

# LISTA DE SECUENCIAS

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Gly Xaa Ser Phe Ser Xaa Xaa Tyr Xaa Xaa Xaa

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Xaa Xaa

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Gly Phe Ser Phe Ser Ala Gly Tyr Trp Ile Cys  
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Gly Phe Ser Phe Ser Ala Gly Tyr Trp Ile Ser  
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Gly Phe Ser Phe Ser Gly Asn Tyr Tyr Met Ser  
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Cys Thr Tyr Ala Gly Arg Ser Gly Ser Thr Tyr Tyr Ala Asn Trp Val  
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Asn Gly

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Asn Ala

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| Cys | Thr | Tyr | Ala | Gly | Arg | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Asn | Trp | Val |
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| Cys | Thr | Tyr | Ala | Gly | Arg | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Asn | Trp | Val |
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| Ser | Thr | Tyr | Ala | Gly | Arg | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Asn | Trp | Val |
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| Ser | Thr | Tyr | Ala | Gly | Arg | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Asn | Trp | Val |
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| Ser | Thr | Tyr | Ala | Gly | Arg | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Asn | Trp | Val |
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Asn Ser

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| Ser | Thr | Tyr | Ala | Gly | Arg | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Asn | Trp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Asn Thr

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| Cys | Ile | Tyr | Ala | Gly | Ser | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Ser | Trp | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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| Ser | Ile | Tyr | Ala | Gly | Ser | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Ser | Trp | Ala |
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Lys Gly

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| Cys | Ile | Tyr | Thr | Gly | Ser | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Ser | Trp | Ala |
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Lys Gly

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<400> 51

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Tyr | Tyr | Asp | Thr | Gly | Ser | Asn | Val | Phe | Phe | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 52

<211> 13

<212> PRT

<213> Secuencia artificial

<220>

<223> CDRL3

<400> 52

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Tyr | Tyr | Asp | Ser | Gly | Ser | Ser | Val | Phe | Phe | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 53

<211> 13

<212> PRT

<213> Secuencia artificial

<220>

<223> CDRL3

<400> 53

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Tyr | Tyr | Asp | Ala | Gly | Ser | Ser | Val | Phe | Phe | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 54

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

<220>  
<223> CDRL3

<400> 54

Gln Ser Tyr Tyr Asp Thr Gly Ser Ser Val Phe Phe Asn  
1 5 10

<210> 55  
<211> 9  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL3

<400> 55

Gln Ser Ala Asp Gly Ser Ser Tyr Ala  
1 5

<210> 56  
<211> 9  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL3

<400> 56

Gln Ser Ala Asp Ser Ser Ser Tyr Ala  
1 5

<210> 57  
<211> 9  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL3

<400> 57

Gln Ser Ala Asp Ala Ser Ser Tyr Ala  
1 5

<210> 58  
<211> 9  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL3

<400> 58

Gln Ser Ala Asp Thr Ser Ser Tyr Ala  
1 5

<210> 59  
<211> 12  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL3

<400> 59

Leu Gly Gly Tyr Tyr Ser Ser Gly Trp Tyr Phe Ala  
1 5 10

<210> 60  
<211> 111  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Región VL de conejo de Ab 4122

<400> 60

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

Gly Thr Val Thr Ile Met Cys Gln Ala Ser Gln Ser Ile Ser Asn Trp  
20 25 30

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

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

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

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

Asn Val Phe Phe Ala Phe Gly Gly Gly Thr Lys Val Val Val Glu  
100 105 110

<210> 61  
<211> 333  
<212> ADN  
<213> Secuencia artificial

<220>  
<223> Región VL de conejo de Ab 4122

<400> 61  
gacattgtga tgacccagac tccagcctcc gtgtctgaac ctgtgggagg cacagtcacc  
60

atcatgtgcc aggccagtca gagcattagc aattggttag cctggtatca acagaaacca  
120

gggcagcctc ccaagctcct gatctaccag gcatccaaac tggcatctgg ggtcccatcg  
180

cggttcaaag gcagtggatc tgggacagag tacactctca ccatcagcga cctggagtgt  
240

gccgatgctg ccacttacta ctgtcaaagc tattatgata gtggtagtaa tgtttttttt  
300

gctttcggcg gagggaccaa ggtggtggtc gaa  
333

<210> 62  
<211> 119  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Región VH de conejo de Ab 4122

<400> 62

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

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

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

Ala Cys Thr Tyr Ala Gly Arg Ser Gly Ser Thr Tyr Tyr Ala Asn Trp  
50 55 60

Val Asn Gly Arg Phe Thr Ile Pro Lys Thr Ser Ser Thr Thr Val Thr  
65 70 75 80

Leu Gln Met Thr Ser Leu Ser Gly Ala Asp Thr Ala Ser Tyr Phe Cys  
85 90 95

Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly Pro Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> 63  
<211> 357  
<212> ADN  
<213> Secuencia artificial

<220>  
<223> Región VH de conejo de Ab 4122

<400> 63  
ctgtcgttgg aggagtccgg gggagacctg gtcaagcctg gggcatccct gacactcacc  
60

tgcacagcct ctggattctc cttcagtgcc ggctattgga tatgttgggt ccgccaggct  
120

ccagggaagg ggctggagtg gatcgcatgc acttatgctg gtcgtagtgg tagcacttac  
180

tacgcgaact ggggtgaatgg ccgattcacc atccccaaaa cctcgtcgac cacggtgact  
240

ctgcaaatga ccagtctgtc aggcgcggac acggccagct atttctgtgc gagaggtaat  
300

gctggtgttg ctgttggtgc cttgtggggc ccaggcaccc tggtcaccgt ctcgagt  
357

<210> 64  
<211> 111  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGKV1-5 de región V de 4122 gL1

<400> 64

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

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

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

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

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

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

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

<210> 65  
<211> 121  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV3-7 de región V de 4122 gH6

<400> 65

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

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

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

Ile Ala Cys Thr Tyr Ala Gly Arg Ser Gly Ser Thr Tyr Tyr Ala Asn  
50 55 60

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

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

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 66  
<211> 121  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV3-7 de región V de 4122 gH4

<400> 66

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

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

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

Ile Ala Ser Thr Tyr Ala Gly Arg Ser Gly Ser Thr Tyr Tyr Ala Asn  
50 55 60

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

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

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 67

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGHV2-70 de región V de 4122 gH3

<400> 67

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

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

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

Ile Ala Cys Thr Tyr Ala Gly Arg Ser Gly Ser Thr Tyr Tyr Ala Asn  
50 55 60

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

Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr  
85 90 95

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 68  
<211> 121  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV2-70 de región V de 4122 gH5

<400> 68

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

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

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

Ile Ala Ser Thr Tyr Ala Gly Arg Ser Gly Ser Thr Tyr Tyr Ala Asn  
50 55 60

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

Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr  
85 90 95

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 69  
<211> 111  
<212> PRT  
<213> Secuencia artificial

<220>

<223> Región VL de conejo de Ab 4129

<400> 69

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

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

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

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

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

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

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

<210> 70

<211> 333

<212> ADN

<213> Secuencia artificial

<220>

<223> Región VL de conejo de Ab 4129

<400> 70

gacattgtga tgacccagac tccagcctcc gtggaggcag ctgtgggagg cacagtcacc  
60

atcaattgcc aagccagtca gagcattagc agttggttat cctggtatca gcagaaacca  
120

gggcagcctc ccaagctcct gatctatggt gcatccaatc tggcatctgg ggtcccatca  
180

cggttcagcg gcagtggatc tgggacacag ttcagtctca ccatcagcga cctggagtgt  
240

gccgatgctg ccacttacta ctgtcaaagc tattatgata gtggtagtag tgtttttttt  
300

aatttcggcg gagggaccaa ggtggtcgtc aaa  
333

<210> 71  
<211> 119  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Región VH de conejo de Ab 4129

<400> 71

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

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

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

Ala Cys Ile Tyr Ala Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser Trp  
50 55 60

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

Leu Gln Met Thr Ser Leu Thr Gly Ala Asp Thr Ala Thr Tyr Phe Cys  
85 90 95

Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly Pro Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> 72  
<211> 357  
<212> ADN  
<213> Secuencia artificial

<220>

<223> Región VH de conejo de Ab 4129

<400> 72

cagtcgttgg aggagtccgg gggagacctg gttaagcctg gggcatccct gacactcacc  
60

tgcacagcct ctggattctc cttcagtgcc ggctattgga tatgttgggt ccgccaggct  
120

ccaggggaagg ggctggagtg gatcgcatgc atttatgctg gtagtagtgg tagcacttac  
180

tacgcgagct gggcgaaagg ccgattcacc atccccaaaa cctcgtcgac cacggtgact  
240

ctgcaaatga ccagtctgac aggcgcggac acggccacct atttctgtgc gagaggtaat  
300

gctggtgttg ctgttggtgc cttgtggggc ccaggcaccc tcgtcaccgt ctcgagt  
357

<210> 73

<211> 111

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGKV1-5 de región V de 4129 gL3

<400> 73

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

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

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Gly | Ala | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Tyr Asp Ser Gly Ser

85

90

95

Ser Val Phe Phe Asn Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 100 105 110

&lt;210&gt; 74

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Secuencia artificial

&lt;220&gt;

&lt;223&gt; Armazón IGHV3-7 de región V de 4129 gH1

&lt;400&gt; 74

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

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

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

Ile Ala Cys Ile Tyr Ala Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
 50 55 60

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

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

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
 100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
 115 120

&lt;210&gt; 75

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Secuencia artificial

<220>

<223> Armazón IGHV3-7 de región V de 4129 gH4

<400> 75

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

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

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

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

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

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

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 76

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGHV2-70 de región V de 4129 gH3

<400> 76

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

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

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

Ile Ala Cys Ile Tyr Ala Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln  
65 70 75 80

Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr  
85 90 95

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 77  
<211> 121  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV2-70 de región V de 4129 gH5

<400> 77

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

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

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

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

Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp Ser Ser Lys Thr Gln  
65 70 75 80

Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr  
85 90 95

Tyr Cys Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly  
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 78  
<211> 107  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Región VL de conejo de Ab 4131

<400> 78

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

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

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

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

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

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

Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys  
100 105

<210> 79  
<211> 321  
<212> ADN

<213> Secuencia artificial

<220>

<223> Región VL de conejo de Ab 4131

<400> 79

gacattgtga tgacccagac tccagcctcc gtgtctgaac ctgtgggagg ctcagtcacc  
60

atcaagtgcc aggccagtca gagcttttac aacctcttag cctggtatca gcagaaacca  
120

gggcagcctc ccaaactcct gatctatgat gcatccgatc tggcatctgg ggtcccatcg  
180

cggttcaaag gcagtggatc tgggactgat ttcactctca ccatcagcga cctggagtgt  
240

gccgatgctg ccgcttacta ctgtcaaagt gctgatggta gtagttacgc tttcggcgga  
300

gggaccgagg tggtcgtcaa a  
321

<210> 80

<211> 120

<212> PRT

<213> Secuencia artificial

<220>

<223> Región VH de conejo de Ab 4131

<400> 80

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Thr | Leu | Thr | Cys | Thr | Ala | Ser | Gly | Val | Ser | Phe | Ser | Ser | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Trp | Ile | Tyr | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Cys | Ile | Tyr | Thr | Gly | Ser | Ser | Gly | Ser | Thr | Tyr | Tyr | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Lys | Gly | Arg | Phe | Thr | Val | Ser | Glu | Thr | Ser | Ser | Thr | Thr | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |

Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe  
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 81  
<211> 360  
<212> ADN  
<213> Secuencia artificial

<220>  
<223> Región VH de conejo de Ab 4131

<400> 81  
caggagcaat tggaggagtc cgggggaggc ctggtcaagc ctgagggatc cctgacactc  
60

acctgcacag cctctggagt ctccttcagt agcagctatt ggatatactg ggtccgccag  
120

gctccagga aggggctgga gtggatcgca tgcatttata ctggtagtag tggtagcact  
180

tactacgca gctgggcgaa aggccgattc accgtctccg aaacctcgtc gaccacgggtg  
240

actctgcaaa tgaccagtct gacagccgcg gacacggcca cctatttctg tgcgagagca  
300

agcgcttgga cctacggcat ggacctctgg ggcccgggca cctcgtcgcac cgtctcgagt  
360

<210> 82  
<211> 107  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGKV1-12 de región V de 4131 gL8

<400> 82

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

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

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

Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val Pro Ser Arg Phe Lys 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 Ser Ala Asp Gly Ser Ser Tyr  
85 90 95

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

<210> 83

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGKV1-12 de región V de 4131 gL3

<400> 83

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

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

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

Tyr Asp Ala Ser Asp Leu Ala 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 Ser Ala Asp Gly Ser Ser Tyr  
85 90 95

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

<210> 84  
<211> 121  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV3-7 de región V de 4131 gH5

<400> 84

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

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

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

Ile Ala Cys Ile Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Val Ser Glu Asp Ser Ala Lys Thr Ser  
65 70 75 80

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

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

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 85  
<211> 121  
<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGHV3-7 de región V de 4131 gH4

<400> 85

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

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

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

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

Trp Ala Lys Gly Arg Phe Thr Val Ser Glu Asp Ser Ala Lys Thr Ser  
65 70 75 80

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

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

Arg Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 86

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGHV4-31 de región V de 4131 gH6

<400> 86

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

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Val Ser Phe Ser Ser Ser

20

25

30

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

Ile Ala Cys Ile Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
 50 55 60

Trp Ala Lys Gly Arg Phe Thr Val Ser Glu Asp Ser Ser Lys Thr Gln  
 65 70 75 80

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

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

Arg Gly Thr Leu Val Thr Val Ser Ser  
 115 120

&lt;210&gt; 87

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Secuencia artificial

&lt;220&gt;

&lt;223&gt; Armazón IGHV4-31 de región V de 4131 gH3

&lt;400&gt; 87

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

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

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

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

Trp Ala Lys Gly Arg Phe Thr Val Ser Glu Asp Ser Ser Lys Thr Gln

|                                      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65                                   |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |
| Val                                  | Ser | Leu | Lys | Leu | Ser | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala | Val | Tyr |
|                                      |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr                                  | Cys | Ala | Arg | Ala | Ser | Ala | Trp | Thr | Tyr | Gly | Met | Asp | Leu | Trp | Gly |
|                                      |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg                                  | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |     |
|                                      |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |
| <210> 88                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| <211> 112                            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| <212> PRT                            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| <213> Secuencia artificial           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| <220>                                |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| <223> Región VL de conejo de Ab 4133 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| <400> 88                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala                                  | Gln | Val | Leu | Thr | Gln | Thr | Pro | Ser | Pro | Val | Ser | Ala | Val | Val | Gly |
| 1                                    |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly                                  | Thr | Val | Ser | Ile | Ser | Cys | Gln | Ala | Ser | Gln | Ser | Val | Tyr | Asn | Asn |
|                                      |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn                                  | Asn | Leu | Ser | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Pro | Pro | Lys | Leu |
|                                      |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu                                  | Ile | Tyr | Asp | Ala | Ser | Lys | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe |
|                                      | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys                                  | Gly | Ser | Gly | Ser | Gly | Thr | Gln | Phe | Thr | Leu | Thr | Ile | Ser | Gly | Val |
| 65                                   |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln                                  | Cys | Asp | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Leu | Gly | Gly | Tyr | Tyr | Ser |
|                                      |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser                                  | Gly | Trp | Tyr | Phe | Ala | Phe | Gly | Gly | Gly | Thr | Lys | Val | Val | Val | Lys |
|                                      |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

<210> 89

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

<220>  
<223> Región VL de conejo de Ab 4133

<400> 89  
gcgcaagtgc tgacccagac tccatctccc gtgtctgcag ttgtgggagg cacagtcagc  
60

atcagttgcc aggccagtca gagtgtttat aataacaaca acttattcctg gtatcagcag  
120

aaaccagggc agcctcccaa gctcttgatc tacgatgcat ccaaattggc atctggggtc  
180

ccatcccggc tcaaaggcag tggatctggg acacagttca ctctcaccat cagcggcgctg  
240

cagtgtgacg atgctgccac ttactactgt ctaggcgggtt attatagtag tggttggtat  
300

tttgctttcg gcggagggac caaggtgggtg gtcaaa  
336

<210> 90  
<211> 122  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Región VH de conejo de Ab 4133

<400> 90

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

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

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

Ile Gly Cys Leu Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Thr Val

65

70

75

80

Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe  
85 90 95

Cys Ala Arg Asp Leu Gly Tyr Glu Ile Asp Gly Tyr Gly Gly Leu Trp  
100 105 110

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

<210> 91

<211> 366

<212> ADN

<213> Secuencia artificial

<220>

<223> Región VH de conejo de Ab 4133

<400> 91

caggagcagc tgggtggagtc cgggggaggc ctgggtccagc ctgagggatc cctgacacta  
60

acctgcacag cttctggatt ctccttcagt ggcaactact acatgtgctg ggtccgccag  
120

gctccaggga aggggctgga gtggatcgga tgcctttata ctggtagtag tggtagcaca  
180

tattacgcga gctgggcgaa aggccgattc accatctcca aaacctcgtc gaccacggtg  
240

actctgcaaa tgaccagtct gacagccgag gacacggcca cctattttctg tgcgagagat  
300

ctaggttatg aaattgatgg ttatgggggc ttgtggggcc agggcaccct cgtcaccgtc  
360

tcgagt

366

<210> 92

<211> 112

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGKV1D-13 de región V de 4133 gL7

<400> 92

Ala Gln Val Leu 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 Ser Val Tyr Asn Asn  
20 25 30

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

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

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

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

Ser Gly Trp Tyr Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 93

<211> 112

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGKV1D-13 de región V de 4133 gL1

<400> 93

Ala Gln Val Leu 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 Ser Val Tyr Asn Asn  
20 25 30

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

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

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

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

Ser Gly Trp Tyr Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 94

<211> 123

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGHV3-21 de región V de 4133 gH1

<400> 94

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

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

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

Ile Gly Cys Leu Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
50 55 60

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

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

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

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

<210> 95  
<211> 123  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV3-21 de región V de 4133 gH4

<400> 95

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

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

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

Ile Gly Ser Leu Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
50 55 60

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

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

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

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

<210> 96  
<211> 123  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV4-4 de región V de 4133 gH3

<400> 96

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

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

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

Ile Gly Cys Leu Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
50 55 60

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

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

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

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

<210> 97

<211> 123

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGHV4-4 de región V de 4133 gH3

<400> 97

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

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

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

Ile Gly Ser Leu Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser  
50 55 60

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

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

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

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

<210> 98  
<211> 10  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH1 Ab 4447

<400> 98

Gly Phe Ser Leu Ser Asn Tyr Ala Val Ser  
1 5 10

<210> 99  
<211> 17  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH2 Ab 4447

<400> 99

Ile Ile Tyr Ile Glu Thr Gly Thr Thr Trp Tyr Ala Asn Trp Ala Lys  
1 5 10 15

Gly

<210> 100  
<211> 17

<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH3 Ab 4447

<400> 100

Glu Pro Tyr Glu Pro Tyr Asp Asp Ser Asn Ile Tyr Tyr Gly Met Asp  
1 5 10 15

Pro

<210> 101  
<211> 13  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL1 Ab4447

<400> 101

Gln Ala Ser Gln Ser Val Val Ser Gly Asn Tyr Leu Ala  
1 5 10

<210> 102  
<211> 7  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL2 Ab4447

<400> 102

Ser Ala Ser Thr Leu Ala Ser  
1 5

<210> 103  
<211> 13  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL3 Ab4447

<400> 103

Leu Gly Glu Phe Ser Cys Ser Ser His Asp Cys Asn Ala  
1 5 10

<210> 104  
<211> 13  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Variante 1 de CDRL3 Ab4447

<400> 104

Leu Gly Glu Phe Ser Ser Ser Ser His Asp Ser Asn Ala  
1 5 10

<210> 105  
<211> 13  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Variante 2 de CDRL3 Ab4447

<400> 105

Leu Gly Glu Phe Ser Cys Ser Ser His Asp Ser Asn Ala  
1 5 10

<210> 106  
<211> 13  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Variante 3 de CDRL3 Ab4447

<400> 106

Leu Gly Glu Phe Ser Ser Ser Ser His Asp Cys Asn Ala  
1 5 10

<210> 107  
<211> 113  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Región VL de conejo de Ab 4447

<400> 107

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

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

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

Leu Ile His Ser Ala Ser Thr Leu Ala Ser Gly Val Ser Ser Arg Phe  
50 55 60

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

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

Ser Ser His Asp Cys Asn Ala Phe Gly Gly Gly Thr Glu Val Val Val  
100 105 110

Lys

<210> 108

<211> 339

<212> ADN

<213> Secuencia artificial

<220>

<223> Región VL de conejo de Ab 4447

<400> 108

gccaagtgc tgaccagac tccgtcccct gtgtctgcac ctgtgggagg cacagtcacc  
60

atcaattgcc aggccagtca gagtgttggt agtggcaatt acctagcctg gcttcagcag  
120

aaaccagggc agcctcccaa gcaactgac cattctgcat ccactctggc atctggggtc  
180

tcatcgcggt tcagcggcag tggatctggg acacaattca ctctcaccat cagcggcgtg  
240

cagtgtgaag atgctgccac ttactactgt ctaggcgaat ttagttgtag tagtcatgat  
300

tgtaatgctt tcggcggagg gaccgaggtg gtggtcaaa  
339

<210> 109

<211> 123

<212> PRT

<213> Secuencia artificial

<220>

<223> Región VH de conejo de Ab 4447

<400> 109

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

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

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

Ile Ile Tyr Ile Glu Thr Gly Thr Thr Trp Tyr Ala Asn Trp Ala Lys  
50 55 60

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

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

Pro Tyr Glu Pro Tyr Asp Asp Ser Asn Ile Tyr Tyr Gly Met Asp Pro  
100 105 110

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

<210> 110

<211> 369

<212> ADN

<213> Secuencia artificial

<220>

<223> Región VH de conejo de Ab 4447

<400> 110

cagtcgctgg aggagtccgg gggtcgcctg gtcacgcctg ggacacccct gacactcacc  
60

tgcaccgtct ctggattctc cctcagtaac tatgcagtaa gctgggtccg ccaggctcca  
120

ggggagggac tggaatggat cgggatcatt tatattgaaa ctggtaccac atggtacgcg  
180

aactgggcga aaggccgatt caccatctcc aaaacctcga ccacggtgga tctgacaatc  
240

accagtccgt caaccgagga cacggccacc tatttctgtg ccagagaacc ttatgaacct  
300

tatgatgata gtaatattta ctacggcatg gaccctggg gccagggcac cctcgtcacc  
360

gtctcgagt  
369

<210> 111

<211> 113

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGKV1D-13 de región V de 4447 gL1

<400> 111

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Val | Leu | 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 | Ser | Val | Val | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | His | Ser | Ala | Ser | Thr | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Ser Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80 |
| Gln | Pro | Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Leu | Gly | Glu | Phe | Ser | Cys |    |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | His | Asp | Cys | Asn | Ala | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Lys

<210> 112  
 <211> 113  
 <212> PRT  
 <213> Secuencia artificial

<220>  
 <223> Armazón IGKV1D-13 de región V de 4447 gL2

<400> 112

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Val | Leu | 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 | Ser | Val | Val | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | His | Ser | Ala | Ser | Thr | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Ser | Gly | Thr | Gln | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Leu | Gly | Glu | Phe | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | His | Asp | Ser | Asn | Ala | Phe | Gly | Gly | Gly | Thr | Lys | Val | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Lys

<210> 113  
<211> 126  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV3-48 de región V de 4447 gH1

<400> 113

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

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

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

Gly Ile Ile Tyr Ile Glu Thr Gly Thr Thr Trp Tyr Ala Asn Trp Ala  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Lys Asp Ser Ala Lys Asn Ser 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 Glu Pro Tyr Glu Pro Tyr Asp Asp Ser Asn Ile Tyr Tyr Gly  
100 105 110

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

<210> 114  
<211> 126  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV4-59 de región V de 4447 gH3

<400> 114

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Tyr  
20 25 30

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

Gly Ile Ile Tyr Ile Glu Thr Gly Thr Thr Trp Tyr Ala Asn Trp Ala  
50 55 60

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

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

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

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

<210> 115  
<211> 10  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH1 Ab 4450

<400> 115

Gly Phe Ser Leu Asn Asn Tyr Val Met Val  
1 5 10

<210> 116  
<211> 16  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH2 Ab 4450

<400> 116

Ile Ile Tyr Val Ser Gly Asn Ala Tyr Tyr Ala Ser Trp Ala Lys Gly  
1 5 10 15

<210> 117

<211> 12

<212> PRT

<213> Secuencia artificial

<220>

<223> CDRH3 Ab 4450

<400> 117

Asp Ala Gly His Ser Asp Val Asp Val Leu Asp Ile  
1 5 10

<210> 118

<211> 13

<212> PRT

<213> Secuencia artificial

<220>

<223> CDRL1 Ab 4450

<400> 118

Gln Ser Ser Gln Ser Ile Tyr Asn Asn Asn Asp Leu Ala  
1 5 10

<210> 119

<211> 7

<212> PRT

<213> Secuencia artificial

<220>

<223> CDRL2 Ab 4450

<400> 119

Glu Ala Ser Lys Leu Ala Ser  
1 5

<210> 120

<211> 11

<212> PRT

<213> Secuencia artificial

<220>  
<223> CDRL3 Ab 4450

<400> 120

Gln Gly Gly Gly Ser Gly Gly Asp Gly Ile Ala  
1 5 10

<210> 121  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Variante 1 de CDRL3 de Ab 4450

<400> 121

Gln Gly Gly Gly Ser Gly Gly Glu Gly Ile Ala  
1 5 10

<210> 122  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Variante 2 de CDRL3 de Ab 4450

<400> 122

Gln Gly Gly Gly Ser Gly Gly Asp Ala Ile Ala  
1 5 10

<210> 123  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Variante 3 de CDRL3 de Ab 4450

<400> 123

Gln Gly Gly Gly Ser Gly Gly Asp Ser Ile Ala  
1 5 10

<210> 124  
<211> 111  
<212> PRT

<213> Secuencia artificial

<220>

<223> Región VL de conejo de Ab 4450

<400> 124

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

Gly Thr Val Thr Ile Asn Cys Gln Ser Ser Gln Ser Ile Tyr Asn Asn  
20 25 30

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

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

Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Gly Val  
65 70 75 80

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

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

<210> 125

<211> 333

<212> ADN

<213> Secuencia artificial

<220>

<223> Región VL de conejo de Ab 4450

<400> 125

gccattgata tgaccagac tccatcccc gtgtctgcag ctgtgggagg cacagtcacc  
60

atcaattgcc agtccagtca gagtatttat aataataatg acttagcctg gtatcagcag  
120

aaaccagggc agcctcccaa gctcctgatac tacgaagcat ccaaactggc atctggggtc  
180

ccatcgcggt tcaaaggcag tggatctggg acacagttca ctctcaccat cagtggcgtg  
240

cagtgtgatg atgctgccac ttactactgt cagggcgggtg gtagtggtgg tgatggcatt  
300

gctttcggcg gagggaccaa ggtggtcgtc gaa  
333

<210> 126

<211> 117

<212> PRT

<213> Secuencia artificial

<220>

<223> Región VH de conejo de Ab 4450

<400> 126

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

Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Tyr Val  
20 25 30

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

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

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

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

Gly His Ser Asp Val Asp Val Leu Asp Ile Trp Gly Pro Gly Thr Leu  
100 105 110

Val Thr Val Ser Ser  
115

<210> 127

<211> 351

<212> ADN  
 <213> Secuencia artificial  
  
 <220>  
 <223> Región VH de conejo de Ab 4450  
  
 <400> 127  
 cagtcggtgg aggagtccgg gggtcgctg gtcacgcctg gggcaccctt gacactcacc  
 60  
  
 tgcacagtct ctggattctc cctcaataac tatgtaatgg tctgggtccg ccaggctcca  
 120  
  
 gggaaggggc tggaatggat cggaatcatt tatgttagtg gtaatgcata ctacgcgagc  
 180  
  
 tgggcaaaag gccgattcac catctccaga acctcgacca cgggtggatct gaaagtgacc  
 240  
  
 agtctgacaa ccgaggacac ggccacctat ttctgtgcca gagatgctgg tcatagtgat  
 300  
  
 gtcgatgttt tggatatattg gggcccgggc accctcgta ccgtctcgag t  
 351

<210> 128  
 <211> 111  
 <212> PRT  
 <213> Secuencia artificial

<220>  
 <223> Armazón IGKV1-6 de región V de 4450 gL1

<400> 128

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ile | Asp | 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 | Ser | Ser | Gln | Ser | Ile | Tyr | Asn | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asp | Leu | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Tyr | Glu | Ala | Ser | Lys | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Ser | Gly | Thr | Gln | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

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

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

<210> 129

<211> 120

<212> PRT

<213> Secuencia artificial

<220>

<223> Armazón IGHV3-66 de región V de 4450 gH1

<400> 129

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

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

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

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

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

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

Arg Asp Ala Gly His Ser Asp Val Asp Val Leu Asp Ile Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 130

<211> 120

<212> PRT  
<213> Secuencia artificial

<220>  
<223> Armazón IGHV4-59 de región V de 4450 gH3

<400> 130

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Tyr  
20 25 30

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

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

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

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

Arg Asp Ala Gly His Ser Asp Val Asp Val Leu Asp Ile Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 131  
<211> 10  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH1 dAbH1

<400> 131

Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn  
1 5 10

<210> 132  
<211> 16  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH2 dAbH1

<400> 132

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Trp | Ala | Ser | Gly | Thr | Thr | Phe | Tyr | Ala | Thr | Trp | Ala | Lys | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 133  
<211> 13  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRH3 dAbH1

<400> 133

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Pro | Gly | Tyr | Ser | Thr | Ala | Pro | Tyr | Phe | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

<210> 134  
<211> 12  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL1 dAbL1

<400> 134

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Ser | Pro | Ser | Val | Trp | Ser | Asn | Phe | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |

<210> 135  
<211> 7  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL2 dAbL1

<400> 135

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Ser | Lys | Leu | Thr | Ser |
| 1   |     |     |     | 5   |     |     |

<210> 136  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CDRL3 dAbL1

<400> 136

Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr  
1 5 10

<210> 137  
<211> 121  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Dominio variable de cadena pesada de anticuerpo anti-albúmina (no  
ds)

<400> 137

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 138

<211> 121

<212> PRT

<213> Secuencia artificial

<220>

<223> Dominio variable de cadena pesada de anticuerpo anti-albúmina (ds)

<400> 138

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 139

<211> 110

<212> PRT

<213> Secuencia artificial

<220>

<223> Dominio variable de cadena ligera de anticuerpo anti-albúmina (no ds)

<400> 139

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn  
20 25 30

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

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

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

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

Ser Asp Thr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105 110

<210> 140

<211> 112

<212> PRT

<213> Secuencia artificial

<220>

<223> Dominio variable de cadena ligera de anticuerpo anti-albúmina (ds)

<400> 140

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

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn  
20 25 30

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

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

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

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

Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr  
100 105 110

<210> 141  
<211> 1304  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> CD45 humano

<400> 141

Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp  
1 5 10 15

Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly  
20 25 30

Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp Pro Leu  
35 40 45

Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu Arg Glu  
50 55 60

Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn Thr Ser  
65 70 75 80

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

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

Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser  
115 120 125

Ala Ala Asn Ala Lys Leu Asn Pro Thr Pro Gly Ser Asn Ala Ile Ser  
130 135 140

Asp Val Pro Gly Glu Arg Ser Thr Ala Ser Thr Phe Pro Thr Asp Pro  
145 150 155 160

Val Ser Pro Leu Thr Thr Thr Leu Ser Leu Ala His His Ser Ser Ala  
165 170 175

Ala Leu Pro Ala Arg Thr Ser Asn Thr Thr Ile Thr Ala Asn Thr Ser  
180 185 190

Asp Ala Tyr Leu Asn Ala Ser Glu Thr Thr Thr Leu Ser Pro Ser Gly  
195 200 205

Ser Ala Val Ile Ser Thr Thr Thr Ile Ala Thr Thr Pro Ser Lys Pro  
210 215 220

Thr Cys Asp Glu Lys Tyr Ala Asn Ile Thr Val Asp Tyr Leu Tyr Asn  
225 230 235 240

Lys Glu Thr Lys Leu Phe Thr Ala Lys Leu Asn Val Asn Glu Asn Val  
245 250 255

Glu Cys Gly Asn Asn Thr Cys Thr Asn Asn Glu Val His Asn Leu Thr  
260 265 270

Glu Cys Lys Asn Ala Ser Val Ser Ile Ser His Asn Ser Cys Thr Ala  
275 280 285

Pro Asp Lys Thr Leu Ile Leu Asp Val Pro Pro Gly Val Glu Lys Phe  
290 295 300

Gln Leu His Asp Cys Thr Gln Val Glu Lys Ala Asp Thr Thr Ile Cys  
305 310 315 320

Leu Lys Trp Lys Asn Ile Glu Thr Phe Thr Cys Asp Thr Gln Asn Ile

325

330

335

Thr Tyr Arg Phe Gln Cys Gly Asn Met Ile Phe Asp Asn Lys Glu Ile  
 340 345 350

Lys Leu Glu Asn Leu Glu Pro Glu His Glu Tyr Lys Cys Asp Ser Glu  
 355 360 365

Ile Leu Tyr Asn Asn His Lys Phe Thr Asn Ala Ser Lys Ile Ile Lys  
 370 375 380

Thr Asp Phe Gly Ser Pro Gly Glu Pro Gln Ile Ile Phe Cys Arg Ser  
 385 390 395 400

Glu Ala Ala His Gln Gly Val Ile Thr Trp Asn Pro Pro Gln Arg Ser  
 405 410 415

Phe His Asn Phe Thr Leu Cys Tyr Ile Lys Glu Thr Glu Lys Asp Cys  
 420 425 430

Leu Asn Leu Asp Lys Asn Leu Ile Lys Tyr Asp Leu Gln Asn Leu Lys  
 435 440 445

Pro Tyr Thr Lys Tyr Val Leu Ser Leu His Ala Tyr Ile Ile Ala Lys  
 450 455 460

Val Gln Arg Asn Gly Ser Ala Ala Met Cys His Phe Thr Thr Lys Ser  
 465 470 475 480

Ala Pro Pro Ser Gln Val Trp Asn Met Thr Val Ser Met Thr Ser Asp  
 485 490 495

Asn Ser Met His Val Lys Cys Arg Pro Pro Arg Asp Arg Asn Gly Pro  
 500 505 510

His Glu Arg Tyr His Leu Glu Val Glu Ala Gly Asn Thr Leu Val Arg  
 515 520 525

Asn Glu Ser His Lys Asn Cys Asp Phe Arg Val Lys Asp Leu Gln Tyr  
 530 535 540

Ser Thr Asp Tyr Thr Phe Lys Ala Tyr Phe His Asn Gly Asp Tyr Pro  
545 550 555 560

Gly Glu Pro Phe Ile Leu His His Ser Thr Ser Tyr Asn Ser Lys Ala  
565 570 575

Leu Ile Ala Phe Leu Ala Phe Leu Ile Ile Val Thr Ser Ile Ala Leu  
580 585 590

Leu Val Val Leu Tyr Lys Ile Tyr Asp Leu His Lys Lys Arg Ser Cys  
595 600 605

Asn Leu Asp Glu Gln Gln Glu Leu Val Glu Arg Asp Asp Glu Lys Gln  
610 615 620

Leu Met Asn Val Glu Pro Ile His Ala Asp Ile Leu Leu Glu Thr Tyr  
625 630 635 640

Lys Arg Lys Ile Ala Asp Glu Gly Arg Leu Phe Leu Ala Glu Phe Gln  
645 650 655

Ser Ile Pro Arg Val Phe Ser Lys Phe Pro Ile Lys Glu Ala Arg Lys  
660 665 670

Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu Pro Tyr Asp  
675 680 685

Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala Gly Ser Asn  
690 695 700

Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro Arg Lys Tyr  
705 710 715 720

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

Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val Thr Arg Cys  
740 745 750

Glu Glu Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro Ser Met Glu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 755 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Glu | Gly | Thr | Arg | Ala | Phe | Gly | Asp | Val | Val | Val | Lys | Ile | Asn | Gln | His |  |  |
| 770 |     |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |  |
| Lys | Arg | Cys | Pro | Asp | Tyr | Ile | Ile | Gln | Lys | Leu | Asn | Ile | Val | Asn | Lys |  |  |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     | 800 |     |  |  |
| Lys | Glu | Lys | Ala | Thr | Gly | Arg | Glu | Val | Thr | His | Ile | Gln | Phe | Thr | Ser |  |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |  |
| Trp | Pro | Asp | His | Gly | Val | Pro | Glu | Asp | Pro | His | Leu | Leu | Leu | Lys | Leu |  |  |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |  |  |
| Arg | Arg | Arg | Val | Asn | Ala | Phe | Ser | Asn | Phe | Phe | Ser | Gly | Pro | Ile | Val |  |  |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |  |  |
| Val | His | Cys | Ser | Ala | Gly | Val | Gly | Arg | Thr | Gly | Thr | Tyr | Ile | Gly | Ile |  |  |
| 850 |     |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |  |  |
| Asp | Ala | Met | Leu | Glu | Gly | Leu | Glu | Ala | Glu | Asn | Lys | Val | Asp | Val | Tyr |  |  |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |  |  |
| Gly | Tyr | Val | Val | Lys | Leu | Arg | Arg | Gln | Arg | Cys | Leu | Met | Val | Gln | Val |  |  |
|     |     |     |     | 885 |     |     |     |     | 890 |     |     |     |     | 895 |     |  |  |
| Glu | Ala | Gln | Tyr | Ile | Leu | Ile | His | Gln | Ala | Leu | Val | Glu | Tyr | Asn | Gln |  |  |
|     |     |     | 900 |     |     |     |     | 905 |     |     |     |     | 910 |     |     |  |  |
| Phe | Gly | Glu | Thr | Glu | Val | Asn | Leu | Ser | Glu | Leu | His | Pro | Tyr | Leu | His |  |  |
|     |     | 915 |     |     |     |     | 920 |     |     |     |     | 925 |     |     |     |  |  |
| Asn | Met | Lys | Lys | Arg | Asp | Pro | Pro | Ser | Glu | Pro | Ser | Pro | Leu | Glu | Ala |  |  |
|     | 930 |     |     |     |     | 935 |     |     |     |     | 940 |     |     |     |     |  |  |
| Glu | Phe | Gln | Arg | Leu | Pro | Ser | Tyr | Arg | Ser | Trp | Arg | Thr | Gln | His | Ile |  |  |
| 945 |     |     |     |     | 950 |     |     |     |     | 955 |     |     |     |     | 960 |  |  |
| Gly | Asn | Gln | Glu | Glu | Asn | Lys | Ser | Lys | Asn | Arg | Asn | Ser | Asn | Val | Ile |  |  |
|     |     |     |     | 965 |     |     |     |     | 970 |     |     |     |     | 975 |     |  |  |

Pro Tyr Asp Tyr Asn Arg Val Pro Leu Lys His Glu Leu Glu Met Ser  
980 985 990

Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp Asp Ser Asp  
995 1000 1005

Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser  
1010 1015 1020

Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu Lys  
1025 1030 1035

Glu Thr Ile Gly Asp Phe Trp Gln Met Ile Phe Gln Arg Lys Val  
1040 1045 1050

Lys Val Ile Val Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu  
1055 1060 1065

Ile Cys Ala Gln Tyr Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp  
1070 1075 1080

Ile Glu Val Asp Leu Lys Asp Thr Asp Lys Ser Ser Thr Tyr Thr  
1085 1090 1095

Leu Arg Val Phe Glu Leu Arg His Ser Lys Arg Lys Asp Ser Arg  
1100 1105 1110

Thr Val Tyr Gln Tyr Gln Tyr Thr Asn Trp Ser Val Glu Gln Leu  
1115 1120 1125

Pro Ala Glu Pro Lys Glu Leu Ile Ser Met Ile Gln Val Val Lys  
1130 1135 1140

Gln Lys Leu Pro Gln Lys Asn Ser Ser Glu Gly Asn Lys His His  
1145 1150 1155

Lys Ser Thr Pro Leu Leu Ile His Cys Arg Asp Gly Ser Gln Gln  
1160 1165 1170

Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu Leu Glu Ser Ala Glu

|                                                                 |    |      |    |      |
|-----------------------------------------------------------------|----|------|----|------|
| 1175                                                            |    | 1180 |    | 1185 |
| Thr Glu Glu Val Val Asp Ile Phe Gln Val Val Lys Ala Leu Arg     |    |      |    |      |
| 1190                                                            |    | 1195 |    | 1200 |
| Lys Ala Arg Pro Gly Met Val Ser Thr Phe Glu Gln Tyr Gln Phe     |    |      |    |      |
| 1205                                                            |    | 1210 |    | 1215 |
| Leu Tyr Asp Val Ile Ala Ser Thr Tyr Pro Ala Gln Asn Gly Gln     |    |      |    |      |
| 1220                                                            |    | 1225 |    | 1230 |
| Val Lys Lys Asn Asn His Gln Glu Asp Lys Ile Glu Phe Asp Asn     |    |      |    |      |
| 1235                                                            |    | 1240 |    | 1245 |
| Glu Val Asp Lys Val Lys Gln Asp Ala Asn Cys Val Asn Pro Leu     |    |      |    |      |
| 1250                                                            |    | 1255 |    | 1260 |
| Gly Ala Pro Glu Lys Leu Pro Glu Ala Lys Glu Gln Ala Glu Gly     |    |      |    |      |
| 1265                                                            |    | 1270 |    | 1275 |
| Ser Glu Pro Thr Ser Gly Thr Glu Gly Pro Glu His Ser Val Asn     |    |      |    |      |
| 1280                                                            |    | 1285 |    | 1290 |
| Gly Pro Ala Ser Pro Ala Leu Asn Gln Gly Ser                     |    |      |    |      |
| 1295                                                            |    | 1300 |    |      |
| <210> 142                                                       |    |      |    |      |
| <211> 226                                                       |    |      |    |      |
| <212> PRT                                                       |    |      |    |      |
| <213> Secuencia artificial                                      |    |      |    |      |
| <220>                                                           |    |      |    |      |
| <223> CD79a humano                                              |    |      |    |      |
| <400> 142                                                       |    |      |    |      |
| Met Pro Gly Gly Pro Gly Val Leu Gln Ala Leu Pro Ala Thr Ile Phe |    |      |    |      |
| 1                                                               |    | 5    | 10 | 15   |
| Leu Leu Phe Leu Leu Ser Ala Val Tyr Leu Gly Pro Gly Cys Gln Ala |    |      |    |      |
|                                                                 | 20 |      | 25 | 30   |
| Leu Trp Met His Lys Val Pro Ala Ser Leu Met Val Ser Leu Gly Glu |    |      |    |      |

[illegible]

<213> Secuencia artificial

<220>

<223> CD79b humano

<400> 143

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

Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg Ser Glu  
20 25 30

Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp Gln  
35 40 45

Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His  
50 55 60

Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys Gln  
65 70 75 80

Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met  
85 90 95

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

Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn Asn  
115 120 125

Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly  
130 135 140

Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly  
145 150 155 160

Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro  
165 170 175

Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu Glu  
180 185 190

Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu  
195 200 205

Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu  
210 215 220

His Pro Gly Gln Glu  
225

<210> 144  
<211> 44  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia GCN4 (7P14P)

<400> 144

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

Leu Leu Pro Lys Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys  
20 25 30

Lys Leu Val Gly Glu Arg His His His His His  
35 40

<210> 145  
<211> 132  
<212> ADN  
<213> Secuencia artificial

<220>  
<223> Secuencia GCN4 (7P14P)

<400> 145

gctagcggag gcggaagaat gaaacaactt gaaccaaggttgaagaatt gcttccgaaa  
60

aattatcact tggaaaatga ggttgccaga ttaaagaaat tagttggcga acgcatcac  
120

catcaccatc ac  
132

<210> 146  
<211> 262  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de ds scFv 52SR4

<400> 146

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

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

Asn Tyr Ala Ser Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
35 40 45

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

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

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

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly Gly Gly  
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
115 120 125

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

Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Leu Leu Thr  
145 150 155 160

Asp Tyr Gly Val Asn Trp Val Arg Gln Ser Pro Gly Lys Cys Leu Glu  
165 170 175

Trp Leu Gly Val Ile Trp Gly Asp Gly Ile Thr Asp Tyr Asn Ser Ala  
180 185 190

Leu Lys Ser Arg Leu Ser Val Thr Lys Asp Asn Ser Lys Ser Gln Val  
195 200 205

Phe Leu Lys Met Asn Ser Leu Gln Ser Gly Asp Ser Ala Arg Tyr Tyr  
210 215 220

Cys Val Thr Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
225 230 235 240

Val Ser Ser Ala Ala Ala His His His His His His Glu Gln Lys Leu  
245 250 255

Ile Ser Glu Glu Asp Leu  
260

<210> 147  
<211> 792  
<212> ADN  
<213> Secuencia artificial

<220>  
<223> Secuencia de ds scFv 52SR4

<400> 147  
gatgcggtgg tgaccagga aagcgcgctg accagcagcc cgggcgaaac cgtgaccctg  
60

acctgccgca gcagcaccgg cgcggtgacc accagcaact atgcgagctg ggtgcaggaa  
120

aaaccggatc atctgtttac cggcctgatt ggcggcacca acaaccgcgc gccgggctg  
180

ccggcgcgct ttagcggcag cctgattggc gataaagcgg cgctgaccat taccggcgcg  
240

cagaccgaag atgaagcgat ttatttttgc gtgctgtggt atagcgacca ttgggtgttt  
300

ggctgcggca ccaaactgac cgtgctgggt ggaggcgggt gctcaggcgg aggtggctca  
360

ggcgggtggcg ggtctggcgg cggcggcagc gatgtgcagc tgcagcagag cggcccgggc  
420

ctggtggcgc cgagccagag cctgagcatt acctgcaccg tgagcggcctt tctcctgacc  
480

gattatggcg tgaactgggt gcgccagagc ccgggcaaatt gcctggaatg gctgggcgtg  
540

atttggggcg atggcattac cgattataac agcgcgctga aaagccgcct gagcgtgacc  
600

aaagataaca gcaaaagcca ggtgtttctg aaaatgaaca gcctgcagag cggcgatagc  
660

gcgcgctatt attgcgtgac cggcctgttt gattattggg gccagggcac caccctgacc  
720

gtgagcagcg cggccgcca tcaccatcac catcacgaac agaaactgat tagcgaagaa  
780

gatctgtaat ag  
792

<210> 148  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador

<400> 148

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

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

<220>  
<223> Secuencia enlazadora de bisagra

<400> 149

Asp Lys Thr His Thr Cys Ala Ala  
1 5

<210> 150  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>

<223> Secuencia enlazadora de bisagra

<400> 150

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
1 5 10

<210> 151

<211> 18

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia enlazadora de bisagra

<400> 151

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Thr Cys Pro Pro Cys  
1 5 10 15

Pro Ala

<210> 152

<211> 25

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia enlazadora de bisagra

<400> 152

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Thr Cys Pro Pro Cys  
1 5 10 15

Pro Ala Thr Cys Pro Pro Cys Pro Ala  
20 25

<210> 153

<211> 30

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia enlazadora de bisagra

<400> 153

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Gly | Lys | Pro | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Asn | Ser | Leu | Val | Met | Ser | Asp | Thr | Ala | Gly | Thr | Cys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

<210> 154

<211> 31

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia enlazadora de bisagra

<400> 154

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Gly | Lys | Pro | Thr | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Val | Ser | Val | Val | Met | Ala | Glu | Val | Asp | Gly | Thr | Cys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |

<210> 155

<211> 15

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia enlazadora de bisagra

<400> 155

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Thr | His | Thr | Cys | Cys | Val | Glu | Cys | Pro | Pro | Cys | Pro | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |

<210> 156

<211> 26

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia enlazadora de bisagra

<400> 156

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Lys | Thr | His | Thr | Cys | Pro | Arg | Cys | Pro | Glu | Pro | Lys | Ser | Cys | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala  
20 25

<210> 157  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia enlazadora de bisagra

<400> 157

Asp Lys Thr His Thr Cys Pro Ser Cys Pro Ala  
1 5 10

<210> 158  
<211> 7  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 158

Ser Gly Gly Gly Gly Ser Glu  
1 5

<210> 159  
<211> 6  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 159

Asp Lys Thr His Thr Ser  
1 5

<210> 160  
<211> 6  
<212> PRT  
<213> Secuencia artificial

<220>

<223> Secuencia de enlazador flexible

<400> 160

Ser Gly Gly Gly Gly Ser  
1 5

<210> 161

<211> 11

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia de enlazador flexible

<400> 161

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

<210> 162

<211> 16

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia de enlazador flexible

<400> 162

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

<210> 163

<211> 21

<212> PRT

<213> Secuencia artificial

<220>

<223> Secuencia de enlazador flexible

<400> 163

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

Gly Gly Gly Gly Ser  
20

<210> 164  
<211> 26  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 164

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
20 25

<210> 165  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 165

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

<210> 166  
<211> 16  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<220>  
<221> característica\_misc  
<222> (7)..(7)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 166

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser  
1 5 10 15

<210> 167  
<211> 21

<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<220>  
<221> característica\_misc  
<222> (7)..(7)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>  
<221> característica\_misc  
<222> (12)..(12)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 167

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser  
1 5 10 15

Gly Ala Ser Ala Ser  
20

<210> 168  
<211> 26  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<220>  
<221> característica\_misc  
<222> (7)..(7)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>  
<221> característica\_misc  
<222> (12)..(12)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>  
<221> característica\_misc  
<222> (17)..(17)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 168

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser

1 5 10 15

Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser  
20 25

<210> 169  
<211> 31  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<220>  
<221> característica\_misc  
<222> (7)..(7)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>  
<221> característica\_misc  
<222> (12)..(12)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>  
<221> característica\_misc  
<222> (17)..(17)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>  
<221> característica\_misc  
<222> (22)..(22)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 169

Ala Ala Ala Gly Ser Gly Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser  
1 5 10 15

Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser  
20 25 30

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

<220>  
<223> Secuencia de enlazador flexible

<220>  
<221> característica\_misc  
<222> (7)..(7)  
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 170

Ala Ala Ala Gly Ser Gly Xaa Ser Gly Ala Ser Ala Ser  
1 5 10

<210> 171  
<211> 28  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 171

Pro Gly Gly Asn Arg Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr  
1 5 10 15

Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr  
20 25

<210> 172  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 172

Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr  
1 5 10

<210> 173  
<211> 6  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 173

Ala Thr Thr Thr Gly Ser  
1 5

<210> 174  
<400> 174  
000

<210> 175  
<211> 21  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 175

Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Ser Pro Pro Ser Lys Glu  
1 5 10 15

Ser His Lys Ser Pro  
20

<210> 176  
<211> 15  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 176

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

<210> 177  
<211> 15  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 177

Gly Gly Gly Gly Ile Ala Pro Ser Met Val Gly Gly Gly Gly Ser  
1 5 10 15

<210> 178  
<211> 15  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 178

Gly Gly Gly Gly Lys Val Glu Gly Ala Gly Gly Gly Gly Gly Ser  
1 5 10 15

<210> 179  
<211> 15  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 179

Gly Gly Gly Gly Ser Met Lys Ser His Asp Gly Gly Gly Gly Ser  
1 5 10 15

<210> 180  
<211> 15  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 180

Gly Gly Gly Gly Asn Leu Ile Thr Ile Val Gly Gly Gly Gly Ser  
1 5 10 15

<210> 181  
<211> 15  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 181

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

<210> 182  
<211> 12  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 182

Gly Gly Glu Lys Ser Ile Pro Gly Gly Gly Gly Ser  
1 5 10

<210> 183  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 183

Arg Pro Leu Ser Tyr Arg Pro Pro Phe Pro Phe Gly Phe Pro Ser Val  
1 5 10 15

Arg Pro

<210> 184  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 184

Tyr Pro Arg Ser Ile Tyr Ile Arg Arg Arg His Pro Ser Pro Ser Leu  
1 5 10 15

Thr Thr

<210> 185  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 185

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Ser | His | Leu | Ser | His | Ile | Leu | Pro | Ser | Phe | Gly | Leu | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Phe Asn

<210> 186  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 186

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Val | Ser | Pro | Phe | Thr | Phe | Pro | Arg | Leu | Ser | Asn | Ser | Trp | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Pro Ala

<210> 187  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 187

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Ala | His | Phe | Pro | Arg | Ser | Ile | Pro | Arg | Pro | Gly | Pro | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Arg Thr

<210> 188  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 188

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Gly | Pro | Ser | Ala | Pro | Ser | His | Arg | Ser | Leu | Pro | Ser | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Phe Gly

<210> 189  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 189

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Asn | Ser | Ile | His | Phe | Leu | His | Pro | Leu | Leu | Val | Ala | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Gly Ala

<210> 190  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 190

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ser | Leu | Ser | Gly | Val | Leu | Gln | Val | Arg | Tyr | Leu | Ser | Pro | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Asp Leu

<210> 191  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 191

Ser Pro Gln Tyr Pro Ser Pro Leu Thr Leu Thr Leu Pro Pro His Pro  
1 5 10 15

Ser Leu

<210> 192  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 192

Asn Pro Ser Leu Asn Pro Pro Ser Tyr Leu His Arg Ala Pro Ser Arg  
1 5 10 15

Ile Ser

<210> 193  
<211> 17  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 193

Leu Pro Trp Arg Thr Ser Leu Leu Pro Ser Leu Pro Leu Arg Arg Arg  
1 5 10 15

Pro

<210> 194  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 194

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Leu | Phe | Ala | Lys | Gly | Pro | Val | Gly | Leu | Leu | Ser | Arg | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Pro Pro

<210> 195  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 195

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Pro | Ala | Pro | Val | Val | Ser | Leu | Arg | Ser | Ala | His | Ala | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Pro Tyr

<210> 196  
<211> 17  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 196

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Pro | Thr | Pro | Pro | Arg | Val | Arg | Ser | Tyr | Thr | Cys | Cys | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Pro

<210> 197  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 197

Pro Asn Val Ala His Val Leu Pro Leu Leu Thr Val Pro Trp Asp Asn  
1 5 10 15

Leu Arg

<210> 198  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador flexible

<400> 198

Cys Asn Pro Leu Leu Pro Leu Cys Ala Arg Ser Pro Ala Val Arg Thr  
1 5 10 15

Phe Pro

<210> 199  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador

<400> 199

Gly Ala Pro Ala Pro Ala Ala Pro Ala Pro Ala  
1 5 10

<210> 200  
<211> 4  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador

<400> 200

Pro Pro Pro Pro  
1

<210> 201  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 201

Asp Leu Cys Leu Arg Asp Trp Gly Cys Leu Trp  
1 5 10

<210> 202  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 202

Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp  
1 5 10

<210> 203  
<211> 15  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 203

Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Gly Asp  
1 5 10 15

<210> 204  
<211> 20

<212> PRT  
<213> Secuencia artificial  
  
<220>  
<223> Secuencias de enlazador  
  
<400> 204

Gln Arg Leu Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp  
1 5 10 15

Glu Asp Asp Glu  
20

<210> 205  
<211> 20  
<212> PRT  
<213> Secuencia artificial  
  
<220>  
<223> Secuencias de enlazador  
  
<400> 205

Gln Gly Leu Ile Gly Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp  
1 5 10 15

Gly Arg Ser Val  
20

<210> 206  
<211> 21  
<212> PRT  
<213> Secuencia artificial  
  
<220>  
<223> Secuencias de enlazador  
  
<400> 206

Gln Gly Leu Ile Gly Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp  
1 5 10 15

Gly Arg Ser Val Lys  
20

<210> 207  
<211> 15

<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 207

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Ile | Cys | Leu | Pro | Arg | Trp | Gly | Cys | Leu | Trp | Glu | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

<210> 208  
<211> 18  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 208

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Met | Glu | Asp | Ile | Cys | Leu | Pro | Arg | Trp | Gly | Cys | Leu | Trp | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Asp Asp

<210> 209  
<211> 16  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 209

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asp | Ile | Cys | Leu | Pro | Arg | Trp | Gly | Cys | Leu | Trp | Glu | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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

<220>  
<223> Secuencias de enlazador

<400> 210

Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu Asp  
1 5 10 15

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

<220>  
<223> Secuencias de enlazador

<400> 211

Arg Leu Met Glu Asp Ile Cys Leu Ala Arg Trp Gly Cys Leu Trp Glu  
1 5 10 15

Asp Asp

<210> 212  
<211> 20  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 212

Glu Val Arg Ser Phe Cys Thr Arg Trp Pro Ala Glu Lys Ser Cys Lys  
1 5 10 15

Pro Leu Arg Gly  
20

<210> 213  
<211> 20  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 213

Arg Ala Pro Glu Ser Phe Val Cys Tyr Trp Glu Thr Ile Cys Phe Glu  
1 5 10 15

Arg Ser Glu Gln  
20

<210> 214  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencias de enlazador

<400> 214

Glu Met Cys Tyr Phe Pro Gly Ile Cys Trp Met  
1 5 10

<210> 215  
<211> 11  
<212> PRT  
<213> Secuencia artificial

<220>  
<223> Secuencia de enlazador

<400> 215

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