

<110> LG CHEM, LTD.
<120> ANTICUERPO ANTI-LILRB1 Y USOS DEL MISMO
<130> OPP20204082KR
<150> 10-2019-0173414
<151> 23-12-2019
<150> 10-2020-0061907
<151> 22-05-2020
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<400> 1
Gln Gly Asp Ser Leu Arg Asn Phe Tyr Ala Ser
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<220>
<223> CDR-L2 de E3 o E3.1 (Kabat)

<400> 2
Gly Lys Asn Asn Arg Pro Ser
1 5

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<220>
<223> CDR-L3 de E3 o E3.1 (Kabat)

<400> 3
Asn Ser Arg Asp Ser Ser Gly Ser His Leu Thr Gly Val
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<223> CDR-H1 de E3 o E3.1 (Kabat)

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

<210> 6
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<223> CDR-H3 de E3 o E3.1 (Kabat)

<400> 6
Asp Thr Tyr Tyr Tyr Gly Ser Gly Arg Ser Asn Ala Phe Asp Ile
1 5 10 15

<210> 7
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<400> 7
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Gln Gln Tyr Asp Asn Leu Pro
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<400> 10
Asp Tyr Ala Met His
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Gly

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Val Gly Asp Ser Ser Gly Trp Ser Asp Ala Phe Asp Ile
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Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
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Ser Tyr Ala Ile Ser
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Gly

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Gly

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<400> 29
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Gly

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<400> 31
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Ser Tyr Asp Ile His
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<400> 35
Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu Gln
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Gly

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<400> 38
Gly Arg Asn Asn Arg Pro Ser
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1 5 10 15

Gly

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<400> 42
Asp Ala Gly Ser Ser Ser Asp Tyr
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<223> CDR-L1 de F12 (Kabat)

<400> 43

Ala Gly Thr Ser Ser Asp Ile Gly Asp Tyr Asp Tyr Val Ser
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Asp Val Ser Arg Arg Pro Ser
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<400> 45

Ala Ser Tyr Thr Ser Ser Ser Val Val Val
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<223> CDR-H1 de F12 (Kabat)

<400> 46

Ser Tyr Trp Ile Gly
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<223> CDR-H2 de F12 (Kabat)

<400> 47
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Gly

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<400> 48
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1 5 10

<210> 49
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<400> 49
Arg Ala Ser Gln Ser Ile Ser Arg Tyr Leu Asn
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<223> CDR-L2 de B9 (Kabat)

<400> 50
Gly Ala Ser Ser Leu Gln Ser
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<223> CDR-L3 de B9 (Kabat)

<400> 51

Gln Gln Ala Tyr Gly Phe Pro Leu Thr
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<210> 52

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<223> CDR-H1 de B9 (Kabat)

<400> 52

Ser Tyr Ala Ile Ser
1 5

<210> 53

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<220>

<223> CDR-H2 de B9 (Kabat)

<400> 53

Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
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Gly

<210> 54

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<223> CDR-H3 de B9 (Kabat)

<400> 54

Gly Glu Ile Ala Val Ala Gln Asn Trp Asp Tyr Tyr Gly Met Asp Val
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<210> 55

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<400> 55

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<400> 56

Asp	Val	Ser	Lys	Arg	Pro	Ser
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<400> 57

Ser	Ser	Tyr	Ser	Ser	Ser	Ser	Thr	Leu	Val	Val
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<223> CDR-H1 de G11 (Kabat)

<400> 58

Ser	Tyr	Trp	Ile	Gly
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<210> 59

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<400> 59
Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 60
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<400> 60
Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val
1 5 10

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<220>
<223> CDR-L1 de G6 (Kabat)

<400> 61
Gln Gly Asp Ser Leu Arg Arg Tyr Tyr Ala Thr
1 5 10

<210> 62
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<400> 62
Gly Gln Asn Tyr Arg Pro Ser
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<210> 63
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<223> CDR-L3 de G6 (Kabat)

<400> 63

Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
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<210> 64

<211> 5

<212> PRT

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<223> CDR-H1 de G6 (Kabat)

<400> 64

Ser Tyr Tyr Met His
1 5

<210> 65

<211> 17

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<220>

<223> CDR-H2 de G6 (Kabat)

<400> 65

Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 66

<211> 10

<212> PRT

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<223> CDR-H3 de G6 (Kabat)

<400> 66

Gly Trp Gly Tyr Ser Ser Ser Phe Asp Tyr
1 5 10

<210> 67

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<400> 67
Ser Gly Ser Ser Ser Asn Ile Gly Thr Asn Thr Val Asn
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Ser Asn Asp Gln Arg Pro Ser
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<400> 69
Glu Thr Trp Asp Asp Ser Leu Lys Gly Pro Val
1 5 10

<210> 70
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Ser Tyr Ala Met Ser
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<400> 71
Thr Ile Ser Gly Ser Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 72
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<212> PRT
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<400> 72
Glu Trp Glu Leu Gly Asp Ala Phe Asp Ile
1 5 10

<210> 73
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<400> 73
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 74
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<400> 74
Ala Ala Ser Ser Leu Gln Ser
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<400> 76
Ser Tyr Ala Met Ser
1 5

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<400> 77
Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

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Asp Arg Gly Ser Tyr Gly Tyr Tyr Tyr Gly Met Asp Val
1 5 10

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<400> 79
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

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<400> 80
Ala Ala Ser Ser Leu Gln Ser
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Gly Tyr Tyr Met His
1 5

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<400> 83
Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
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Gly

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<400> 84
Ala Gly Ala Ser Ile Val Gly Ala Thr Ala Leu Asp Tyr
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<400> 85
Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn Tyr Val Gln
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<210> 86
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Glu Asp Asn Gln Arg Pro Ser
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<210> 87
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<400> 87
Gln Ser Tyr Asp Thr Gly Asn Arg Asn Tyr Val
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<400> 88
Ser Tyr Thr Ile Ser
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<223> CDR-H2 de E4 (Kabat)

<400> 89
Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe Gln
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Gly

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<220>
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<400> 90
Gly Pro Ser Leu Asn Tyr Ala Gly Tyr Phe Asp Asn

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<400> 91
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
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<400> 92
Gly Lys Glu Lys Arg Pro Ser
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<223> CDR-L3 de E12 (Kabat)

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<210> 94
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<400> 94
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<210> 95
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<400> 95
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

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<220>
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<400> 96
Glu Arg Gly Ser Gly Met Asp Val
1 5

<210> 97
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<220>
<223> CDR-L1 de D1 (Kabat)

<400> 97
Lys Ala Ser Gln Asp Ile Asp Asp Asp Met Asn
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Glu Ala Ser Thr Leu Val Pro

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Leu Gln His Asp Lys Phe Pro Tyr Thr
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<400> 100
Ser Tyr Gly Ile Ser
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1 5 10 15

Gly

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Arg Gly Val Asp Glu Gly Asp Tyr
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<223> CDR-L1 de E6 (Kabat)

<400> 103
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<223> CDR-L2 de E6 (Kabat)

<400> 104
Arg Asp Asp Gln Arg Pro Ser
1 5

<210> 105
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L3 de E6 (Kabat)

<400> 105
Gln Ser Tyr Asp Ser Ser Ser Trp Val
1 5

<210> 106
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de E6 (Kabat)

<400> 106

Thr Tyr Asp Ile Thr
1 5

<210> 107
<211> 17
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de E6 (Kabat)

<400> 107
Trp Met Asn Pro Asn Ser Gly Asn Ser Arg Ser Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 108
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de E6 (Kabat)

<400> 108
Gly Asp Tyr Ser Gly Val Val Leu Thr Ala Thr Ala Leu Asp Tyr
1 5 10 15

<210> 109
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de E9 (Kabat)

<400> 109
Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Tyr
1 5 10

<210> 110
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de E9 (Kabat)

<400> 110
Arg Asn Asn Gln Arg Pro Ser
1 5

<210> 111
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L3 de E9 (Kabat)

<400> 111
Ala Ala Trp Asp Asp Ser Leu Ser Gly Trp Val
1 5 10

<210> 112
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de E9 (Kabat)

<400> 112
Ser Tyr Gly Met His
1 5

<210> 113
<211> 17
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de E9 (Kabat)

<400> 113
Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 114
<211> 14
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de E9 (Kabat)

<400> 114
Glu Asp Arg Ile Ala Ala Ala Gly Met Arg Glu Leu Asp Tyr
1 5 10

<210> 115
<211> 16
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de A11 (Kabat)

<400> 115
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 116
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de A11 (Kabat)

<400> 116
Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 117
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L3 de A11 (Kabat)

<400> 117
Met Gln Gly Thr His Trp Pro Pro Tyr Thr
1 5 10

<210> 118
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de A11 (Kabat)

<400> 118
Ser Tyr Ala Met Thr
1 5

<210> 119
<211> 17
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de A11 (Kabat)

<400> 119
Gly Ile Ser Ser Asp Gly Thr Thr Thr Tyr Ala Asp Ser Val Arg
1 5 10 15

Gly

<210> 120
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de A11 (Kabat)

<400> 120
Asp Gln Leu Leu Gly Trp Asp Ala Leu Asn Val
1 5 10

<210> 121
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de E3 o E3.1 (IGMT)

<400> 121
Ser Leu Arg Asn Phe Tyr
1 5

<210> 122
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de E3 o E3.1 (IGMT)

<400> 122
Gly Lys Asn
1

<210> 123
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de E3 o E3.1 (IGMT)

<400> 123
Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 124
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de E3 o E3.1 (IGMT)

<400> 124
Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 125
<211> 17
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de E3 o E3.1 (IGMT)

<400> 125
Ala Arg Asp Thr Tyr Tyr Tyr Gly Ser Gly Arg Ser Asn Ala Phe Asp
1 5 10 15

Ile

<210> 126
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de B3 (IGMT)

<400> 126
Gln Asp Ile Ser Asn Tyr
1 5

<210> 127
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de B3 (IGMT)

<400> 127
Asp Ala Ser
1

<210> 128
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de B3 (IGMT)

<400> 128
Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 129
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de B3 (IGMT)

<400> 129
Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 130
<211> 15
<212> PRT
<213> Secuencia artificial

<220>

<223> CDR-H3 de B3 (IGMT)

<400> 130
Ala Arg Val Gly Asp Ser Ser Gly Trp Ser Asp Ala Phe Asp Ile
1 5 10 15

<210> 131
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de A10 (IGMT)

<400> 131
Gln Ser Val Ser Ser Asn
1 5

<210> 132
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de A10 (IGMT)

<400> 132
Gly Ala Ser
1

<210> 133
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de A10 (IGMT)

<400> 133
Gly Gly Thr Phe Ser Ser Tyr Ala
1 5

<210> 134
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de A10 (IGMT)

<400> 134
Ile Ile Pro Ile Phe Gly Thr Ala
1 5

<210> 135
<211> 14
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de A10 (IGMT)

<400> 135
Ala Arg Gly Gly Leu Gly Glu Leu Asp Asn Trp Phe Asp Pro
1 5 10

<210> 136
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de G1 (IGMT)

<400> 136
Lys Leu Gly Asp Arg Tyr
1 5

<210> 137
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de G1 (IGMT)

<400> 137
Lys Asp Ser
1

<210> 138
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de G1 (IGMT)

<400> 138
Gly Gly Thr Phe Ser Ser Tyr Gly
1 5

<210> 139
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de G1 (IGMT)

<400> 139
Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 140
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de G1 (IGMT)

<400> 140
Ala Arg Val Gly Val Ala Gly Lys Leu Asp Tyr
1 5 10

<210> 141
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de G9 (IGMT)

<400> 141
Ser Ser Asp Val Gly Gly Tyr Asn Tyr
1 5

<210> 142
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de G9 (IGMT)

<400> 142

Asp Val Ser
1

<210> 143
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de G9 (IGMT)

<400> 143
Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 144
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de G9 (IGMT)

<400> 144
Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 145
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de G9 (IGMT)

<400> 145
Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val
1 5 10

<210> 146
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de H2 (IGMT)

<400> 146
Ser Leu Arg Asn Tyr Tyr

1 5

<210> 147
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de H2 (IGMT)

<400> 147
Gly Asn Asn
1

<210> 148
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de H2 (IGMT)

<400> 148
Gly Tyr Thr Phe Thr Ser Tyr Asp
1 5

<210> 149
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de H2 (IGMT)

<400> 149
Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 150
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de H2 (IGMT)

<400> 150
Ala Arg Asp Gly Gly Asp Ala Phe Asp Ile
1 5 10

<210> 151
<211> 6
<212> PRT
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<220>
<223> CDR-L1 de H11 (IGMT)

<400> 151
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 152
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de H11 (IGMT)

<400> 152
Gly Arg Asn
1

<210> 153
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de H11 (IGMT)

<400> 153
Gly Tyr Thr Phe Thr Ser Tyr Tyr
1 5

<210> 154
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de H11 (IGMT)

<400> 154
Ile Asn Pro Ser Gly Gly Ser Thr
1 5

<210> 155
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de H11 (IGMT)

<400> 155
Ala Arg Asp Ala Gly Ser Ser Ser Asp Tyr
1 5 10

<210> 156
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de F12 (IGMT)

<400> 156
Ser Ser Asp Ile Gly Asp Tyr Asp Tyr
1 5

<210> 157
<211> 3
<212> PRT
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<220>
<223> CDR-L2 de F12 (IGMT)

<400> 157
Asp Val Ser
1

<210> 158
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de F12 (IGMT)

<400> 158
Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 159

<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de F12 (IGMT)

<400> 159
Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 160
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de F12 (IGMT)

<400> 160
Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val
1 5 10

<210> 161
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de B9 (IGMT)

<400> 161
Gln Ser Ile Ser Arg Tyr
1 5

<210> 162
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de B9 (IGMT)

<400> 162
Gly Ala Ser
1

<210> 163
<211> 8

<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de B9 (IGMT)

<400> 163
Gly Gly Thr Phe Ser Ser Tyr Ala
1 5

<210> 164
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
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<400> 164
Ile Ile Pro Ile Phe Gly Thr Ala
1 5

<210> 165
<211> 18
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de B9 (IGMT)

<400> 165
Ala Arg Gly Glu Ile Ala Val Ala Gln Asn Trp Asp Tyr Tyr Gly Met
1 5 10 15

Asp Val

<210> 166
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de G11 (IGMT)

<400> 166
Ser Ser Asp Val Gly Gly Tyr Asn Tyr
1 5

<210> 167
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de G11 (IGMT)

<400> 167
Asp Val Ser
1

<210> 168
<211> 8
<212> PRT
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<220>
<223> CDR-H1 de G11 (IGMT)

<400> 168
Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 169
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
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<400> 169
Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 170
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de G11 (IGMT)

<400> 170
Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val
1 5 10

<210> 171

<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de G6 (IGMT)

<400> 171
Ser Leu Arg Arg Tyr Tyr
1 5

<210> 172
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de G6 (IGMT)

<400> 172
Gly Gln Asn
1

<210> 173
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de G6 (IGMT)

<400> 173
Gly Tyr Thr Phe Thr Ser Tyr Tyr
1 5

<210> 174
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de G6 (IGMT)

<400> 174
Ile Ile Pro Ile Phe Gly Thr Ala
1 5

<210> 175
<211> 12

<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de G6 (IGMT)

<400> 175
Ala Arg Gly Trp Gly Tyr Ser Ser Ser Phe Asp Tyr
1 5 10

<210> 176
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de F11 (IGMT)

<400> 176
Ser Ser Asn Ile Gly Thr Asn Thr
1 5

<210> 177
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de F11 (IGMT)

<400> 177
Ser Asn Asp
1

<210> 178
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de F11 (IGMT)

<400> 178
Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 179
<211> 8
<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-H2 de F11 (IGMT)

<400> 179

Ile Ser Gly Ser Gly Asp Ser Thr
1 5

<210> 180

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-H3 de F11 (IGMT)

<400> 180

Ala Arg Glu Trp Glu Leu Gly Asp Ala Phe Asp Ile
1 5 10

<210> 181

<211> 6

<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-L1 de D3 (IGMT)

<400> 181

Gln Ser Ile Ser Ser Tyr
1 5

<210> 182

<211> 3

<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-L2 de D3 (IGMT)

<400> 182

Ala Ala Ser
1

<210> 183

<211> 8

<212> PRT

<213> Secuencia artificial

<220>
<223> CDR-H1 de D3 (IGMT)

<400> 183
Gly Ser Thr Phe Ser Ser Tyr Ala
1 5

<210> 184
<211> 8
<212> PRT
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<220>
<223> CDR-H2 de D3 (IGMT)

<400> 184
Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 185
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de D3 (IGMT)

<400> 185
Ala Lys Asp Arg Gly Ser Tyr Gly Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 186
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de B12 (IGMT)

<400> 186
Gln Ser Ile Ser Ser Tyr
1 5

<210> 187
<211> 3
<212> PRT
<213> Secuencia artificial

<220>

<223> CDR-L2 de B12 (IGMT)

<400> 187

Ala Ala Ser
1

<210> 188

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-H1 de B12 (IGMT)

<400> 188

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 189

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-H2 de B12 (IGMT)

<400> 189

Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 190

<211> 15

<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-H3 de B12 (IGMT)

<400> 190

Thr Arg Ala Gly Ala Ser Ile Val Gly Ala Thr Ala Leu Asp Tyr
1 5 10 15

<210> 191

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> CDR-L1 de E4 (IGMT)

<400> 191
Ser Gly Ser Ile Ala Ser Asn Tyr
1 5

<210> 192
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de E4 (IGMT)

<400> 192
Glu Asp Asn
1

<210> 193
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de E4 (IGMT)

<400> 193
Gly Gly Thr Phe Ser Ser Tyr Thr
1 5

<210> 194
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de E4 (IGMT)

<400> 194
Ile Ile Pro Ile Leu Gly Ile Ala
1 5

<210> 195
<211> 14
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de E4 (IGMT)

<400> 195
Val Arg Gly Pro Ser Leu Asn Tyr Ala Gly Tyr Phe Asp Asn
1 5 10

<210> 196
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de E12 (IGMT)

<400> 196
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 197
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de E12 (IGMT)

<400> 197
Gly Lys Glu
1

<210> 198
<211> 8
<212> PRT
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<220>
<223> CDR-H1 de E12 (IGMT)

<400> 198
Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 199
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de E12 (IGMT)

<400> 199

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 200
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de E12 (IGMT)

<400> 200
Ala Arg Glu Arg Gly Ser Gly Met Asp Val
1 5 10

<210> 201
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de D1 (IGMT)

<400> 201
Gln Asp Ile Asp Asp Asp
1 5

<210> 202
<211> 3
<212> PRT
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<220>
<223> CDR-L2 de D1 (IGMT)

<400> 202
Glu Ala Ser
1

<210> 203
<211> 8
<212> PRT
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<220>
<223> CDR-H1 de D1 (IGMT)

<400> 203
Gly Tyr Thr Phe Thr Ser Tyr Gly

1 5

<210> 204
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de D1 (IGMT)

<400> 204
Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 205
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de D1 (IGMT)

<400> 205
Ala Ser Arg Gly Val Asp Glu Gly Asp Tyr
1 5 10

<210> 206
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de E6 (IGMT)

<400> 206
Ser Gly Asn Ile Ala Ser Asn Tyr
1 5

<210> 207
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de E6 (IGMT)

<400> 207
Arg Asp Asp
1

<210> 208
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
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<400> 208
Gly Tyr Thr Phe Thr Thr Tyr Asp
1 5

<210> 209
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de E6 (IGMT)

<400> 209
Met Asn Pro Asn Ser Gly Asn Ser
1 5

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

<220>
<223> CDR-H3 de E6 (IGMT)

<400> 210
Ala Thr Gly Asp Tyr Ser Gly Val Val Leu Thr Ala Thr Ala Leu Asp
1 5 10 15

Tyr

<210> 211
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de E9 (IGMT)

<400> 211
Ser Ser Asn Ile Gly Asn Asn Tyr

1 5

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

<220>
<223> CDR-L2 de E9 (IGMT)

<400> 212
Arg Asn Asn
1

<210> 213
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de E9 (IGMT)

<400> 213
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 214
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de E9 (IGMT)

<400> 214
Ile Lys Gln Asp Gly Ser Glu Lys
1 5

<210> 215
<211> 16
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de E9 (IGMT)

<400> 215
Ala Arg Glu Asp Arg Ile Ala Ala Ala Gly Met Arg Glu Leu Asp Tyr
1 5 10 15

<210> 216
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L1 de A11 (IGMT)

<400> 216
Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
1 5 10

<210> 217
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-L2 de A11 (IGMT)

<400> 217
Leu Gly Ser
1

<210> 218
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H1 de A11 (IGMT)

<400> 218
Gly Phe Ser Phe Thr Ser Tyr Ala
1 5

<210> 219
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H2 de A11 (IGMT)

<400> 219
Ile Ser Ser Asp Gly Thr Thr Thr
1 5

<210> 220
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> CDR-H3 de A11 (IGMT)

<400> 220
Ala Arg Asp Gln Leu Leu Gly Trp Asp Ala Leu Asn Val
1 5 10

<210> 221
<211> 116
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (E3)

<400> 221
Ser Tyr 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 Asn Phe Tyr Ala
20 25 30

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

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

Thr 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 Arg Asp Ser Ser Gly Ser His
85 90 95

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

Pro Ala Ala Ala
115

<210> 222
<211> 124
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (E3 o E3.1)

<400> 222
Gln 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 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 Ile Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Thr Tyr Tyr Tyr Gly Ser Gly Arg Ser Asn Ala Phe Asp
100 105 110

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

<210> 223
<211> 110
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (B3)

<400> 223
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 Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

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

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

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

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

Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Thr Ala Ala Ala
100 105 110

<210> 224
<211> 122
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (B3)

<400> 224
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Val Gly Asp Ser Ser Gly Trp Ser Asp Ala Phe Asp Ile Trp
100 105 110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 225
<211> 114
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (A10)

<400> 225
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val 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
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

Ala Ala

<210> 226
<211> 121
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (A10)

<400> 226
Gln Met 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 Ile 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 Gly Gly Leu Gly Glu Leu Asp Asn Trp Phe Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 227
<211> 112
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (G1)

<400> 227
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

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

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

Lys Asp Ser Gln Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Gly Thr Gly Val
85 90 95

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

<210> 228
<211> 118
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (G1)

<400> 228
Glu 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

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

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

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

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

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

Leu Val Thr Val Ser Ser

<210> 229
 <211> 112
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Región variable de cadena ligera (B9)

<400> 229
 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 Ser Arg Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr His Cys Gln Gln Ala Tyr Gly Phe Pro Leu
 85 90 95
 Thr Leu Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Ala Ala Ala
 100 105 110

<210> 230
 <211> 125
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Región variable de cadena pesada (B9)

<400> 230
 Gln Val Gln Leu Val Glu 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 Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Glu Ile Ala Val Ala Gln Asn Trp Asp Tyr Tyr Gly Met
 100 105 110

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

<210> 231
<211> 114
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (H11)

<400> 231

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

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

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

Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Ser Ser Gly Asn His
 85 90 95

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

Ala Ala

<210> 232
<211> 117
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (H11)

<400> 232
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

Ala Arg Asp Ala Gly Ser Ser Ser Asp Tyr Trp Gly Arg Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 233
<211> 118
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (G9)

<400> 233
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Met Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Thr Leu Asp Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

Gly Gln Pro Ala Ala Ala
115

<210> 234
<211> 120
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (G9)

<400> 234
Gln Val Gln Leu Val Gln Pro Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

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

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

Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 235
<211> 114
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (H2)

<400> 235
Ser Tyr 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 Asn Tyr Tyr Ala
20 25 30

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

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

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

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Asp Ser Thr Tyr Asn His
85 90 95

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

Ala Ala

<210> 236

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena pesada (H2)

<400> 236

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

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

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

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

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

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

Ala Arg Asp Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 237

<211> 116

<212> PRT

<213> Secuencia artificial

<220>

<223> RegiÃ³n variable de cadena ligera (F12)

<400> 237
Gln Ser Val Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Asp Val Ser Arg Arg Pro Ser Gly Val Pro Asp Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Tyr Thr Ser Ser
 85 90 95

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

Pro Ala Ala Ala
 115

<210> 238
<211> 120
<212> PRT
<213> Secuencia artificial

<220>
<223> RegiÃ³n variable de cadena pesada (F12)

<400> 238
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30

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

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

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

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

Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 239

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena ligera (G11)

<400> 239

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

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

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

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ser Ser Ser
85 90 95

Ser Thr Leu Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

Gln Pro Ala Ala Ala
115

<210> 240

<211> 120

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena pesada (G11)

<400> 240

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

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

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

Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 241
<211> 114
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (G6)

<400> 241
Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

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

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

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

Asn Ser Gly Thr 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 Arg Asp Ser Ser Gly Asn His
85 90 95

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

Ala Ala

<210> 242
<211> 119
<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena pesada (G6)

<400> 242

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20 25 30

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

35 40 45

Gly 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 Glu Ser Thr Ser Thr Ala Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Trp Gly Tyr Ser Ser Ser Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Thr Val Thr Val Ser Ser

115

<210> 243

<211> 116

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena ligera (F11)

<400> 243

Gln Ser Val Leu Thr Gln Pro Pro Ser Thr Ser Gly Thr Pro Gly Gln

1 5 10 15

Thr Phe Ser Ile Phe Cys Ser Gly Ser Ser Ser Asn Ile Gly Thr Asn

20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

35 40 45

Ile Tyr Ser Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Thr Trp Asp Asp Ser Leu
85 90 95

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

Pro Ala Ala Ala
115

<210> 244
<211> 119
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (F11)

<400> 244
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

Ala Arg Glu Trp Glu Leu Gly Asp Ala Phe Asp Ile Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 245
<211> 112
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (D3)

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

<210> 246
 <211> 122
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> Región variable de cadena pesada (D3)

<400> 246
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly 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 Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Arg Gly Ser Tyr Gly Tyr Tyr Tyr Gly Met Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 247

<211> 112
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (B12)

<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 Ser Ile Ser Ser Tyr
20 25 30

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

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

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

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

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

<210> 248
<211> 122
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (B12)

<400> 248
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

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

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

<210> 249
<211> 118
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (E4)

<400> 249
Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

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

Gly Asn Arg Asn Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu
100 105 110

Gly Gln Pro Ala Ala Ala
115

<210> 250
<211> 121
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (E4)

<400> 250
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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 251

<211> 114

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena ligera (E12)

<400> 251

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

Gly Lys Glu Lys 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 Arg Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Gly Ser Thr Thr Asp Tyr
85 90 95

Met Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly Gln Pro Ala
100 105 110

Ala Ala

<210> 252
<211> 117
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena pesada (E12)

<400> 252
Gln 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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Glu Arg Gly Ser Gly Met Asp Val Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 253
<211> 112
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (D1)

<400> 253
Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly
1 5 10 15

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

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Ala Ile Ser Ile Ile
35 40 45

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

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

Glu Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Lys Phe Pro Tyr
85 90 95

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

<210> 254

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena pesada (D1)

<400> 254

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

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

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

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

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

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

Ala Ser Arg Gly Val Asp Glu Gly Asp Tyr Trp Gly Gln Gly Thr Met
100 105 110

Val Thr Val Ser Ser
115

<210> 255

<211> 116

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena ligera (E6)

<400> 255

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Leu Ser Cys Thr Gly Ser Ser Gly Asn Ile Ala Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln His Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

Ile Tyr Arg Asp Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

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

Ser Ser Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Ala Ala Ala
115

<210> 256

<211> 124

<212> PRT

<213> Secuencia artificial

<220>

<223> Región variable de cadena pesada (E6)

<400> 256

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

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

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

Gly Trp Met Asn Pro Asn Ser Gly Asn Ser Arg Ser Ala Gln Lys Phe
50 55 60

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

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

<210> 257
 <211> 116
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Región variable de cadena ligera (E9)

<400> 257
 Gln Ser Glu Leu Thr Gln Leu Pro Ser Ala Ser Glu Thr Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
 20 25 30
 Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95
 Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Ala Ala Ala
 115

<210> 258
 <211> 123
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Región variable de cadena pesada (E9)

<400> 258
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

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

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

Ala Arg Glu Asp Arg Ile Ala Ala Ala Gly Met Arg Glu Leu Asp Tyr
100 105 110

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

<210> 259
<211> 118
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (A11)

<400> 259
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

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

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

Thr His Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Ala Ala Ala
115

<210> 260
<211> 120
<212> PRT
<213> Secuencia artificial

<220>

<223> RegiÃ³n variable de cadena pesada (A11)

<400> 260
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Glu Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Ala Arg Asp Gln Leu Leu Gly Trp Asp Ala Leu Asn Val Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 261
<211> 348
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regiÃ³n variable de cadena ligera (E3)

<400> 261
tctatgagc tgactcagga cctgtctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccagg gagacagcct cagaaacttt tatgcaagct ggtaccagca gaagtcagga 120

caggccccag ttcttgcatt gtatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccacctcagg aaacacagct tccttgacca tcaactggggc tcaggcggaa 240

gatgaggctg actattactg taactcccg gacagcagtg gtagccattt gacgggcgta 300

ttcggcggag ggaccaaggt caccgtccta ggtcagcccg cggccgca 348

<210> 262
<211> 372
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la región variable de cadena pesada (E3 o E3.1)

<400> 262
caggtgcagc tggaggagtc tgggggaggc ttgtacagc ctgggggggc cctgagactc 60
tctgtgcag cctctggatt cacctttagc agctatgcc ttagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggttag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa tacgtgtat 240
ctgcaaatga ttagcctgag agctgaggac acggctgtgt attactgtgc gagagatacg 300
tattactatg gttcggggag aagtaatgct ttgatatat ggggccaggg aaccctggtc 360
accgtctcga gt 372

<210> 263
<211> 330
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la región variable de cadena ligera (B3)

<400> 263
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggcgagtca ggacattagc aactatttga attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat ttactttca ccatcagcag cctgcagcct 240
gaagatattg caacatatta ctgtcaacag tatgataatc tcccttcgg cgagaggacc 300
aaagtggata tcaaacgtac cgcggccgca 330

<210> 264
<211> 366
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la región variable de cadena pesada (B3)

<400> 264
gaggtgcagc tgttggagtc tgggggaggc ttgtacagc ctggcaggtc cctgagactc 60
tctgtgcag cctctggatt cacctttgat gattatgcc tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
cttcaaatga acagtctgag agccgaggac acggccgtgt attactgtgc gagagttggg 300
gatagcagtg gctggtccga tgcttttgat atctggggcc aagggacaat ggtcaccgtc 360
tcgagt 366

<210> 265
<211> 342
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena ligera (A10)

<400> 265
gatattgtga tgacacagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctatggt gcatcacca gggccaccgg tatcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcagcag tatggtagct cacctcggat gtacactttt 300
ggccagggga ccaaagtgga tatcaaacgt accgcggccg ca 342

<210> 266
<211> 363
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena pesada (A10)

<400> 266
caaatgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggtggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag agtcacgatt accgcggaca aatccatcag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggcggc 300
ctcggggagt tggacaactg gttcgacccc tggggccagg gaacctggt caccgtctcg 360
agt 363

<210> 267
<211> 336
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena ligera (G1)

<400> 267
tcctatgagc tgactcagcc accctcactg tccgtgtccc caggacagac agccagcatc 60
acctgctcag gatataaact gggagataga tatgtttcct ggtatcagca gaagacaggc 120
cagtcccctg tgggtggcat ctataaagat agccagcggc cctcaggggt ccctgaacga 180
ttctctgget ccaactctgg gaacacagcc actctgacca tcagcgggac ccaggctatg 240
gatgaggctg actattactg tcaggcgtgg gacagcggca ctgggggtatt cggcggaggg 300
accaagctga cgcctcctagg tcagcccgcg gccgca 336

<210> 268
<211> 354
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena pesada (G1)

<400> 268
gaagtgcagc tgggtcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cttctggagg caccttcagc agctatggta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat 180
gcacaggagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctat 240
atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagtaggg 300
gtggctggta aacttgacta ctggggccaa ggaaccctgg tcaccgtctc gagt 354

<210> 269
<211> 354
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena ligera (G9)

<400> 269

cagtctgcgc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60
tctgcactg gaagcagcag tgacgttggg ggttataact atgtctcctg gtaccagcaa 120
caccagggca aagcccccaa actcatgatt tatgatgtca gtaatcggcc ctcagggggt 180
tctgatcgct tctctggctc caagtctggc aacatggcct ccctgacat ctctgggctc 240
caggctgagg acgaggctga ttattactgc agtcatata caggaagcag cactctcgac 300
gtgctattcg gcgaggggac caagctgacc gtcttaggtc agcccgcggc cgca 354

<210> 270
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena pesada (G9)

<400> 270
caggtgcagc tgggtcagcc tggagcagag gtgaaaaagc cggggggagtc tctgaagatc 60
tctgtgaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaagg gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180
agcccgctct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240
ctgcagtgga gcagcctgaa ggccctggac accgccatgt attactgtgc gagtcaatat 300
tacgatgggg gttactacat ggacgtctgg ggccaggga ccttggtcac cgtctcgagt 360

360

<210> 271
<211> 342
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena ligera (H2)

<400> 271
tcttatgagc tgactcagga ccctgctgtg tcgggtggcct tgggacagac agtcaggatc 60
acatgccaag gagacagcct cagaaactat tatgcaagct ggtaccagca gaagccagga 120
caggcccccta ttctgtcat ctctggtaac aacaacggc cctcgggggat ccagaccga 180
ttctctggct ccagctcagg agacacagct tccttgacca tctctggggc tcaggcggaa 240
gatgaggctg actattactg taactcccta gacagcactt ataaccatcc gatattcggc 300

ggagggacca aggtcacgt cctaggtcag cccgcggccg ca342

<210> 272<211> 351<212> ADN<213> Secuencia artificial<220><223> Gen que codifica para la regi3n variable de cadena pesada (H2)<400> 272caggtccagc ttgtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc60tcctgcaagg cttctggata caccttcacc agttatgata tccactgggt gcgacaggcc120actggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat180gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac240atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatggg300ggtgatgctt ttgatatctg gggccaagga accctggtca cegtctcgag t351<210> 273<211> 342<212> ADN<213> Secuencia artificial<220><223> Gen que codifica para la regi3n variable de cadena ligera (H11)<400> 273tcctatgagc tgactcagga ccctgctgcg tctgtggcct tgggacagac agtcaggatc60acatgccaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagccagga120caggccccctg tagttgtcat ctatggtaga aacaaccggc cctcagggat cccagaccga180ttctctgget ccagctcagg agacacagct tccttgacca tcaactgggc tcaggcggaa240gatgaggctg actattactg taagtcccgg gacagcagtg gtaaccatta tgtcttcgga300actgggacca agctgaccgt cctaggtcag cccgcggccg ca342<210> 274<211> 351<212> ADN<213> Secuencia artificial<220><223> Gen que codifica para la regi3n variable de cadena pesada (H11)

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<400> 274
caggtgcagc tgggtcagtc tggggctgag gtgaagaagc ctggggcctc agtgaagggt 60
tcttgaagg catctggata caccttacc agctactata tgactgggt ggcacaggcc 120
cctggacaag ggcttgagt gatgggaata atcaacccta gtggtggtag cacaagctac 180
gcacagaagt tccagggcag agtcacatg accagggaca cgtccacgag cacagtctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatgcc 300
ggcagctcgt ccgattactg gggccgtggc accctggta cgtctcgag t 351

<210> 275
<211> 348
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regiÃ³n variable de cadena ligera (F12)

<400> 275
cagtctgtgc tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60
tcttgcgtg gaaccagcag tgacattggt gattatgact atgtctctg gtaccaacag 120
caccagggca agactcccaa actcatgatt tatgatgtca gtagggggcc ctcaggggtc 180
cctgatcgt tctctggctc caagtctggc aacacggcct ccctgacat ctctgggtc 240
cagactgagg acgaggctga ttattactgc gcctcatata caagcagcag cgtcgtggtc 300
ttcggcggag ggaccaagct gaccgtccta ggtcagcccg cggccgca 348

<210> 276
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regiÃ³n variable de cadena pesada (F12)

<400> 276
caggtgcagc tgggtcagtc tggagcagag gtgaaaagc cgggggagtc tctgaagatc 60
tcttgaagg gttctggata cagctttacc agctactgga tcggctgggt ggcacagatg 120
cccgggaaag gcctggagt gatggggatc atctatctg gtgactctga taccagatac 180
agcccgctct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240
ctgcagtgga gcagcctgaa ggctcggac accgcatgt attactgtgc gactcaatat 300

tacgatgggg gttactacat ggacgtctgg ggccagggca ccctggtcac cgtctcgagt 360

360

<210> 277

<211> 336

<212> ADN

<213> Secuencia artificial

<220>

<223> Gen que codifica para la regiÃ³n variable de cadena ligera (B9)

<400> 277

gacatccaga tgaccagtc tccatctec ctgtctgcat ctgtaggaga cagagtcacc 60

atcactgcc gggcaagtca gagcattagc aggtatttaa attggtatca gcagaaacca 120

gggaaagccc ccaagctcct gatctatggt gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcagcct 240

gaagatttcg caactacca ttgtcaacag gcttacggtt tccccctcac tctcggcgga 300

gggaccaagg tggagatcaa acgtaccgcg gccgca 336

<210> 278

<211> 375

<212> ADN

<213> Secuencia artificial

<220>

<223> Gen que codifica para la regiÃ³n variable de cadena de pesada (B9)

<400> 278

caggtgcagc tggaggagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcttgcaagg cttctggagg caccttcage agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtgc gatgggaggg atcatcccta tctttgttac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggaa 300

atagcagtgg ctcaaaactg ggactactac ggtatggacg tctggggcca gggcacctg 360

gtcacctgtc cgagt 375

<210> 279

<211> 351

<212> ADN

<213> Secuencia artificial

<220>
<223> Gen que codifica para la regiÃ³n variable de cadena ligera (G11)

<400> 279
cagtctgcgc tgactcagcc tcgctcagtg tccgggtctc ctggacagtc agtcaccatc 60
tcttgactg gaaccagcag tgatgttggg ggtataact atgtctctg gtaccaacag 120
caccagga aagccccaa actcatgatt tatgatgtca gtaagcggcc ctcaggggtc 180
cctgatcgt tctctggctc caagtctggc aacacggcct ccctgacaat ctctgggctc 240
caggctgagg acgaggctga ttattactgc agtcatatt caagcagcag cactctcgtg 300
gtttcggcg gagggaccaa gctgaccgtc ctaggtcagc ccgcggccgc a 351

<210> 280
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regiÃ³n variable de cadena pesada (G11)

<400> 280
caggtccagc tggtagcagc tggagcagag gtgaaaaagc cgggggagtc tctgaagatc 60
tctgtgaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120
cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180
agcccgctct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagtcaatat 300
tacgatgggg gttactacat ggacgtctgg ggccaggga ccttggtcac cgtctcagat 360

360

<210> 281
<211> 342
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regiÃ³n variable de cadena ligera (G6)

<400> 281
tctatgagc tgactcagga cctgtctgtg tctgtggcct tgggacagac agtcacgatc 60
acatgccaag gagacagcct cagaaggtat tatgcaacct ggtaccagca gaagccagga 120

caggccctg tcctgtcat ctatgtcaa aactaccggc cctcggggat cccagaccga 180
ttctctggct ccaactcagg aaccacagct tccttgacca tcaactggggc tcaggcggaa 240
gatgaggctg actattactg taactccggg gacagcagtg gtaacctatg ggtattcggc 300
ggagggacca agctgaccgt cctaggtcag cccgcggccg ca 342

<210> 282
<211> 357
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la región variable de cadena pesada (G6)

<400> 282
gagggtgcagc tgggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60
tcttgaagg catctggata cacctcacc agctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttgttac agcaaactac 180
gcacagaagt tcagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt actactgtgc gagagggtgg 300
gggtatagca gctcgttga ctactggggg caagggacca cggtcaccgt ctcgagt 357

<210> 283
<211> 348
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la región variable de cadena ligera (F11)

<400> 283
cagtctgtgc tgactcagcc accctcaacg tctgggaccc ccgggcagac gttctccatt 60
tttgttctg gaagcagttc gaacatcgga actaatactg ttaattggtg ccagcagctc 120
ccaggaacgg ccccaaact cctcatctat agtaatgatc agcggccctc aggggtccct 180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240
tctgaggatg aggctgatta ttactgtgaa acatgggatg acagcctgaa aggcccggtg 300
ttcggcgggg ggaccaaggt caccgtccta ggtcagcccg cggccgca 348

<210> 284
<211> 357

<212> ADN
 <213> Secuencia artificial

<220>
 <223> Gen que codifica para la región variable de cadena pesada (F11)

<400> 284
 gaggtgcagc tgggtggagtc tgggggaggc ttgtccagc ctgggggggc cctgaaactc 60
 tctgtgcag cgtctggatt cacctttagc agctatgcca tgagctgggt ccgccgggct 120
 ccagggaagg ggctggagtg ggtctcaact attagtggta gtggtgatag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acaacctgag agccgaggac acggccgtat attactgtgc gagagaatgg 300
 gaactaggcg atgcttttga tatctggggc cgtggcaccc tggtcaccgt ctcgagt 357

<210> 285
 <211> 336
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Gen que codifica para la región variable de cadena ligera (D3)

<400> 285
 gacatccaga tgaccagtc tccatctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcg gggcaagtca gaggattagc agctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccggtggac gttcggccaa 300
 gggaccaagg tggaaatcaa acgtaccgcg gccgca 336

<210> 286
 <211> 366
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Gen que codifica para la región variable de cadena pesada (D3)

<400> 286
 gaggtgcagc tgttggagtc tgggggaggc gtgtccagc ctgggaggtc cctgagactc 60
 tctgtgcag cctctggatc cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagacaga 300
ggcagctatg gttactacta cggtatggac gtctggggcc aagggacaat ggtcaccgtc 360
tcgagt 366

<210> 287
<211> 336
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena ligera (B12)

<400> 287
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcactlgcc gggcaagtca gaggcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta ccctccggac gttcggccaa 300
gggaccaagg tggagatcaa acgtaccgcg gccgca 336

<210> 288
<211> 366
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena pesada (B12)

<400> 288
caggtccagc tggtagcagc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaactac 180
gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtac gagagccggt 300
gcttctatag tgggagctac cgcgcttgac tactggggcc agggaaccct ggtcaccgtc 360
tcgagt 366

<210> 289
<211> 354
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena ligera (E4)

<400> 289
aattttatgc tgactcagcc ccactctgtg tcggagtctc cgggaaagac ggtaaccatc 60
tctgcaccc gcagcagtgg cagcattgcc agcaactatg tgcagtggta ccagcagcgc 120
ccgggcagtt cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtcctt 180
gatcggttct ctggetccat cgacagctcc tccaactctg cctccctcac catctctgga 240
ctgaagactg aggacgaggc tgactactac tgcagtctt atgataccgg caatcggaat 300
tatgtcttcg gaactgggac ccagtcacc gtctaggtc agcccgcggc cgca 354

<210> 290
<211> 363
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena pesada (E4)

<400> 290
caggtgcagc tgggtcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcttgaagg cttctggagg caccttcagc agctatacta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaagg atcatcceta tccttggtat agcaaactac 180
gcacagaagt tccagggcag agtcacatg accagggaca tgtccacaga cacagcctac 240
atggagttga gcagcctgac atatgatgac acggccgtat attttgtgt gagaggccct 300
agtcttaatt atgccggcta tttgacaac tggggccagg gcaccctggt caccgtctcg 360

agt 363

<210> 291
<211> 342
<212> ADN
<213> Secuencia artificial

<220>
<223> Gen que codifica para la regi3n variable de cadena ligera (E12)

<400> 291
 tcctatgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60
 acatgccaaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagtcagga 120
 caggccccctg tacttgtcat ctatggtaaa gaaaagcggc cctcagggat cccagaccga 180
 ttctctgget ccagctcagg aaacacagct tccttgacca tcaactggggc tcgggcggaa 240
 gatgaggctg actattactg taactcccg ggcagcacta ctgactatat ggtgttcggc 300
 gggggggaccc agctcacctg cctaggtcag cccgcggccg ca 342

<210> 292
 <211> 351
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Gen que codifica para la regiÃ³n variable de cadena pesada (E12)

<400> 292
 caggtgcagc tgggtggagtc cggggggaggc ttagttcagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agctgaggac acggtctgtg attactgtgc gagagaacgg 300
 ggaagtggta tggacgtctg gggccaagga accctgggtca ccgtctcgag t 351

<210> 293
 <211> 336
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Gen que codifica para la regiÃ³n variable de cadena ligera (D1)

<400> 293
 gaaacgacac tcacgcagtc tccagcattc atgtcagcga ctccaggaga caaagtcaac 60
 atctcctgca aagccagcca agacattgat gatgatatga actggtacca acagaaacca 120
 ggagaagctg ctatttccat tattcaagaa gctagtactc tcgttcctgg aatcccacct 180
 cgattcagtg gcagcgggta tggaacagat ttaccctca caattaataa catagaatct 240
 gaggatgctg catattactt ctgtctacaa catgataagt tcccgtacac ttttgccag 300

gggaccaagc tggagatcaa acgtaccgcg gccgca

336

<210> 294

<211> 351

<212> ADN

<213> Secuencia artificial

<220>

<223> Gen que codifica para la regi3n variable de cadena pesada (D1)

<400> 294

gaagtgcagc tggtcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcttgcagg cttctggta caccttacc agctatgga tcagctgggt gcgacaggcc 120

cctggacaag ggcttgatg gatgggatgg atcaacccta acagtgggtg cacaactat 180

gcacagaagt ttcaggcag ggtcacatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gaggcgggg 300

gttgatgagg gggactactg gggccaagg acaatggtca ccgtctcag t 351

<210> 295

<211> 348

<212> ADN

<213> Secuencia artificial

<220>

<223> Gen que codifica para la regi3n variable de cadena ligera (E6)

<400> 295

aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac gggtaccctc 60

tctgcaccg gcagcagcgg caacattgcc agtaactatg tgagtggtta ccagcaccgc 120

ccgggcagtg ccccccaccac tgtgatctac cgggatgacc aaagaccctc tggagtcct 180

gatcgcttct ctggctccat cgacagtcca tccaactctg cctccctcac gatctctgga 240

ctgaggcctg aggacgaggc tgactattac tgcagttt atgtagcag ctcttggtg 300

ttcggcggag ggaccaagct gaccgtccta ggtcagccc cggccgca 348

<210> 296

<211> 372

<212> ADN

<213> Secuencia artificial

<220>

<223> Gen que codifica para la regi3n variable de cadena pesada (E6)

<400> 296
caggtccagc ttgtgcagtc tggagcagag gtgaagaagc ctggggcctc agtgaaggtc 60
tcttgaagg cttctggata caccttcacc acttatgata tcacctgggt gcgacaggcc 120
cctggacaag gccttgagt gatgggatgg atgaaccga acagtggtaa ctacgctct 180
gcacagaagt tccagggcag agtcagcatg accagtgact cctccataag cacagcctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aacaggagac 300
tactcgggtg tgggtactaac tgcaacagca cttgactact gggggccaggg aacctggtc 360
accgtctcga gt 372

<210> 297
<211> 348
<212> ADN
<213> Secuencia artificial
<220>
<223> Gen que codifica para la regiÃ³n variable de cadena ligera (E9)

<400> 297
cagtctgagc tgactcagct accctcagcg tctgagacc cggggcagag ggtcaccatc 60
tcttgttctg gaagcagctc caacatcgga aataattatg tatactggta ccagcaactc 120
cccggaaagg cccccaaact cctcatctat aggaataatc agcggccctc aggggtccct 180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggtccgg 240
tccgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgag tggttgggtg 300
ttcggcggag ggaccaagct gaccgtccta ggtcagcccg cggccgca 348

<210> 298
<211> 369
<212> ADN
<213> Secuencia artificial
<220>
<223> Gen que codifica para la regiÃ³n variable de cadena pesada (E9)

<400> 298
caggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggaggtc cctgagactc 60
tctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
ccaggaagg ggctggagt ggtggccaac ataaagcaag atggaagtga gaaatactat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa cacgctgtat 240

ctccaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagaggac 300

cgtatagcag cagctgggat gcgggagttg gactactggg gccagggcac cctggtcacc 360

gtctcgagt 369

<210> 299

<211> 354

<212> ADN

<213> Secuencia artificial

<220>

<223> Gen que codifica para la regiÃ³n variable de cadena ligera (A11)

<400> 299

gatattgtga tgaccagtc tccactctcc ctgcccgtca cccttgaga gccggcctcc 60

atctcctgca ggtctagtc gagcctctg catagtaatg gatacaacta tttggattgg 120

tacctgcaga agccagggca gtctccacag ctctgatct attgggttc taaccgggcc 180

tccgggggtcc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaac 240

agcagagtgg aggctgagga tgttgggggt tattactgca tgcaaggtag acactggcct 300

ccgtacacct ttggccaggg gaccaagggt gagatcaaac gtaccgggcg cgca 354

<210> 300

<211> 360

<212> ADN

<213> Secuencia artificial

<220>

<223> Gen que codifica para la regiÃ³n variable de cadena pesada (A11)

<400> 300

gaggtgcagc tgttgagtc tgggggaggg ttggaacagc ctgggggggt cctgagactc 60

tcctgtgcag cctctggatt ctctttacc agctacgcca tgacctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaggt attagtagtg atgggaccac tacaacctac 180

gcggactccg tgagggggcg gttcaccatc tccagagaca acgccaagaa cacggtgtat 240

ctccaaatga acagtctgag agacgaggac acggctgtgt attattgtgc aagagatcaa 300

ttgtgggct gggatgctct gaatgtctgg ggccaaggga caatggtcac cgtctcgagt 360

360

<210> 301

<211> 216

<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (E3)

<400> 301
Ser Tyr 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 Asn Phe Tyr Ala
20 25 30
Ser Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Met Tyr
35 40 45
Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60
Thr 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 Arg Asp Ser Ser Gly Ser His
85 90 95
Leu Thr Gly Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110
Pro Ala Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160
Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205
Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 302
<211> 451
<212> PRT
<213> Secuencia artificial

<220>

<223> Cadena pesada (E3 o E3.1)

<400> 302

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

Ala Arg Asp Thr Tyr Tyr Tyr Gly Ser Gly Arg Ser Asn Ala Phe Asp
100 105 110

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

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

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

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

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

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

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

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

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

Leu Gly Lys
450

<210> 303
<211> 212
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (B3)

<400> 303
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 Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

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

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

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

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

<210> 304
 <211> 449
 <212> PRT
 <213> Secuencia artificial

 <220>
 <223> Cadena pesada (B3)

<400>	304
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg	
1	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
20	30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35	45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val	
50	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85	95

Ala Arg Val Gly Asp Ser Ser Gly Trp Ser Asp Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270

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

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

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

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

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

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

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

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

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

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

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

Lys

<210> 305
<211> 216
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (A10)

<400> 305
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val 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

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

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

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

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

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

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

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

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

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

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

180 185 190
Leu Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 306
<211> 448
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (A10)

<400> 306
Gln Met 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 Ile 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 Gly Gly Leu Gly Glu Leu Asp Asn Trp Phe Asp Pro Trp Gly
100 105 110

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- <210> 307
- <211> 212
- <212> PRT
- <213> Secuencia artificial
- <220>
- <223> Cadena ligera (G1)

<400> 307

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

1 5 10 15

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

20 25 30

Ser Trp Tyr Gln Gln Lys Thr Gly Gln Ser Pro Val Val Val Ile Tyr

35 40 45

Lys Asp Ser Gln Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser

50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met

65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Gly Thr Gly Val

85 90 95

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

100 105 110

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

115 120 125

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

130 135 140

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

145 150 155 160

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser

165 170 175

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser

180 185 190

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

195 200 205

Thr Glu Cys Ser

210

<210> 308

<211> 445

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena pesada (G1)

<400> 308

Glu 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

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

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

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

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

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

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

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

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

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

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

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 309

<211> 218

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena ligera (G9)

<400> 309

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

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

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

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Met Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

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

Ser Thr Leu Asp Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

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

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

<210> 310
<211> 447
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (G9)

<400> 310
Gln Val Gln Leu Val Gln Pro Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

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

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

Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val Trp Gly Gln
100 105 110

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

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

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

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

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

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 311
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (H2)

<400> 311
Ser Tyr 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 Asn Tyr Tyr Ala
20 25 30

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

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

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

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Asp Ser Thr Tyr Asn His
85 90 95

Pro Ile Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln Pro Ala
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> 312
<211> 444

<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (H2)

<400> 312
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Asp Ile His Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Gly Gly Asp Ala Phe Asp Ile 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205
Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220
Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255
Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe

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

<210> 313
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (H11)

<400> 313
Ser Tyr Glu Leu Thr Gln Asp Pro Ala Ala 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 Val Val Ile Tyr
35 40 45
Gly Arg Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

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

Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Ser Ser Gly Asn His
85 90 95

Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Ala
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> 314
<211> 444
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (H11)

<400> 314
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Ala Gly Ser Ser Ser Asp Tyr Trp Gly Arg 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

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

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

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

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

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

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

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

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

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

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

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser

385 390 395 400

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 315
 <211> 216
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cadena ligera (F12)

<400> 315
 Gln Ser Val Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15

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

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

Met Ile Tyr Asp Val Ser Arg Arg Pro Ser Gly Val Pro Asp Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80

Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Tyr Thr Ser Ser
 85 90 95

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

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 316
<211> 447
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (F12)

<400> 316
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

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

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

Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val Trp Gly Gln
100 105 110

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

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

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

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

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

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro

210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- <210> 317
- <211> 214
- <212> PRT
- <213> Secuencia artificial
- <220>
- <223> Cadena ligera (B9)
- <400> 317

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 Ser Arg Tyr
20 25 30

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

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

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

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

Thr Leu Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Ala 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 Leu Tyr
180 185 190

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

Phe Asn Arg Gly Glu Cys
210

<210> 318

<211> 452

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena pesada (B9)

<400> 318

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

325 330 335

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

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

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

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

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

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

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

Ser Leu Gly Lys
450

<210> 319
<211> 217
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (G11)

<400> 319
Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ser Ser Ser
85 90 95

Ser Thr Leu Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
130 135 140

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
145 150 155 160

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
180 185 190

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
195 200 205

Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 320
<211> 447
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (G11)

<400> 320
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

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

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

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

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

Ala Ser Gln Tyr Tyr Asp Gly Gly Tyr Tyr Met Asp Val Trp Gly Gln
100 105 110

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

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

130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys

435 440 445

<210> 321
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (G6)

<400> 321
Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

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

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

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

Asn Ser Gly Thr 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 Arg Asp Ser Ser Gly Asn His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Ala
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> 322
<211> 446
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (G6)

<400> 322
Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly 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 Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Trp Gly Tyr Ser Ser Ser Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125
Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190
Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220
Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
225 230 235 240
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

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

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

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

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

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

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

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

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

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

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

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

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

<210> 323
<211> 216
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (F11)

<400> 323
Gln Ser Val Leu Thr Gln Pro Pro Ser Thr Ser Gly Thr Pro Gly Gln
1 5 10 15

Thr Phe Ser Ile Phe Cys Ser Gly Ser Ser Ser Asn Ile Gly Thr Asn
20 25 30

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

Ile Tyr Ser Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Thr Trp Asp Asp Ser Leu
85 90 95

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

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 324

<211> 446

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena pesada (F11)

<400> 324

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

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

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

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

370 375 380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400
Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 325
<211> 212
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (D3)

<400> 325
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 Ser Ser Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Ala Ala Ala
100 105 110
Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
115 120 125
Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
130 135 140
Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
145 150 155 160
Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser

165 170 175

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
180 185 190

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

Thr Glu Cys Ser
210

<210> 326

<211> 449

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena pesada (D3)

<400> 326

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly 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 Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Asp Arg Gly Ser Tyr Gly Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270

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

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

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

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

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

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

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

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

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

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

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

Lys

- <210> 327
- <211> 214
- <212> PRT
- <213> Secuencia artificial

<220>

<223> Cadena ligera (B12)

<400> 327

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 Ser Ser Tyr
20 25 30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Ala 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 Leu 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> 328

<211> 449

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena pesada (B12)

<400> 328
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

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

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

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270

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

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

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

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

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

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

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

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

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

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

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

Lys

<210> 329
<211> 218
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (E4)

<400> 329
Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15

Thr Val Thr Ile Ser Cys Thr Arg Ser Ser Gly Ser Ile Ala Ser Asn
 20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ser Pro Thr Thr Val
 35 40 45

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
 65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Thr

85 90 95

Gly Asn Arg Asn Tyr Val Phe Gly Thr Gly Thr Gln Leu Thr Val Leu
100 105 110

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

Glu Glu Ile Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
130 135 140

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

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
165 170 175

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
180 185 190

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
195 200 205

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 330
<211> 448
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (E4)

<400> 330
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

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

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

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

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

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

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 331
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (E12)

<400> 331
Ser Tyr 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 Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Gly Lys Glu Lys 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 Arg Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Gly Ser Thr Thr Asp Tyr
85 90 95

Met Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly Gln Pro Ala
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> 332
<211> 444
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (E12)

<400> 332
Gln 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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Glu Arg Gly Ser Gly Met Asp Val 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 Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

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

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

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

<210> 333
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (D1)

<400> 333
Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly
1 5 10 15
Asp Lys Val Asn Ile Ser Cys Lys Ala Ser Gln Asp Ile Asp Asp Asp
20 25 30

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Ala Ile Ser Ile Ile
35 40 45

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

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

Glu Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Lys Phe Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Ala 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 Leu 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> 334
<211> 444
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (D1)

<400> 334
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe

50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ser Arg Gly Val Asp Glu Gly Asp Tyr Trp Gly Gln Gly Thr Met
 100 105 110
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser 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 Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
 340 345 350
 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

355 360 365
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 385 390 395 400
 Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
 405 410 415
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 420 425 430
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 335
 <211> 216
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Cadena ligera (E6)

<400> 335
 Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15

Thr Val Thr Leu Ser Cys Thr Gly Ser Ser Gly Asn Ile Ala Ser Asn
 20 25 30

Tyr Val Gln Trp Tyr Gln His Arg Pro Gly Ser Ala Pro Thr Thr Val
 35 40 45

Ile Tyr Arg Asp Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
 65 70 75 80

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

Ser Ser Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110

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

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 336
<211> 451
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (E6)

<400> 336

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

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

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

Gly Trp Met Asn Pro Asn Ser Gly Asn Ser Arg Ser Ala Gln Lys Phe
50 55 60

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

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

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

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

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

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val

180	185	190
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn		
195	200	205
Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser		
210	215	220
Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly		
225	230	235
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
245	250	255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln		
260	265	270
Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
275	280	285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr		
290	295	300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
305	310	315
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile		
325	330	335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		
340	345	350
Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser		
355	360	365
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		
370	375	380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		
385	390	395
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val		
405	410	415
Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met		
420	425	430
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser		
435	440	445
Leu Gly Lys		
450		

<210> 337
 <211> 216
 <212> PRT

<213> Secuencia artificial

<220>

<223> Cadena ligera (E9)

<400> 337

Gln Ser Glu Leu Thr Gln Leu Pro Ser Ala Ser Glu Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn

20 25 30

Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu

35 40 45

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser

50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg

65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu

85 90 95

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln

100 105 110

Pro Ala Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu

115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr

130 135 140

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

145 150 155 160

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

165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His

180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys

195 200 205

Thr Val Ala Pro Thr Glu Cys Ser

210 215

<210> 338

<211> 450

<212> PRT

<213> Secuencia artificial

<220>

<223> Cadena pesada (E9)

<400> 338
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Asp Arg Ile Ala Ala Ala Gly Met Arg Glu Leu Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
 195 200 205
 Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
 210 215 220
 Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
 260 265 270
 Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg

290 295 300

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

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

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

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

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

Gly Lys
450

<210> 339
<211> 220
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (A11)

<400> 339

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

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

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

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

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

Thr His Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Ala Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

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

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

<210> 340
<211> 447
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada (A11)

<400> 340
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Glu Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Ala Arg Asp Gln Leu Leu Gly Trp Asp Ala Leu Asn Val Trp Gly Gln

100 105 110
 Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg

405 410 415

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

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

<210> 341
<211> 327
<212> PRT
<213> Secuencia artificial

<220>
<223> Fc de IgG4

<400> 341
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

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

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

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

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

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

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

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

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

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

<210> 342
<211> 102
<212> PRT
<213> Secuencia artificial

<220>
<223> Región constante kappa

<400> 342
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
1 5 10 15

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
35 40 45

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

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

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

Phe Asn Arg Gly Glu Cys

<210> 343
 <211> 100
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Región constante lambda

<400> 343
 Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
 1 5 10 15

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

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
 35 40 45

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
 50 55 60

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
 65 70 75 80

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

Thr Glu Cys Ser
 100

<210> 344
 <211> 106
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Región constante lambda CL.1

<400> 344
 Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser
 1 5 10 15

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

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

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

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
 85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 100 105

<210> 345
<211> 110
<212> PRT
<213> Secuencia artificial

<220>
<223> Región variable de cadena ligera (E3.1)

<400> 345
Ser Tyr 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 Asn Phe Tyr Ala
 20 25 30

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

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

Thr 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 Arg Asp Ser Ser Gly Ser His
 85 90 95

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

<210> 346
<211> 330
<212> PRT
<213> Secuencia artificial

<220>
<223> Gen que codifica para la región variable de cadena ligera (E3.1)

<400> 346
Thr Cys Cys Thr Ala Thr Gly Ala Gly Cys Thr Gly Ala Cys Thr Cys
 1 5 10 15

Ala Gly Gly Ala Cys Cys Cys Thr Gly Cys Thr Gly Thr Gly Thr Cys
 20 25 30

Thr Gly Thr Gly Gly Cys Cys Thr Thr Gly Gly Gly Ala Cys Ala Gly
35 40 45

Ala Cys Ala Gly Thr Cys Ala Gly Gly Ala Thr Cys Ala Cys Ala Thr
50 55 60

Gly Cys Cys Ala Gly Gly Gly Ala Gly Ala Cys Ala Gly Cys Cys Thr
65 70 75 80

Cys Ala Gly Ala Ala Ala Cys Thr Thr Thr Thr Ala Thr Gly Cys Ala
85 90 95

Ala Gly Cys Thr Gly Gly Thr Ala Cys Cys Ala Gly Cys Ala Gly Ala
100 105 110

Ala Gly Thr Cys Ala Gly Gly Ala Cys Ala Gly Gly Cys Cys Cys Cys
115 120 125

Ala Gly Thr Thr Cys Thr Thr Gly Thr Cys Ala Thr Gly Thr Ala Thr
130 135 140

Gly Gly Thr Ala Ala Ala Ala Ala Cys Ala Ala Cys Cys Gly Gly Cys
145 150 155 160

Cys Cys Thr Cys Ala Gly Gly Gly Ala Thr Cys Cys Cys Ala Gly Ala
165 170 175

Cys Cys Gly Ala Thr Thr Cys Thr Cys Thr Gly Gly Cys Thr Cys Cys
180 185 190

Ala Cys Cys Thr Cys Ala Gly Gly Ala Ala Ala Cys Ala Cys Ala Gly
195 200 205

Cys Thr Thr Cys Cys Thr Thr Gly Ala Cys Cys Ala Thr Cys Ala Cys
210 215 220

Thr Gly Gly Gly Gly Cys Thr Cys Ala Gly Gly Cys Gly Gly Ala Ala
225 230 235 240

Gly Ala Thr Gly Ala Gly Gly Cys Thr Gly Ala Cys Thr Ala Thr Thr
245 250 255

Ala Cys Thr Gly Thr Ala Ala Cys Thr Cys Cys Cys Gly Gly Gly Ala
260 265 270

Cys Ala Gly Cys Ala Gly Thr Gly Gly Thr Ala Gly Cys Cys Ala Thr
275 280 285

Thr Thr Gly Ala Cys Gly Gly Gly Cys Gly Thr Ala Thr Thr Cys Gly
290 295 300

Gly Cys Gly Gly Ala Gly Gly Gly Ala Cys Cys Ala Ala Gly Gly Thr
305 310 315 320

Cys Ala Cys Cys Gly Thr Cys Cys Thr Ala
325 330

<210> 347
<211> 216
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera (E3.1)

<400> 347
Ser Tyr 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 Asn Phe Tyr Ala
20 25 30
Ser Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Met Tyr
35 40 45
Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60
Thr 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 Arg Asp Ser Ser Gly Ser His
85 90 95
Leu Thr Gly Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110
Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145 150 155 160
Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205
Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 348
<211> 650
<212> PRT
<213> Secuencia artificial

<220>

<223> LILRB1(AAH15731)

<400> 348

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

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

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

Cys Gln Gly Gly Gln Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50 55 60

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

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

Arg Cys Tyr Tyr Gly Ser Asp Thr Ala Gly Arg Ser Glu Ser Ser Asp
100 105 110

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

Ala Gln Pro Ser Pro Val Val Asn Ser Gly Gly Asn Val Thr Leu Gln
130 135 140

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

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

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

Trp Trp Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Glu Trp
195 200 205

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

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

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

Leu Tyr Lys Asp Gly Glu Arg Asp Phe Leu Gln Leu Ala Gly Ala Gln
260 265 270

Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser

275 280 285
 Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser
 290 295 300
 Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly
 305 310 315 320
 Gln Phe Tyr Asp Arg Val Ser Leu Ser Val Gln Pro Gly Pro Thr Val
 325 330 335
 Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Gln Gly Trp Met
 340 345 350
 Gln Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala Asp Asp Pro Trp Arg
 355 360 365
 Leu Arg Ser Thr Tyr Gln Ser Gln Lys Tyr Gln Ala Glu Phe Pro Met
 370 375 380
 Gly Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
 385 390 395 400
 Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp Pro Leu Glu
 405 410 415
 Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly
 420 425 430
 Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
 435 440 445
 Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
 450 455 460
 Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Phe
 465 470 475 480
 Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
 485 490 495
 Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
 500 505 510
 Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
 515 520 525
 Glu Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly
 530 535 540
 Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val
 545 550 555 560
 Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser
 565 570 575
 Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln

580 585 590
Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala
595 600 605
Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg
610 615 620
Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val
625 630 635 640
Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
645 650

<210> 349
<211> 598
<212> PRT
<213> Secuencia artificial

<220>
<223> LILRB2(AAH36827)

<400> 349
Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1 5 10 15
Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp
20 25 30
Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser
35 40 45
Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50 55 60
Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn
65 70 75 80
Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr
85 90 95
Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro
100 105 110
Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala
115 120 125
Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys
130 135 140
Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu
145 150 155 160
Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser
165 170 175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Thr Leu Ala Ile His
595

<210> 350
<211> 631
<212> PRT
<213> Secuencia artificial

<220>
<223> LILRB3(XP_006726377)

<400> 350
Met Thr Pro Ala Leu Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
1 5 10 15

Pro Arg Thr Arg Val Gln Ala Gly Pro Phe Pro Lys Pro Thr Leu Trp
20 25 30

Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Ser Pro Val Thr Ile Trp
35 40 45

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

Ser Pro Glu Pro Leu Asp Arg Asn Asn Pro Leu Glu Pro Lys Asn Lys
65 70 75 80

Ala Arg Phe Ser Ile Pro Ser Met Thr Glu His His Ala Gly Arg Tyr
85 90 95

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

Leu Glu Leu Val Met Thr Gly Phe Tyr Asn Lys Pro Thr Leu Ser Ala

115	120	125			
Leu Pro Ser Pro Val Val Ala Ser Gly Gly Asn Met Thr Leu Arg Cys					
130	135	140			
Gly Ser Gln Lys Gly Tyr His His Phe Val Leu Met Lys Glu Gly Glu					
145	150	155	160		
His Gln Leu Pro Arg Thr Leu Asp Ser Gln Gln Leu His Ser Gly Gly					
165	170	175			
Phe Gln Ala Leu Phe Pro Val Gly Pro Val Asn Pro Ser His Arg Trp					
180	185	190			
Arg Phe Thr Cys Tyr Tyr Tyr Tyr Met Asn Thr Pro Gln Val Trp Ser					
195	200	205			
His Pro Ser Asp Pro Leu Glu Ile Leu Pro Ser Gly Val Ser Arg Lys					
210	215	220			
Pro Ser Leu Leu Thr Leu Gln Gly Pro Val Leu Ala Pro Gly Gln Ser					
225	230	235	240		
Leu Thr Leu Gln Cys Gly Ser Asp Val Gly Tyr Asp Arg Phe Val Leu					
245	250	255			
Tyr Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Gln Gln Pro					
260	265	270			
Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro					
275	280	285			
Ser His Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser Ser					
290	295	300			
Glu Trp Ser Ala Pro Ser Asp Pro Leu Asn Ile Leu Met Ala Gly Gln					
305	310	315	320		
Ile Tyr Asp Thr Val Ser Leu Ser Ala Gln Pro Gly Pro Thr Val Ala					
325	330	335			
Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Trp Gln Phe Asp					
340	345	350			
Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala His Pro Pro Leu Arg Leu					
355	360	365			
Arg Ser Met Tyr Gly Ala His Lys Tyr Gln Ala Glu Phe Pro Met Ser					
370	375	380			
Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Tyr					
385	390	395	400		
Ser Ser Asn Pro His Leu Leu Ser Phe Pro Ser Glu Pro Leu Glu Leu					
405	410	415			
Met Val Ser Gly His Ser Gly Gly Ser Ser Leu Pro Pro Thr Gly Pro					

420 425 430
Pro Ser Thr Pro Gly Leu Gly Arg Tyr Leu Glu Val Leu Ile Gly Val
435 440 445
Ser Val Ala Phe Val Leu Leu Leu Phe Leu Leu Leu Phe Leu Leu Leu
450 455 460
Arg Arg Gln Arg His Ser Lys His Arg Thr Ser Asp Gln Arg Lys Thr
465 470 475 480
Asp Phe Gln Arg Pro Ala Gly Ala Ala Glu Thr Glu Pro Lys Asp Arg
485 490 495
Gly Leu Leu Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Glu Glu Asn
500 505 510
Leu Tyr Ala Ala Val Lys Asp Thr Gln Ser Glu Asp Arg Val Glu Leu
515 520 525
Asp Ser Gln Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala
530 535 540
Pro Val Lys His Ser Ser Pro Arg Arg Glu Met Ala Ser Pro Pro Ser
545 550 555 560
Ser Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Val Glu Glu
565 570 575
Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Ser Gln Asp
580 585 590
Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr
595 600 605
Glu Pro Pro Pro Ser Gln Glu Gly Glu Pro Pro Ala Glu Pro Ser Ile
610 615 620
Tyr Ala Thr Leu Ala Ile His
625 630

<210> 351
<211> 448
<212> PRT
<213> Secuencia artificial

<220>
<223> LILRB4(NP_001265355)

<400> 351
Met Ile Pro Thr Phe Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
1 5 10 15
Pro Arg Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
20 25 30

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

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

Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
65 70 75 80

Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
85 90 95

Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro
100 105 110

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

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

Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala
145 150 155 160

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

Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr
180 185 190

Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His
195 200 205

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

Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp
225 230 235 240

Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg
245 250 255

His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu
260 265 270

Ser Leu Leu Leu Phe Leu Leu Leu Gln His Trp Arg Gln Gly Lys His
275 280 285

Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala
290 295 300

Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro
305 310 315 320

Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asn Thr
325 330 335

Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Gln Ser Pro His Asp
340 345 350

Glu Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro
355 360 365

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

Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu
385 390 395 400

Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Arg Leu His
405 410 415

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

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

<210> 352
<211> 590
<212> PRT
<213> Secuencia artificial

<220>
<223> LILRB5(NP_006831)

<400> 352
Met Thr Leu Thr Leu Ser Val Leu Ile Cys Leu Gly Leu Ser Val Gly
1 5 10 15

Pro Arg Thr Cys Val Gln Ala Gly Thr Leu Pro Lys Pro Thr Leu Trp
20 25 30

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

Cys Gln Gly Pro Leu Glu Thr Glu Glu Tyr Arg Leu Asp Lys Glu Gly
50 55 60

Leu Pro Trp Ala Arg Lys Arg Gln Asn Pro Leu Glu Pro Gly Ala Lys
65 70 75 80

Ala Lys Phe His Ile Pro Ser Thr Val Tyr Asp Ser Ala Gly Arg Tyr
85 90 95

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

Leu Glu Leu Val Ala Thr Gly Phe Tyr Ala Glu Pro Thr Leu Leu Ala
115 120 125

Leu Pro Ser Pro Val Val Ala Ser Gly Gly Asn Val Thr Leu Gln Cys
 130 135 140

Asp Thr Leu Asp Gly Leu Leu Thr Phe Val Leu Val Glu Glu Glu Gln
 145 150 155 160

Lys Leu Pro Arg Thr Leu Tyr Ser Gln Lys Leu Pro Lys Gly Pro Ser
 165 170 175

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

Phe Arg Cys Tyr Tyr Tyr Tyr Arg Lys Asn Pro Gln Val Trp Ser Asn
 195 200 205

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

Ser Leu Leu Ile Pro Gln Gly Ser Val Val Ala Arg Gly Gly Ser Leu
 225 230 235 240

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

Lys Glu Gly Glu His Asp Leu Val Gln Gly Ser Gly Gln Gln Pro Gln
 260 265 270

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

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

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly Leu Ile
 305 310 315 320

Pro Asp Ile Pro Ala Leu Ser Val Gln Pro Gly Pro Lys Val Ala Ser
 325 330 335

Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp His Gln Ile Asp Thr
 340 345 350

Phe Phe Leu Thr Lys Glu Gly Ala Ala His Pro Pro Leu Cys Leu Lys
 355 360 365

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

Val Thr Ser Ala Gln Gly Gly Thr Tyr Arg Cys Tyr Ser Ala Ile Arg
 385 390 395 400

Ser Tyr Pro Tyr Leu Leu Ser Ser Pro Ser Tyr Pro Gln Glu Leu Val
 405 410 415

Val Ser Gly Pro Ser Gly Asp Pro Ser Leu Ser Pro Thr Gly Ser Thr
 420 425 430

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

Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Thr Gly Val Ser
450 455 460

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

His Arg His Gln Ser Lys His Arg Thr Ser Ala His Phe Tyr Arg Pro
485 490 495

Ala Gly Ala Ala Gly Pro Glu Pro Lys Asp Gln Gly Leu Gln Lys Arg
500 505 510

Ala Ser Pro Val Ala Asp Ile Gln Glu Glu Ile Leu Asn Ala Ala Val
515 520 525

Lys Asp Thr Gln Pro Lys Asp Gly Val Glu Met Asp Ala Arg Ala Ala
530 535 540

Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu
545 550 555 560

Thr Leu Arg Arg Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu Arg Glu
565 570 575

Pro Pro Ala Glu Pro Ser Ile Tyr Ala Pro Leu Ala Ile His
580 585 590

<210> 353
<211> 489
<212> PRT
<213> Secuencia artificial

<220>
<223> LILRA1(NP_006854)

<400> 353
Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Arg Leu Ser Leu Gly
1 5 10 15

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

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

Cys Gln Gly Ile Leu Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50 55 60

Lys Thr Ala Pro Trp Ile Thr Arg Ile Pro Gln Glu Ile Val Lys Lys
65 70 75 80

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

85 90 95

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

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

Ala Leu Pro Ser Pro Val Val Thr Ser Gly Gly Asn Val Thr Leu His
130 135 140

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

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

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

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

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

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

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

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

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

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

Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly
305 310 315 320

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

Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Gly Pro Phe
340 345 350

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

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

Ser Pro Val Thr Ser Ala His Ser Gly Thr Tyr Arg Cys Tyr Gly Ser

385 390 395 400
Leu Ser Ser Asn Pro Tyr Leu Leu Ser His Pro Ser Asp Ser Leu Glu
 405 410 415
Leu Met Val Ser Gly Ala Ala Glu Thr Leu Ser Pro Pro Gln Asn Lys
 420 425 430
Ser Asp Ser Lys Ala Gly Ala Ala Asn Thr Leu Ser Pro Ser Gln Asn
 435 440 445
Lys Thr Ala Ser His Pro Gln Asp Tyr Thr Val Glu Asn Leu Ile Arg
 450 455 460
Met Gly Ile Ala Gly Leu Val Leu Val Val Leu Gly Ile Leu Leu Phe
465 470 475 480
Glu Ala Gln His Ser Gln Arg Ser Leu
 485

<210> 354
<211> 466
<212> PRT
<213> Secuencia artificial

<220>
<223> LILRA2(AAH17412)

<400> 354
Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
 1 5 10 15
Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
 20 25 30
Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
 35 40 45
Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
 50 55 60
Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
 65 70 75 80
Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
 85 90 95
Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
 100 105 110
Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
 115 120 125
Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
 130 135 140

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

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

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

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

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

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

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

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
260 265 270

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

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

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
305 310 315 320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
325 330 335

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

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
355 360 365

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
370 375 380

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

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

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
420 425 430

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

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

Gly Arg
465

- <210> 355
- <211> 439
- <212> PRT
- <213> Secuencia artificial
- <220>
- <223> LILRA3(AAH28208)

<400> 355
Met Thr Ser Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Asp
1 5 10 15

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

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

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

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

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

Cys Cys Ile Tyr Gly Ser His Thr Val Gly Leu Ser Glu Ser Ser Asp
100 105 110

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

Ala Leu Pro Ser Pro Val Val Thr Ser Gly Gly Asn Val Thr Ile Gln
130 135 140

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

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

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

Trp Ser Tyr Arg Cys Tyr Gly Tyr Asp Ser Arg Ala Pro Tyr Val Trp
195 200 205

Ser Leu Pro Ser Asp Leu Leu Gly Leu Leu Val Pro Gly Val Ser Lys

210 215 220

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

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

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

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

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

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

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

Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Gln Gly Gly Met
340 345 350

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

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

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

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

Leu Val Val Ser Gly Ala Ala Glu Thr Leu Ser Pro Pro Gln Asn Lys
420 425 430

Ser Asp Ser Lys Ala Gly Glu
435

<210> 356
<211> 499
<212> PRT
<213> Secuencia artificial

<220>
<223> LILRA4(NP_036408)

<400> 356
Met Thr Leu Ile Leu Thr Ser Leu Leu Phe Phe Gly Leu Ser Leu Gly
1 5 10 15

Pro Arg Thr Arg Val Gln Ala Glu Asn Leu Pro Lys Pro Ile Leu Trp
 20 25 30

Ala Glu Pro Gly Pro Val Ile Thr Trp His Asn Pro Val Thr Ile Trp
 35 40 45

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

Asn Ser Met Ser Arg His Ile Leu Lys Thr Leu Glu Ser Glu Asn Lys
 65 70 75 80

Val Lys Leu Ser Ile Pro Ser Met Met Trp Glu His Ala Gly Arg Tyr
 85 90 95

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

Leu Glu Leu Val Val Thr Ala Tyr Ser Arg Pro Thr Leu Ser Ala Leu
 115 120 125

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

Ser Arg Leu Gly Leu Gly Arg Phe Thr Leu Ile Glu Glu Gly Asp His
 145 150 155 160

Arg Leu Ser Trp Thr Leu Asn Ser His Gln His Asn His Gly Lys Phe
 165 170 175

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

Phe Arg Cys Tyr Gly Tyr Glu Asn Asn Thr Pro Tyr Val Trp Ser Glu
 195 200 205

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

Ser Leu Leu Thr Leu Gln Gly Pro Val Val Thr Pro Gly Glu Asn Leu
 225 230 235 240

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

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

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

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

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly Gln Ile
 305 310 315 320

Ser Asp Arg Pro Ser Leu Ser Val Gln Pro Gly Pro Thr Val Thr Ser
325 330 335

Gly Glu Lys Val Thr Leu Leu Cys Gln Ser Trp Asp Pro Met Phe Thr
340 345 350

Phe Leu Leu Thr Lys Glu Gly Ala Ala His Pro Pro Leu Arg Leu Arg
355 360 365

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

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

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

Val Ser Gly Ala Thr Glu Thr Leu Asn Pro Ala Gln Lys Lys Ser Asp
420 425 430

Ser Lys Thr Ala Pro His Leu Gln Asp Tyr Thr Val Glu Asn Leu Ile
435 440 445

Arg Met Gly Val Ala Gly Leu Val Leu Leu Phe Leu Gly Ile Leu Leu
450 455 460

Phe Glu Ala Gln His Ser Gln Arg Ser Pro Pro Arg Cys Ser Gln Glu
465 470 475 480

Ala Asn Ser Arg Lys Asp Asn Ala Pro Phe Arg Val Val Glu Pro Trp
485 490 495

Glu Gln Ile

<210> 357

<211> 299

<212> PRT

<213> Secuencia artificial

<220>

<223> LILRA5(NP_067073)

<400> 357

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

Asp Ala Val Ser Pro Ala Leu Met Val Leu Leu Cys Leu Gly Leu Ser
20 25 30

Leu Gly Pro Arg Thr His Val Gln Ala Gly Asn Leu Ser Lys Ala Thr
35 40 45

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

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

<210> 358

<211> 481

<212> PRT

<213> Secuencia artificial

<220>

<223> LILRA6(NP_001347096)

<400> 358
Met Thr Pro Ala Leu Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
1 5 10 15

Pro Arg Thr Arg Val Gln Ala Gly Pro Phe Pro Lys Pro Thr Leu Trp
20 25 30

Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Ser Pro Val Thr Ile Trp
35 40 45

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

Ser Pro Glu Pro Leu Asp Arg Asn Asn Pro Leu Glu Pro Lys Asn Lys
65 70 75 80

Ala Arg Phe Ser Ile Pro Ser Met Thr Gln His His Ala Gly Arg Tyr
85 90 95

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

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

Leu Pro Ser Pro Val Val Ala Ser Gly Gly Asn Met Thr Leu Arg Cys
130 135 140

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

His Gln Leu Pro Arg Thr Leu Asp Ser Gln Gln Leu His Ser Gly Gly
165 170 175

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

Arg Phe Thr Cys Tyr Tyr Tyr Tyr Thr Asn Thr Pro Arg Val Trp Ser
195 200 205

His Pro Ser Asp Pro Leu Glu Ile Leu Pro Ser Gly Val Ser Arg Lys
210 215 220

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

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

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

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

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

Glu Trp Ser Ala Pro Ser Asp Pro Leu Asn Ile Leu Met Ala Gly Gln
305 310 315 320

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

Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Tyr Phe Asp
 340 345 350

Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala His Pro Pro Leu Arg Leu
 355 360 365

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

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

Ser Ser Asn Pro His Leu Leu Ser Phe Pro Ser Glu Pro Leu Glu Leu
 405 410 415

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

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

Ile Arg Met Gly Met Ala Gly Leu Val Leu Val Phe Leu Gly Ile Leu
 450 455 460

Leu Phe Glu Ala Gln His Ser Gln Arg Asn Pro Gln Asp Ala Ala Gly
465 470 475 480

Arg

<210> 359
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra superior de IgG1 humana

<400> 359
Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10