactattgga tgaactgggt gcggcaggct	120
cctggaaaagg gcctcgagtg ggtggccgag atcagattga aatccaataa cttcggaaga	180
tattacgctg caagcgtgaa gggccggttc accatcagca gagatgattc caagaacacg	240
ctgtacctgc agatgaacag cctgaagacc gaggatacgg ccgtgtatta ctgtaccaca	300
tacggcaact acgttgggca ctacttcgac cactggggcc aagggaccac cgtcaccgtc	360
tccagtgcta gcaccaaggg cccatcggtc ttcccectgg caccctctc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga taagaaagtt	660
gagcccaaact cttgtgactc cggcggagga gggagcggcg gaggtggctc cggaggtggc	720
ggagcaccta cttcaagttc tacaaagaaa acacagctac aactggagca tttactgctg	780
gatttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg	840
ctcacattta agttttacat gcccaagaag gccacagaac tgaacatct tcagtgtcta	900
gaagaagaac tcaaacctct ggaggaagtg ctaaatttag ctcaaagcaa aaactttcac	960
ttaagacca gggacttaat cagcaatatc aacgtaatag ttctggaact aaagggatct	1020
gaaacaacat tcatgtgtga atatgctgat gagacagcaa ccattgtaga atttctgaac	1080
agatggatta cctttgccc aagcatcatc tcaacactga cttccggcgg aggaggatcc	1140
ggcggagggtg gctctggcgg tggcggagaa gtgcagctgg tggagtctgg aggaggcttg	1200
gtcaagcctg gcgggtccct gcggctctcc tgtgcagcct ccggattcac atttagcaac	1260
tattggatga actgggtgcy gcaggctcct ggaaagggcc tcgagtgggt ggccgagatc	1320
agattgaaat ccaataactt cggaagatat tacgctgcaa gcgtgaaggg ccggttcacc	1380
atcagcagag atgattccaa gaacacgctg tacctgcaga tgaacagcct gaagaccgag	1440

gatacggccg tgtattactg taccacatac ggcaactacg ttgggcacta cttcgaccac 1500
 tggggccaag ggaccaccgt caccgtctcc agtgctagca ccaagggccc atcggtcttc 1560
 cccctggcac cctctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1620
 aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1680
 gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg 1740
 accgtgccct ccagcagctt gggcaccag acctacatct gcaacgtgaa tcacaagccc 1800
 agcaacacca aggtggataa gaaagttgag cccaaatctt gtgactga 1848

<210> 253

<211> 214

<212> PRT

<213> Secuencia artificial

<220>

<223> cadena ligera de KV9

<400> 253

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

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

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

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

Ser Gly Ser Gly Thr Glu 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

476

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly Arg Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

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

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

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

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

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

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

Cys Asp Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 225 230 235 240

Gly Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
 245 250 255

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr

260					265					270					
Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe	Tyr	Met	Pro
		275					280					285			
Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu
	290					295					300				
Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys	Asn	Phe	His
305					310					315					320
Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu
				325					330					335	
Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr
			340					345					350		
Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Ala	Gln	Ser
		355					360					365			
Ile	Ile	Ser	Thr	Leu	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
	370					375					380				
Ser	Gly	Gly	Gly	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu
385					390					395					400
Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe
				405					410					415	
Thr	Phe	Ser	Asn	Tyr	Trp	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys
			420					425					430		
Gly	Leu	Glu	Trp	Val	Ala	Glu	Ile	Arg	Leu	Lys	Ser	Asn	Asn	Phe	Gly
		435					440					445			
Arg	Tyr	Tyr	Ala	Ala	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp
	450					455					460				
Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu
465					470					475					480
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Thr	Thr	Tyr	Gly	Asn	Tyr	Val	Gly	His
				485					490					495	
Tyr	Phe	Asp	His	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala
			500					505					510		

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
515 520 525

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
530 535 540

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
545 550 555 560

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
565 570 575

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
580 585 590

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
595 600 605

Val Glu Pro Lys Ser Cys Asp
610 615

<210> 256
<211> 1848
<212> ADN
<213> Secuencia artificial

<220>

<223> Fab-IL2-Fab MHLG (constructo de fusión cadena pesada-citoquina)

<400> 256

gaagtgcagc tggaggagtc tggaggagtc ttggtccagc ctggcgggctc cctgcggctc	60
tctctgtgcag cctccggatt cacatttagc aactattgga tgaactgggt gcggcaggct	120
cctggaaagg gcctcgagtg ggtggccgag atcagattga aatccaataa cttcggaaga	180
tattacgctg caagcgtgaa gggccggttc accatcagca gagatgattc caagaacacg	240
ctgtacctgc agatgaacag cctgaagacc gaggatacgg ccgtgtatta ctgtaccaca	300
tacggcaact acgttgggca ctacttcgac cactggggcc aaggggaccac cgtcaccgtc	360
tccagtgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	540
tctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaag ccagcaaca ccaagggtgga taagaaagtt	660
gagcccaaat cttgtgactc cggcggagga gggagcggcg gaggtggctc cggaggtggc	720
ggagcaccta cttcaagtgc tacaagaaa acacagctac aactggagca tttactgctg	780

gatttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg 840
 ctcacattta agttttacat gccaagaag gccacagaac tgaaacatct tcagtgtcta 900
 gaagaagaac tcaaacctct ggaggaagtg ctaaatttag ctcaaagcaa aaactttcac 960
 ttaagaccca gggacttaat cagcaatata aacgtaatag ttctggaact aaagggatct 1020
 gaaacaacat tcatgtgtga atatgctgat gagacagcaa ccattgtaga atttctgaac 1080
 agatggatta cctttgcccc aagcatcctc tcaacactga cttccggcgg aggaggatcc 1140
 ggcggagggtg gctctggcgg tggcggagaa gtgcagctgg tggagtctgg aggaggcttg 1200
 gtccagcctg gcgggtccct gcggctctcc tgtgcagcct ccggattcac atttagcaac 1260
 tattggatga actgggtgcg gcaggctcct ggaaagggcc tcgagtgggt ggccgagatc 1320
 agattgaaat ccaataactt cggaagatat tacgtgcaa gcgtgaaggg ccggttcacc 1380
 atcagcagag atgattccaa gaacacgctg tacctgcaga tgaacagcct gaagaccgag 1440
 gatacggccg tgtattactg taccacatac ggcaactacg ttgggcacta cttcgaccac 1500
 tggggccaag ggaccaccgt caccgtctcc agtgctagca ccaagggccc atcggctctc 1560
 cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1620
 aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1680
 gtgcacacct tcccggtgt cctacagtcc tcaggactct actccctcag cagcgtggtg 1740
 accgtgccct ccagcagctt gggcaccag acctacatct gcaacgtgaa tcacaagccc 1800
 agcaacacca aggtggataa gaaagttgag cccaaatctt gtgactga 1848

<210> 257
 <211> 122
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> MHLG1; VH

<400> 257

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly Arg Tyr Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 258
<211> 366
<212> ADN
<213> Secuencia artificial

<220>
<223> MHLG1; VH

<400> 258
gaagtgcagc tggtaggagtc tggaggaggc ttggtcaagc ctggcgggctc cctgcggctc 60
tcctgtgcag cctccggatt cacatttagc aactattgga tgaactgggt gcggcaggct 120
cctggaaagg gcctcgagtg ggtggccgag atcagattga aatccaataa cttcggaaga 180
tattacgctg caagcgtgaa gggccggttc accatcagca gagatgattc caagaacacg 240
ctgtacctgc agatgaacag cctgaagacc gaggatacgg ccgtgtatta ctgtaccaca 300
tacggcaact acgttgggca ctactcgac cactggggcc aagggaccac cgtcacccgtc 360
tcagtt 366

<210> 259
<211> 109
<212> PRT
<213> Secuencia artificial

<220>
<223> MHLG KV9; VL

<400> 259

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Glu 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
100 105

<210> 260
<211> 327
<212> ADN
<213> Secuencia artificial

<220>
<223> MHLG KV9; VL

<400> 260
gatatccagt tgaccagtc tccatccttc ctgtctgcat ctgtgggcga ccgggtcacc 60
atcacctgca aggccagtca gaatgtggat actaacgtgg cttggtacca gcagaagcca 120
gggcaggcac ctaggcctct gatctattcg gcatactacc ggtacactgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttcaactctca caatctcaag cctgcaacct 240
gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300
ggtaccaagg tggagatcaa gcgtacg 327

<210> 261
<211> 122
<212> PRT
<213> Secuencia artificial

<220>
<223> MHLG; VH

<400> 261

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

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly Arg Tyr Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 262
<211> 366
<212> ADN
<213> Secuencia artificial

<220>
<223> MHLG; VH

<400> 262
gaagtgcagc tgggtggagtc tggaggaggc ttggtccagc ctggcggggtc cctgcgggtc 60
tcctgtgcag cctccggatt cacatttagc aactattgga tgaactgggt gcggcaggct 120
cctggaaagg gcctcgagtg ggtggccgag atcagattga aatccaataa cttcggaaga 180
tattacgtg caagcgtgaa gggccggttc accatcagca gagatgattc caagaacacg 240
ctgtacctgc agatgaacag cctgaagacc gaggatacgg ccgtgtatta ctgtaccaca 300
tacggcaact acgttgggca ctacttcgac cactggggcc aagggaccac cgtcaccgtc 360
tccagt 366

<210> 263
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> KV1 light chain

<400> 263

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Glu 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> 264
<211> 645
<212> ADN
<213> Secuencia artificial

<220>
<223> cadena ligera de KV1

<400> 264
gatatccagt tgacccagtc tccatccttc ctgtctgcat ctgtgggcga ccgggtcacc 60
atcacctgca gggccagtca gaatgtggat actaacttag cttggtacca gcagaagcca 120
gggaaagcac ctaagctcct gatctattcg gcatacctacc gttacactgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttcactctca caatctcaag cctgcaacct 240
gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300
ggtaccaagg tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taactttctat 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> 265
 <211> 214
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> cadena ligera de KV7

<400> 265

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

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

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

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

Ser Gly Ser Gly Thr Glu 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> 266
 <211> 645
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> cadena ligera de KV7

<400> 266
 gatattccagt tgaccacagtc tccatccttc ctgtctgcat ctgtgggcga ccgggtcacc 60
 atcacctgca aggccagtc gaattgtgat actaacgtgg cttggtacca gcagaagcca 120
 gggaaagcac ctaagcctct gatctattcg gcacccctacc ggtacactgg cgtcccatca 180
 aggttcagcg gcagtggatc cgggacagag ttactctca caatctcaag cctgcaacct 240
 gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300
 ggtaccaagg tggagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 267
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 267

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

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Glu Pro Leu Leu

426

35

40

45

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

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

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

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

<210> 268

<211> 122

<212> PRT

<213> Mus musculus

<400> 268

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

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly Arg Tyr Tyr Ala Glu
 50 55 60

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

Ala Tyr Leu Gln Met Ile Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr
 85 90 95

Tyr Cys Thr Ser Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 269

<211> 109

<212> PRT

<213> Secuencia artificial

<220>

<223> KV1; VL

<400> 269

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

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

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

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

Ser Gly Ser Gly Thr Glu 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
 100 105

<210> 270

<211> 327

<212> ADN

<213> Secuencia artificial

<220>

<223> KV1; VL

<400> 270

gatatccagt tgacccagtc tccatccttc ctgtctgcat ctgtgggcga ccgggtcacc 60

atcacctgca gggccagtca gaatgtggat actaacttag cttggtacca gcagaagcca 120

gggaaagcac ctaagctcct gatctattcg gcatactacc gttacactgg cgtcccatca 180

aggttcagcg gcagtggatc cgggacagag ttcactctca caatctcaag cctgcaacct 240

gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300

ggtaccaagg tggagatcaa gcgtacg 327

<210> 271

<211> 109

<212> PRT

<213> Secuencia artificial

<220>

<223> KV7; VL

<400> 271

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

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

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

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

Ser Gly Ser Gly Thr Glu 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
 100 105

<210> 272

<211> 327

<212> ADN

<213> Secuencia artificial

<220>

<223> KV7; VL

<400> 272

gatatccagt tgacccagtc tccatccttc ctgtctgcat ctgtgggcga ccgggtcacc 60

atcacctgca aggccagtca gaatgtggat actaacgtgg cttggtacca gcagaagcca 120

gggaaagcac ctaagcctct gatctattcg gcatcctacc ggtacactgg cgtcccatca 180

aggttcagcg gcagtggatc cgggacagag ttcaactctca caatctcaag cctgcaacct 240

gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300

ggtaccaagg tggagatcaa gcgtacg 327

<210> 273

<211> 19

<212> PRT

<213> Secuencia artificial

<220>

<223> secuencia lider

<400> 273

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly

1

5

10

15

Ala His Ser

<210> 274
 <211> 57
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 274
 atggactgga cctggagaat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 275
 <211> 57
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 275
 atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 276
 <211> 22
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 276

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

Phe Pro Gly Ala Arg Cys
 20

<210> 277
 <211> 66
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 277
 atggacatga gggccccgc tcagctcctg ggctctctgc tgctctgggtt cccaggtgcc 60

aggtgt 66

<210> 278
 <211> 19
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 278

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

Val His Ser

<210> 279
 <211> 57
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 279
 atgggatgga gctgtatcat cctottcttg gtagcaacag ctaccggtgt gcattcc 57

<210> 280
 <211> 57
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 280
 atgggctggt cctgcatcat cctgtttctg gtggctaccg ccactggagt gcattcc 57

<210> 281
 <211> 57
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> secuencia líder

<400> 281
 atgggctggt cctgcatcat cctgtttctg gtcgccacag ccaccggcgt gcactct 57



No. 11-181029- -00000-0000

Fecha: 2011-12-29 16:32:46 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 378 FASENACIONALI
Act. 411 PRESENTACION Folios: 491

PATENTE DE INVENCION ☐

MODELO DE UTILIDAD ☐

Art 33 Decisión 486/00

- ☐ Indicación que solicita una patente
 - ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
 - ☐ Descripción de la invención
 - ☐ Dibujos de ser estos pertinentes
 - ☐ Comprobante de pago de las tasas establecidas (De ser caso formato de descuento)
- Completa ☐ Incompleta ☐

PATENTE DE INVENCION PCT ☒ **MODELO DE UTILIDAD PCT** ☐ **Art .33 Decisión 486/00, Circular Única**

- ☒ Indicación que se solicita una PCT
 - ☒ Copia de la solicitud en español, tal como fue presentada inicialmente (capitulo descriptivo, reivindicatorio, resume)
 - ☒ Dibujos de ser estos pertinentes.
 - ☒ Comprobante de pago de las tasas establecidas (de ser el caso formato de descuento)
- Completa ☒ Incompleta ☐

DISEÑO INDUSTRIAL ☐

(Art. 119 Decisión 486/00)

- ☐ Indicación que se solicita Diseño Industrial
 - ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
 - ☐ Representación gráfica y fotográfica del Diseño industrial o muestra del material que Incorpora el diseño
 - ☐ Comprobante de pago de las tasas establecidas
- Completa ☐ Incompleta ☐

ESQUEMA TRAZADO ☐

(Art. 92 Decisión 486/00)

- ☐ Indicación que se solicita un esquema de trazado
 - ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
 - ☐ Representación grafica de un esquema de trazado
 - ☐ Comprobante de pago de las tasas establecidas
- Completa ☐ Incompleta ☐