LISTADO DE SECUENCIAS

<110> F. Hoffmann-La Roche AG

<120> Anticuerpos biespecíficos específicos para un receptor de tnf coestimulador

<130> P33116-WO

<150> EP15188095.2
<151> 2015-10-02

<150> EP16170363.2
<151> 2016-05-19

<160> 347

<170> PatentIn versión 3.5

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Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
        35                  40                  45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
    50                  55                  60

Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
65                  70                  75                  80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
                85                  90                  95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
            100                 105                 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
        115                 120                 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
    130                 135                 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
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Ser Tyr Ala Ile Ser
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Ser Tyr Ala Met Ser
1 5

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

Gly

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Gly

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Glu Tyr Gly Trp Met Asp Tyr
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Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr
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Glu Tyr Gly Ser Met Asp Tyr
1 5

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<400> 9

Val Asn Tyr Pro Tyr Ser Tyr Trp Gly Asp Phe Asp Tyr
1 5 10

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Asp Val Gly Ala Phe Asp Tyr
1 5

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Asp Val Gly Pro Phe Asp Tyr
1 5

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

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Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
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Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 15
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Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1 5 10

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Asp Ala Ser Ser Leu Glu Ser
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Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 18
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Gly Lys Asn Asn Arg Pro Ser
1 5

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Gln Gln Tyr Leu Thr Tyr Ser Arg Phe Thr
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Gln Gln Tyr Ser Ser Gln Pro Tyr Thr
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Gln Gln Tyr Ile Ser Tyr Ser Met Leu Thr
1 5 10

<210> 22
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Gln Gln Tyr Gln Ala Phe Ser Leu Thr
1 5

<210> 23
<211> 9
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<213> Secuencia artificial

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Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 24
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<213> Secuencia artificial

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Asn Ser Arg Val Met Pro His Asn Arg Val
1 5 10

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<213> Secuencia artificial

<220>
<223> OX40(8H9) VH

<400> 25

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

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

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

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

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

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

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

Thr Val Ser Ser
        115

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<223> OX40(8H9) VL

<400> 26

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20   25   30

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

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

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

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

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

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<223> OX40(49B4) VH

<400> 27

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

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

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

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

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

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

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 28
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<400> 28

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

<210> 29
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<223> OX40(1G4) VH

<400> 29

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

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

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

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

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

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

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

Thr Val Ser Ser
        115
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<223> OX40(1G4) VL

<400> 30

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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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

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

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
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Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

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

<220>
<223> OX40(20B7) VH

<400> 31

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

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

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

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

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

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

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

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

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<223> OX40(20B7) VL

<400> 32

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

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

<220>
<223> OX40(CLC-563) VH

<400> 33

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

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

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

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

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

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

```
Ala Leu Asp Val Gly Ala Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
            100                 105                 110


Thr Val Ser Ser
        115


<210>  34
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<213>  Secuencia artificial

<220>
<223>  OX40(CLC-563)  VL

<400>  34

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


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


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


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


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


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


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


<210>  35
<211>  116
<212>  PRT
<213>  Secuencia artificial

<220>
<223>  OX40(CLC-564)  VH

<400>  35

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


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

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

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

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

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

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

Thr Val Ser Ser
        115


<210>  36
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<400>  36

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

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

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

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

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

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

Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 37
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<220>
<223> OX40(17A9) VH

<400> 37

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 38
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<220>
<223> OX40(17A9) VL

<400> 38

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

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

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

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

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

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

Val Phe Gly Gly Gly Thr Lys Leu Thr Val
            100                 105
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<210> 39
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<212> PRT
<213> Homo sapiens

<400> 39

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Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1               5                   10                  15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
            20                  25                  30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
        35                  40                  45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
    50                  55                  60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65                  70                  75                  80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
                85                  90                  95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
            100                 105                 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
        115                 120                 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
    130                 135                 140

Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145                 150                 155                 160
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Ser Pro Gln

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Ser Tyr Ala Ile Ser
1 5

<210> 41
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<212> PRT
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<223> 4-1BB(25G7) CDR-H1

<400> 41

Ser Tyr Ala Met Ser
1 5

<210> 42
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<223> 4-1BB(12B3,11D5, 9B11, 20G2) CDR-H2

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

Gly

<210> 43
<211> 17
<212> PRT
<213> Secuencia artificial

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<223> 4-1BB(25G7) CDR-H2

<400> 43

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

1 5 10 15

Gly

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

<220>
<223> 4-1BB(12B3) CDR-H3

<400> 44

Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr
1 5 10

<210> 45
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(25G7) CDR-H3

<400> 45

Asp Asp Pro Trp Pro Pro Phe Asp Tyr
1 5

<210> 46
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(11D5) CDR-H3

<400> 46

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

<210> 47
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(9B11) CDR-H3

<400> 47

Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr
1 5 10

<210> 48
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(20G2) CDR-H3

<400> 48

Ser Tyr Tyr Trp Glu Ser Tyr Pro Phe Asp Tyr
1 5 10

<210> 49
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(12B3,11D5, 9B11, 20G2) CDR-L1

<400> 49

Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 50
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<213> Secuencia artificial

<220>
<223> 4-1BB(25G7) CDR-L1

<400> 50

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1 5 10

<210> 51
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(12B3,11D5, 9B11, 20G2) CDR-L2

<400> 51

Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 52
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(25G7) CDR-L2

<400> 52

Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 53
<211> 9
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<220>
<223> 4-1BB(12B3) CDR-L3

<400> 53

Gln Gln Tyr His Ser Tyr Pro Gln Thr
1 5

<210> 54
<211> 10
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<220>
<223> 4-1BB(25G7) CDR-L3

<400> 54

Asn Ser Leu Asp Arg Arg Gly Met Trp Val
1 5 10

<210> 55
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<400> 55

Gln Gln Leu Asn Ser Tyr Pro Gln Thr
1 5

<210> 56
<211> 9
<212> PRT
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<223> 4-1BB(9B11) CDR-L3

<400> 56

Gln Gln Val Asn Ser Tyr Pro Gln Thr
1 5

<210> 57
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(20G2) CDR-L3

<400> 57

Gln Gln Gln His Ser Tyr Tyr Thr
1 5

<210> 58
<211> 120
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(12B3) VH

<400> 58

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

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

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 59
<211> 107
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(12B3) VL

<400> 59

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

<210> 60
<211> 118
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(25G7) VH

<400> 60

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

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

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

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

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

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

```
Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115


<210>  61
<211>  106
<212>  PRT
<213>  Secuencia artificial

<220>
<223>  4-1BB(25G7)  VL

<400>  61

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


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


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


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


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


Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Asp Arg Arg Gly Met Trp
                85                  90                  95


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


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

<220>
<223>  4-1BB(11D5)  VH

<400>  62

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


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

20 25 30

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

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

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

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

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

Thr Thr Val Thr Val Ser Ser
115

<210> 63
<211> 107
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(11D5) VL

<400> 63

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

<210> 64
<211> 120
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(9B11) VH

<400> 64

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

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

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 65
<211> 107
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(9B11) VL

<400> 65

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

35 40 45

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

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

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

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

<210> 66
<211> 120
<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(20G2) VH

<400> 66

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

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

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 67
<211> 106

<212> PRT
<213> Secuencia artificial

<220>
<223> 4-1BB(20G2) VL

<400> 67

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

<210> 68
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) CDR-H1

<400> 68

Ser His Ala Met Ser
1 5

<210> 69
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) CDR-H1

<400> 69

Ser Tyr Ala Met Ser
1 5

<210> 70
<211> 16
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) CDR-H2

<400> 70

Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 71
<211> 17
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) CDR-H2

<400> 71

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

Gly

<210> 72
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) CDR-H3

<400> 72

Gly Trp Leu Gly Asn Phe Asp Tyr
1 5

<210> 73
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) CDR-H3

<400> 73

Gly Trp Phe Gly Gly Phe Asn Tyr
1 5

<210> 74
<211> 12

<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) CDR-L1

<400> 74

Arg Ala Ser Gln Ser Val Ser Arg Ser Tyr Leu Ala
1 5 10

<210> 75
<211> 12
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) CDR-L1

<400> 75

Arg Ala Ser Gln Ser Val Thr Ser Ser Tyr Leu Ala
1 5 10

<210> 76
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) CDR-L2

<400> 76

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 77
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) CDR-L2

<400> 77

Val Gly Ser Arg Arg Ala Thr
1 5

<210> 78
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) CDR-L3

<400> 78

Gln Gln Gly Gln Val Ile Pro Pro Thr
1 5

<210> 79
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) CDR-L3

<400> 79

Gln Gln Gly Ile Met Leu Pro Pro Thr
1 5

<210> 80
<211> 116
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) VH

<400> 80

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

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

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

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

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

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

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

Thr Val Ser Ser
115

<210> 81
<211> 108

<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(28H1) VL

<400> 81

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

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

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

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

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

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

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

<210> 82
<211> 117
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) VH

<400> 82

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

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

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

Val Thr Val Ser Ser
115

<210> 83
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> FAP(4B9) VL

<400> 83

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

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

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

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

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

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

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

<210> 84
<211> 760
<212> PRT
<213> Homo sapiens

<400> 84

Met Lys Thr Trp Val Lys Ile Val Phe Gly Val Ala Thr Ser Ala Val
1 5 10 15

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Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
            20                  25                  30

Asn Ser Glu Glu Asn Thr Met Arg Ala Leu Thr Leu Lys Asp Ile Leu
        35                  40                  45

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

Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
65                  70                  75                  80

Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
                85                  90                  95

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

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
        115                 120                 125

Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly Glu Phe Val Arg Gly Asn
    130                 135                 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145                 150                 155                 160

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

Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile
            180                 185                 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
        195                 200                 205

Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly Lys Phe Leu Ala Tyr Ala
    210                 215                 220

Glu Phe Asn Asp Thr Asp Ile Pro Val Ile Ala Tyr Ser Tyr Tyr Gly
225                 230                 235                 240

Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
                245                 250                 255

Ala Lys Asn Pro Val Val Arg Ile Phe Ile Ile Asp Thr Thr Tyr Pro
            260                 265                 270
```

```
Ala Tyr Val Gly Pro Gln Glu Val Pro Val Pro Ala Met Ile Ala Ser
        275                 280                 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Thr Asp Glu Arg Val
    290                 295                 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
305                 310                 315                 320

Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln
                325                 330                 335

Glu His Ile Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
            340                 345                 350

Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe
        355                 360                 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
    370                 375                 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile
385                 390                 395                 400

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
                405                 410                 415

Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
            420                 425                 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
        435                 440                 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
    450                 455                 460

Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
465                 470                 475                 480

Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
                485                 490                 495

Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
            500                 505                 510

Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
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        515                 520                 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
    530                 535                 540

Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
545                 550                 555                 560

Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly
                565                 570                 575

Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
            580                 585                 590

Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
        595                 600                 605

Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
    610                 615                 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625                 630                 635                 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
                645                 650                 655

Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
            660                 665                 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
        675                 680                 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
    690                 695                 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705                 710                 715                 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
                725                 730                 735

Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
            740                 745                 750

Lys Gln Cys Phe Ser Leu Ser Asp
        755                 760
```

<210> 85
<211> 748
<212> PRT
<213> Secuencia artificial

<220>
<223> ectodominio+cola de poli-lys-tag+his6 de ihu FAP

<400> 85

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
```

210 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
545                 550                 555                 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
                565                 570                 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
            580                 585                 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
        595                 600                 605

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

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

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

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

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

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

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
705                 710                 715                 720
```

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

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

<210> 86
<211> 2244
<212> ADN
<213> Secuencia artificial

<220>
<223> ectodominio+cola de poli-lys-tag+his6 de ihu FAP

<400> 86
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attttaaatg gaacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa 120

tatcttcatc aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180

tataccattt tgagtaatag aaccatgaaa agtgtgaatg cttcaaatta cggcttatca 240

cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac 300

acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360

cctcgtccaa ttcagtattt atgctggtcg cctgttggga gtaaattagc atatgtctat 420

caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaaat aacatttaat 480

ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540

gctacaaaat atgctctctg gtggtctcct aatggaaaat ttttggcata tgcggaattt 600

aatgatacgg atataccagt tattgcctat tcctattatg gcgatgaaca atatcctaga 660

acaataaata ttccataccc aaaggctgga gctaagaatc ccgttgttcg gatatttatt 720

atcgatacca cttaccctgc gtatgtaggt ccccaggaag tgcctgttcc agcaatgata 780

gcctcaagtg attattattt cagttggctc acgtgggtta ctgatgaacg agtatgtttg 840

cagtggctaa aaagagtcca gaatgtttcg gtcctgtcta tatgtgactt cagggaagac 900

tggcagacat gggattgtcc aaagacccag gagcatatag aagaaagcag aactggatgg 960

gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc gtactacaaa 1020

atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat 1080

gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat 1140

tcactgtttt attctagcaa tgaatttgaa gaataccctg gaagaagaaa catctacaga 1200

attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa 1260

aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc 1320

tacggcccag gcatccccat ttccaccctt catgatggac gcactgatca agaaattaaa 1380

atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag 1440

gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct 1500

caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt 1560

cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg 1620

atggtcattg ccttggtgga tggtcgagga acagctttcc aaggtgacaa actcctctat 1680

gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa 1740

ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga 1800

ggatacgttt catcactggc ccttgcatct ggaactggtc ttttcaaatg tggtatagca 1860

gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt 1920

ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca 1980

gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040

tttcaaaact cagcacagat tgctaaagct ctggttaatg cacaagtgga tttccaggca 2100

atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc 2160

cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa 2220

aagggccacc accatcacca tcac 2244

<210> 87
<211> 761
<212> PRT
<213> Mus musculus

<400> 87

Met Lys Thr Trp Leu Lys Thr Val Phe Gly Val Thr Thr Leu Ala Ala
1 5 10 15

Leu Ala Leu Val Val Ile Cys Ile Val Leu Arg Pro Ser Arg Val Tyr
20 25 30

Lys Pro Glu Gly Asn Thr Lys Arg Ala Leu Thr Leu Lys Asp Ile Leu
35 40 45

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

Gln Glu Tyr Leu His Gln Ser Glu Asp Asp Asn Ile Val Phe Tyr Asn
65 70 75 80

Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu Ser Asn Ser Thr Met Lys
85 90 95

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

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
        115                 120                 125

Thr Tyr Tyr Ile Tyr Asp Leu Gln Asn Gly Glu Phe Val Arg Gly Tyr
    130                 135                 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145                 150                 155                 160

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

Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr Gly Arg Glu Asn Arg Ile
            180                 185                 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
        195                 200                 205

Lys Tyr Ala Leu Trp Trp Ser Pro Asp Gly Lys Phe Leu Ala Tyr Val
    210                 215                 220

Glu Phe Asn Asp Ser Asp Ile Pro Ile Ile Ala Tyr Ser Tyr Tyr Gly
225                 230                 235                 240

Asp Gly Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
                245                 250                 255

Ala Lys Asn Pro Val Val Arg Val Phe Ile Val Asp Thr Thr Tyr Pro
            260                 265                 270

His His Val Gly Pro Met Glu Val Pro Val Pro Glu Met Ile Ala Ser
        275                 280                 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Ser Ser Glu Arg Val
    290                 295                 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
305                 310                 315                 320

Cys Asp Phe Arg Glu Asp Trp His Ala Trp Glu Cys Pro Lys Asn Gln
                325                 330                 335

Glu His Val Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
            340                 345                 350
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Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr Ser Tyr Tyr Lys Ile Phe
        355                 360                 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
    370                 375                 380

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

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
                405                 410                 415

Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Asn Ser
            420                 425                 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
        435                 440                 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys Ala Lys Tyr Tyr Ala Leu
    450                 455                 460

Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser Thr Leu His Asp Gly Arg
465                 470                 475                 480

Thr Asp Gln Glu Ile Gln Val Leu Glu Glu Asn Lys Glu Leu Glu Asn
                485                 490                 495

Ser Leu Arg Asn Ile Gln Leu Pro Lys Val Glu Ile Lys Lys Leu Lys
            500                 505                 510

Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
        515                 520                 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
    530                 535                 540

Cys Ser Gln Ser Val Lys Ser Val Phe Ala Val Asn Trp Ile Thr Tyr
545                 550                 555                 560

Leu Ala Ser Lys Glu Gly Ile Val Ile Ala Leu Val Asp Gly Arg Gly
                565                 570                 575

Thr Ala Phe Gln Gly Asp Lys Phe Leu His Ala Val Tyr Arg Lys Leu
            580                 585                 590

Gly Val Tyr Glu Val Glu Asp Gln Leu Thr Ala Val Arg Lys Phe Ile
        595                 600                 605
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Glu Met Gly Phe Ile Asp Glu Glu Arg Ile Ala Ile Trp Gly Trp Ser
    610                 615                 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625                 630                 635                 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
                645                 650                 655

Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
            660                 665                 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
        675                 680                 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
    690                 695                 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705                 710                 715                 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Ile
                725                 730                 735

Ser Ser Gly Arg Ser Gln Asn His Leu Tyr Thr His Met Thr His Phe
            740                 745                 750

Leu Lys Gln Cys Phe Ser Leu Ser Asp
        755                 760


<210>  88
<211>  749
<212>  PRT
<213>  Secuencia artificial

<220>
<223>  Ectodominio+cola de poli-lys-tag+his6 de FAP murino

<400>  88

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

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

Pro Asn Trp Ile Ser Glu Gln Glu Tyr Leu His Gln Ser Glu Asp Asp
        35                  40                  45
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Asn Ile Val Phe Tyr Asn Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu
    50                  55                  60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Lys Glu Leu Glu Asn Ser Leu Arg Asn Ile Gln Leu Pro Lys Val
465                 470                 475                 480

Glu Ile Lys Lys Leu Lys Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Lys Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Thr Tyr Leu Ala Ser Lys Glu Gly Ile Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Phe Leu His
```

545 550 555 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Leu Thr
565 570 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Glu Arg Ile
580 585 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
595 600 605

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

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

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

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

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

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

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

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

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

<210> 89
<211> 2247
<212> ADN
<213> Secuencia artificial

<220>
<223> Ectodominio+cola de poli-lys-tag+his6 de FAP murino

<400> 89
cgtccctcaa gagtttacaa acctgaagga aacacaaaga gagctcttac cttgaaggat 60

attttaaatg gaacattctc atataaaaca tattttccca actggatttc agaacaagaa 120

tatcttcatc aatctgagga tgataacata gtattttata atattgaaac aagagaatca 180
tatatcattt tgagtaatag caccatgaaa agtgtgaatg ctacagatta tggtttgtca 240
cctgatcggc aatttgtgta tctagaaagt gattattcaa agctctggcg atattcatac 300
acagcgacat actacatcta cgaccttcag aatggggaat ttgtaagagg atacgagctc 360
cctcgtccaa ttcagtatct atgctggtcg cctgttggga gtaaattagc atatgtatat 420
caaaacaata tttatttgaa acaaagacca ggagatccac cttttcaaat aacttatact 480
ggaagagaaa atagaatatt taatggaata ccagactggg tttatgaaga ggaaatgctt 540
gccacaaaat atgctctttg gtggtctcca gatggaaaat ttttggcata tgtagaattt 600
aatgattcag atataccaat tattgcctat tcttattatg gtgatggaca gtatcctaga 660
actataaata ttccatatcc aaaggctggg gctaagaatc cggttgttcg tgtttttatt 720
gttgacacca cctaccctca ccacgtgggc ccaatggaag tgccagttcc agaaatgata 780
gcctcaagtg actattattt cagctggctc acatgggtgt ccagtgaacg agtatgcttg 840
cagtggctaa aaagagtgca gaatgtctca gtcctgtcta tatgtgattt cagggaagac 900
tggcatgcat gggaatgtcc aaagaaccag gagcatgtag aagaaagcag aacaggatgg 960
gctggtggat tctttgtttc gacaccagct tttagccagg atgccacttc ttactacaaa 1020
atatttagcg acaaggatgg ttacaaacat attcactaca tcaaagacac tgtggaaaat 1080
gctattcaaa ttacaagtgg caagtgggag gccatatata tattccgcgt aacacaggat 1140
tcactgtttt attctagcaa tgaatttgaa ggttaccctg gaagaagaaa catctacaga 1200
attagcattg gaaactctcc tccgagcaag aagtgtgtta cttgccatct aaggaaagaa 1260
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tatggccctg gcctccccat ttccaccctc catgatggcc gcacagacca agaaatacaa 1380
gtattagaag aaaacaaaga actggaaaat tctctgagaa atatccagct gcctaaagtg 1440
gagattaaga agctcaaaga cgggggactg actttctggt acaagatgat tctgcctcct 1500
cagtttgaca gatcaaagaa gtacccttg ctaattcaag tgtatggtgg tccttgtagc 1560
cagagtgtta agtctgtgtt tgctgttaat tggataactt atctcgcaag taaggagggg 1620
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ggttatgttt catccctggc ccttgcatct ggaactggtc ttttcaaatg tggcatagca 1860
gtggctccag tctccagctg ggaatattac gcatctatct actcagagag attcatgggc 1920
ctcccaacaa aggacgacaa tctcgaacac tataaaaatt caactgtgat ggcaagagca 1980

gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040

tttcagaact cagcacagat tgctaaagct ttggttaatg cacaagtgga tttccaggcg 2100

atgtggtact ctgaccagaa ccatggtata ttatctgggc gctcccagaa tcatttatat 2160

acccacatga cgcacttcct caagcaatgc ttttctttat cagacggcaa aaagaaaaag 2220

aaaaagggcc accaccatca ccatcac 2247

<210> 90
<211> 748
<212> PRT
<213> Secuencia artificial

<220>
<223> Ectodominio+cola de poli-lys-tag+his6 de FAP de macaco

<400> 90

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
```

420 425 430

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

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

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

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
485 490 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
500 505 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
515 520 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
530 535 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
545 550 555 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
565 570 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
580 585 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
595 600 605

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

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

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

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

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

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

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

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

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

<210> 91
<211> 2244
<212> ADN
<213> Secuencia artificial

<220>
<223> Ectodominio+cola de poli-lys-tag+his6 de FAP de macaco

<400> 91
cgccctccaa gagttcataa ctctgaagaa aatacaatga gagcactcac actgaaggat 60

attttaaatg ggacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa 120

tatcttcatc aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180

tataccattt tgagtaacag aaccatgaaa agtgtgaatg cttcaaatta tggcttatca 240

cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac 300

acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360

cctcgtccaa ttcagtattt atgctggtcg cctgttggga gtaaattagc atatgtctat 420

caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaaat aacatttaat 480

ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540

gctacaaaat atgctctctg gtggtctcct aatggaaaat ttttggcata tgcggaattt 600

aatgatacag atataccagt tattgcctat tcctattatg gcgatgaaca atatcccaga 660

acaataaata ttccataccc aaaggccgga gctaagaatc cttttgttcg gatatttatt 720

atcgatacca cttaccctgc gtatgtaggt ccccaggaag tgcctgttcc agcaatgata 780

gcctcaagtg attattattt cagttggctc acgtgggtta ctgatgaacg agtatgtttg 840

cagtggctaa aaagagtcca gaatgtttcg gtcttgtcta tatgtgattt cagggaagac 900

tggcagacat gggattgtcc aaagacccag gagcatatag aagaaagcag aactggatgg 960

gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc atactacaaa 1020

atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat 1080

gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat 1140

tcactgtttt attctagcaa tgaatttgaa gattaccctg gaagaagaaa catctacaga 1200

attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa 1260

aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc 1320

tatggcccag gcatccccat ttccaccctt catgacggac gcactgatca agaaattaaa 1380

atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag 1440

gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct 1500

caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt 1560

cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg 1620

atggtcattg ccttggtgga tggtcgggga acagctttcc aaggtgacaa actcctgtat 1680

gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa 1740

ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga 1800

ggatatgttt catcactggc ccttgcatct ggaactggtc ttttcaaatg tgggatagca 1860

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gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040

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atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc 2160

cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa 2220

aagggccacc accatcacca tcac 2244

<210> 92
<211> 702
<212> PRT
<213> Homo sapiens

<400> 92

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

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

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly

50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

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

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125

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

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145 150 155 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
165 170 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
195 200 205

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210 215 220

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225 230 235 240

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
245 250 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
260 265 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
290 295 300

```
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305                 310                 315                 320

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
                325                 330                 335

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
            340                 345                 350

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
        355                 360                 365

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
    370                 375                 380

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Lys Leu Ser
385                 390                 395                 400

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
                405                 410                 415

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
            420                 425                 430

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
        435                 440                 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
    450                 455                 460

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                 470                 475                 480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                485                 490                 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
            500                 505                 510

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
        515                 520                 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
    530                 535                 540

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                 550                 555                 560
```

```
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                565                 570                 575

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
            580                 585                 590

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
        595                 600                 605

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
    610                 615                 620

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                 630                 635                 640

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                645                 650                 655

Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
            660                 665                 670

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
        675                 680                 685

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
    690                 695                 700
```

<210> 93
<211> 2322
<212> PRT
<213> Homo sapiens

<400> 93

```
Met Gln Ser Gly Pro Arg Pro Pro Leu Pro Ala Pro Gly Leu Ala Leu
1               5                   10                  15

Ala Leu Thr Leu Thr Met Leu Ala Arg Leu Ala Ser Ala Ala Ser Phe
            20                  25                  30

Phe Gly Glu Asn His Leu Glu Val Pro Val Ala Thr Ala Leu Thr Asp
        35                  40                  45

Ile Asp Leu Gln Leu Gln Phe Ser Thr Ser Gln Pro Glu Ala Leu Leu
    50                  55                  60

Leu Leu Ala Ala Gly Pro Ala Asp His Leu Leu Leu Gln Leu Tyr Ser
65                  70                  75                  80
```

```
Gly Arg Leu Gln Val Arg Leu Val Leu Gly Gln Glu Glu Leu Arg Leu
                85                  90                  95

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

Val Leu Thr Val Val Glu Gly Trp Ala Thr Leu Ser Val Asp Gly Phe
        115                 120                 125

Leu Asn Ala Ser Ser Ala Val Pro Gly Ala Pro Leu Glu Val Pro Tyr
    130                 135                 140

Gly Leu Phe Val Gly Gly Thr Gly Thr Leu Gly Leu Pro Tyr Leu Arg
145                 150                 155                 160

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

Gly Arg Ser Leu Leu Arg Pro Leu Thr Pro Asp Val His Glu Gly Cys
            180                 185                 190

Ala Glu Glu Phe Ser Ala Ser Asp Asp Val Ala Leu Gly Phe Ser Gly
        195                 200                 205

Pro His Ser Leu Ala Ala Phe Pro Ala Trp Gly Thr Gln Asp Glu Gly
    210                 215                 220

Thr Leu Glu Phe Thr Leu Thr Thr Gln Ser Arg Gln Ala Pro Leu Ala
225                 230                 235                 240

Phe Gln Ala Gly Gly Arg Arg Gly Asp Phe Ile Tyr Val Asp Ile Phe
                245                 250                 255

Glu Gly His Leu Arg Ala Val Val Glu Lys Gly Gln Gly Thr Val Leu
            260                 265                 270

Leu His Asn Ser Val Pro Val Ala Asp Gly Gln Pro His Glu Val Ser
        275                 280                 285

Val His Ile Asn Ala His Arg Leu Glu Ile Ser Val Asp Gln Tyr Pro
    290                 295                 300

Thr His Thr Ser Asn Arg Gly Val Leu Ser Tyr Leu Glu Pro Arg Gly
305                 310                 315                 320

Ser Leu Leu Leu Gly Gly Leu Asp Ala Glu Ala Ser Arg His Leu Gln
                325                 330                 335
```

```
Glu His Arg Leu Gly Leu Thr Pro Glu Ala Thr Asn Ala Ser Leu Leu
            340                 345                 350

Gly Cys Met Glu Asp Leu Ser Val Asn Gly Gln Arg Arg Gly Leu Arg
        355                 360                 365

Glu Ala Leu Leu Thr Arg Asn Met Ala Ala Gly Cys Arg Leu Glu Glu
    370                 375                 380

Glu Glu Tyr Glu Asp Asp Ala Tyr Gly His Tyr Glu Ala Phe Ser Thr
385                 390                 395                 400

Leu Ala Pro Glu Ala Trp Pro Ala Met Glu Leu Pro Glu Pro Cys Val
                405                 410                 415

Pro Glu Pro Gly Leu Pro Pro Val Phe Ala Asn Phe Thr Gln Leu Leu
            420                 425                 430

Thr Ile Ser Pro Leu Val Val Ala Glu Gly Gly Thr Ala Trp Leu Glu
        435                 440                 445

Trp Arg His Val Gln Pro Thr Leu Asp Leu Met Glu Ala Glu Leu Arg
    450                 455                 460

Lys Ser Gln Val Leu Phe Ser Val Thr Arg Gly Ala Arg His Gly Glu
465                 470                 475                 480

Leu Glu Leu Asp Ile Pro Gly Ala Gln Ala Arg Lys Met Phe Thr Leu
                485                 490                 495

Leu Asp Val Val Asn Arg Lys Ala Arg Phe Ile His Asp Gly Ser Glu
            500                 505                 510

Asp Thr Ser Asp Gln Leu Val Leu Glu Val Ser Val Thr Ala Arg Val
        515                 520                 525

Pro Met Pro Ser Cys Leu Arg Arg Gly Gln Thr Tyr Leu Leu Pro Ile
    530                 535                 540

Gln Val Asn Pro Val Asn Asp Pro Pro His Ile Ile Phe Pro His Gly
545                 550                 555                 560

Ser Leu Met Val Ile Leu Glu His Thr Gln Lys Pro Leu Gly Pro Glu
                565                 570                 575

Val Phe Gln Ala Tyr Asp Pro Asp Ser Ala Cys Glu Gly Leu Thr Phe
```

```
            580                 585                 590

Gln Val Leu Gly Thr Ser Ser Gly Leu Pro Val Glu Arg Arg Asp Gln
        595                 600                 605

Pro Gly Glu Pro Ala Thr Glu Phe Ser Cys Arg Glu Leu Glu Ala Gly
    610                 615                 620

Ser Leu Val Tyr Val His Arg Gly Gly Pro Ala Gln Asp Leu Thr Phe
625                 630                 635                 640

Arg Val Ser Asp Gly Leu Gln Ala Ser Pro Pro Ala Thr Leu Lys Val
                645                 650                 655

Val Ala Ile Arg Pro Ala Ile Gln Ile His Arg Ser Thr Gly Leu Arg
            660                 665                 670

Leu Ala Gln Gly Ser Ala Met Pro Ile Leu Pro Ala Asn Leu Ser Val
        675                 680                 685

Glu Thr Asn Ala Val Gly Gln Asp Val Ser Val Leu Phe Arg Val Thr
    690                 695                 700

Gly Ala Leu Gln Phe Gly Glu Leu Gln Lys Gln Gly Ala Gly Gly Val
705                 710                 715                 720

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

Glu Gln Gly Arg Val Arg Tyr Leu Ser Thr Asp Pro Gln His His Ala
            740                 745                 750

Tyr Asp Thr Val Glu Asn Leu Ala Leu Glu Val Gln Val Gly Gln Glu
        755                 760                 765

Ile Leu Ser Asn Leu Ser Phe Pro Val Thr Ile Gln Arg Ala Thr Val
    770                 775                 780

Trp Met Leu Arg Leu Glu Pro Leu His Thr Gln Asn Thr Gln Gln Glu
785                 790                 795                 800

Thr Leu Thr Thr Ala His Leu Glu Ala Thr Leu Glu Glu Ala Gly Pro
                805                 810                 815

Ser Pro Pro Thr Phe His Tyr Glu Val Val Gln Ala Pro Arg Lys Gly
            820                 825                 830
```

```
Asn Leu Gln Leu Gln Gly Thr Arg Leu Ser Asp Gly Gln Gly Phe Thr
        835                 840                 845

Gln Asp Asp Ile Gln Ala Gly Arg Val Thr Tyr Gly Ala Thr Ala Arg
    850                 855                 860

Ala Ser Glu Ala Val Glu Asp Thr Phe Arg Phe Arg Val Thr Ala Pro
865                 870                 875                 880

Pro Tyr Phe Ser Pro Leu Tyr Thr Phe Pro Ile His Ile Gly Gly Asp
                885                 890                 895

Pro Asp Ala Pro Val Leu Thr Asn Val Leu Leu Val Val Pro Glu Gly
            900                 905                 910

Gly Glu Gly Val Leu Ser Ala Asp His Leu Phe Val Lys Ser Leu Asn
        915                 920                 925

Ser Ala Ser Tyr Leu Tyr Glu Val Met Glu Arg Pro Arg His Gly Arg
    930                 935                 940

Leu Ala Trp Arg Gly Thr Gln Asp Lys Thr Thr Met Val Thr Ser Phe
945                 950                 955                 960

Thr Asn Glu Asp Leu Leu Arg Gly Arg Leu Val Tyr Gln His Asp Asp
                965                 970                 975

Ser Glu Thr Thr Glu Asp Asp Ile Pro Phe Val Ala Thr Arg Gln Gly
            980                 985                 990

Glu Ser Ser Gly Asp Met Ala Trp  Glu Glu Val Arg Gly  Val Phe Arg
        995                 1000                1005

Val Ala  Ile Gln Pro Val Asn  Asp His Ala Pro Val  Gln Thr Ile
    1010                1015                1020

Ser Arg  Ile Phe His Val Ala  Arg Gly Gly Arg Arg  Leu Leu Thr
    1025                1030                1035

Thr Asp  Asp Val Ala Phe Ser  Asp Ala Asp Ser Gly  Phe Ala Asp
    1040                1045                1050

Ala Gln  Leu Val Leu Thr Arg  Lys Asp Leu Leu Phe  Gly Ser Ile
    1055                1060                1065

Val Ala  Val Asp Glu Pro Thr  Arg Pro Ile Tyr Arg  Phe Thr Gln
    1070                1075                1080
```

```
Glu Asp  Leu Arg Lys Arg Arg  Val Leu Phe Val His  Ser Gly Ala
    1085                1090                1095

Asp Arg  Gly Trp Ile Gln Leu  Gln Val Ser Asp Gly  Gln His Gln
    1100                1105                1110

Ala Thr  Ala Leu Leu Glu Val  Gln Ala Ser Glu Pro  Tyr Leu Arg
    1115                1120                1125

Val Ala  Asn Gly Ser Ser Leu  Val Val Pro Gln Gly  Gly Gln Gly
    1130                1135                1140

Thr Ile  Asp Thr Ala Val Leu  His Leu Asp Thr Asn  Leu Asp Ile
    1145                1150                1155

Arg Ser  Gly Asp Glu Val His  Tyr His Val Thr Ala  Gly Pro Arg
    1160                1165                1170

Trp Gly  Gln Leu Val Arg Ala  Gly Gln Pro Ala Thr  Ala Phe Ser
    1175                1180                1185

Gln Gln  Asp Leu Leu Asp Gly  Ala Val Leu Tyr Ser  His Asn Gly
    1190                1195                1200

Ser Leu  Ser Pro Arg Asp Thr  Met Ala Phe Ser Val  Glu Ala Gly
    1205                1210                1215

Pro Val  His Thr Asp Ala Thr  Leu Gln Val Thr Ile  Ala Leu Glu
    1220                1225                1230

Gly Pro  Leu Ala Pro Leu Lys  Leu Val Arg His Lys  Lys Ile Tyr
    1235                1240                1245

Val Phe  Gln Gly Glu Ala Ala  Glu Ile Arg Arg Asp  Gln Leu Glu
    1250                1255                1260

Ala Ala  Gln Glu Ala Val Pro  Pro Ala Asp Ile Val  Phe Ser Val
    1265                1270                1275

Lys Ser  Pro Pro Ser Ala Gly  Tyr Leu Val Met Val  Ser Arg Gly
    1280                1285                1290

Ala Leu  Ala Asp Glu Pro Pro  Ser Leu Asp Pro Val  Gln Ser Phe
    1295                1300                1305

Ser Gln  Glu Ala Val Asp Thr  Gly Arg Val Leu Tyr  Leu His Ser
    1310                1315                1320
```

```
Arg Pro  Glu Ala Trp Ser Asp  Ala Phe Ser Leu Asp  Val Ala Ser
    1325                 1330                 1335

Gly Leu  Gly Ala Pro Leu Glu  Gly Val Leu Val Glu  Leu Glu Val
    1340                 1345                 1350

Leu Pro  Ala Ala Ile Pro Leu  Glu Ala Gln Asn Phe  Ser Val Pro
    1355                 1360                 1365

Glu Gly  Gly Ser Leu Thr Leu  Ala Pro Pro Leu Leu  Arg Val Ser
    1370                 1375                 1380

Gly Pro  Tyr Phe Pro Thr Leu  Leu Gly Leu Ser Leu  Gln Val Leu
    1385                 1390                 1395

Glu Pro  Pro Gln His Gly Ala  Leu Gln Lys Glu Asp  Gly Pro Gln
    1400                 1405                 1410

Ala Arg  Thr Leu Ser Ala Phe  Ser Trp Arg Met Val  Glu Glu Gln
    1415                 1420                 1425

Leu Ile  Arg Tyr Val His Asp  Gly Ser Glu Thr Leu  Thr Asp Ser
    1430                 1435                 1440

Phe Val  Leu Met Ala Asn Ala  Ser Glu Met Asp Arg  Gln Ser His
    1445                 1450                 1455

Pro Val  Ala Phe Thr Val Thr  Val Leu Pro Val Asn  Asp Gln Pro
    1460                 1465                 1470

Pro Ile  Leu Thr Thr Asn Thr  Gly Leu Gln Met Trp  Glu Gly Ala
    1475                 1480                 1485

Thr Ala  Pro Ile Pro Ala Glu  Ala Leu Arg Ser Thr  Asp Gly Asp
    1490                 1495                 1500

Ser Gly  Ser Glu Asp Leu Val  Tyr Thr Ile Glu Gln  Pro Ser Asn
    1505                 1510                 1515

Gly Arg  Val Val Leu Arg Gly  Ala Pro Gly Thr Glu  Val Arg Ser
    1520                 1525                 1530

Phe Thr  Gln Ala Gln Leu Asp  Gly Gly Leu Val Leu  Phe Ser His
    1535                 1540                 1545

Arg Gly  Thr Leu Asp Gly Gly  Phe Arg Phe Arg Leu  Ser Asp Gly
```

1550 1555 1560

Glu His Thr Ser Pro Gly His Phe Phe Arg Val Thr Ala Gln Lys
1565 1570 1575

Gln Val Leu Leu Ser Leu Lys Gly Ser Gln Thr Leu Thr Val Cys
1580 1585 1590

Pro Gly Ser Val Gln Pro Leu Ser Ser Gln Thr Leu Arg Ala Ser
1595 1600 1605

Ser Ser Ala Gly Thr Asp Pro Gln Leu Leu Leu Tyr Arg Val Val
1610 1615 1620

Arg Gly Pro Gln Leu Gly Arg Leu Phe His Ala Gln Gln Asp Ser
1625 1630 1635

Thr Gly Glu Ala Leu Val Asn Phe Thr Gln Ala Glu Val Tyr Ala
1640 1645 1650

Gly Asn Ile Leu Tyr Glu His Glu Met Pro Pro Glu Pro Phe Trp
1655 1660 1665

Glu Ala His Asp Thr Leu Glu Leu Gln Leu Ser Ser Pro Pro Ala
1670 1675 1680

Arg Asp Val Ala Ala Thr Leu Ala Val Ala Val Ser Phe Glu Ala
1685 1690 1695

Ala Cys Pro Gln Arg Pro Ser His Leu Trp Lys Asn Lys Gly Leu
1700 1705 1710

Trp Val Pro Glu Gly Gln Arg Ala Arg Ile Thr Val Ala Ala Leu
1715 1720 1725

Asp Ala Ser Asn Leu Leu Ala Ser Val Pro Ser Pro Gln Arg Ser
1730 1735 1740

Glu His Asp Val Leu Phe Gln Val Thr Gln Phe Pro Ser Arg Gly
1745 1750 1755

Gln Leu Leu Val Ser Glu Glu Pro Leu His Ala Gly Gln Pro His
1760 1765 1770

Phe Leu Gln Ser Gln Leu Ala Ala Gly Gln Leu Val Tyr Ala His
1775 1780 1785

```
Gly Gly  Gly Gly Thr Gln Gln  Asp Gly Phe His Phe  Arg Ala His
    1790                1795                1800

Leu Gln  Gly Pro Ala Gly Ala  Ser Val Ala Gly Pro  Gln Thr Ser
    1805                1810                1815

Glu Ala  Phe Ala Ile Thr Val  Arg Asp Val Asn Glu  Arg Pro Pro
    1820                1825                1830

Gln Pro  Gln Ala Ser Val Pro  Leu Arg Leu Thr Arg  Gly Ser Arg
    1835                1840                1845

Ala Pro  Ile Ser Arg Ala Gln  Leu Ser Val Val Asp  Pro Asp Ser
    1850                1855                1860

Ala Pro  Gly Glu Ile Glu Tyr  Glu Val Gln Arg Ala  Pro His Asn
    1865                1870                1875

Gly Phe  Leu Ser Leu Val Gly  Gly Gly Leu Gly Pro  Val Thr Arg
    1880                1885                1890

Phe Thr  Gln Ala Asp Val Asp  Ser Gly Arg Leu Ala  Phe Val Ala
    1895                1900                1905

Asn Gly  Ser Ser Val Ala Gly  Ile Phe Gln Leu Ser  Met Ser Asp
    1910                1915                1920

Gly Ala  Ser Pro Pro Leu Pro  Met Ser Leu Ala Val  Asp Ile Leu
    1925                1930                1935

Pro Ser  Ala Ile Glu Val Gln  Leu Arg Ala Pro Leu  Glu Val Pro
    1940                1945                1950

Gln Ala  Leu Gly Arg Ser Ser  Leu Ser Gln Gln Gln  Leu Arg Val
    1955                1960                1965

Val Ser  Asp Arg Glu Glu Pro  Glu Ala Ala Tyr Arg  Leu Ile Gln
    1970                1975                1980

Gly Pro  Gln Tyr Gly His Leu  Leu Val Gly Gly Arg  Pro Thr Ser
    1985                1990                1995

Ala Phe  Ser Gln Phe Gln Ile  Asp Gln Gly Glu Val  Val Phe Ala
    2000                2005                2010

Phe Thr  Asn Phe Ser Ser Ser  His Asp His Phe Arg  Val Leu Ala
    2015                2020                2025
```

```
Leu Ala  Arg Gly Val Asn Ala  Ser Ala Val Val Asn  Val Thr Val
    2030                 2035                 2040

Arg Ala  Leu Leu His Val Trp  Ala Gly Gly Pro Trp  Pro Gln Gly
    2045                 2050                 2055

Ala Thr  Leu Arg Leu Asp Pro  Thr Val Leu Asp Ala  Gly Glu Leu
    2060                 2065                 2070

Ala Asn  Arg Thr Gly Ser Val  Pro Arg Phe Arg Leu  Leu Glu Gly
    2075                 2080                 2085

Pro Arg  His Gly Arg Val Val  Arg Val Pro Arg Ala  Arg Thr Glu
    2090                 2095                 2100

Pro Gly  Gly Ser Gln Leu Val  Glu Gln Phe Thr Gln  Gln Asp Leu
    2105                 2110                 2115

Glu Asp  Gly Arg Leu Gly Leu  Glu Val Gly Arg Pro  Glu Gly Arg
    2120                 2125                 2130

Ala Pro  Gly Pro Ala Gly Asp  Ser Leu Thr Leu Glu  Leu Trp Ala
    2135                 2140                 2145

Gln Gly  Val Pro Pro Ala Val  Ala Ser Leu Asp Phe  Ala Thr Glu
    2150                 2155                 2160

Pro Tyr  Asn Ala Ala Arg Pro  Tyr Ser Val Ala Leu  Leu Ser Val
    2165                 2170                 2175

Pro Glu  Ala Ala Arg Thr Glu  Ala Gly Lys Pro Glu  Ser Ser Thr
    2180                 2185                 2190

Pro Thr  Gly Glu Pro Gly Pro  Met Ala Ser Ser Pro  Glu Pro Ala
    2195                 2200                 2205

Val Ala  Lys Gly Gly Phe Leu  Ser Phe Leu Glu Ala  Asn Met Phe
    2210                 2215                 2220

Ser Val  Ile Ile Pro Met Cys  Leu Val Leu Leu Leu  Leu Ala Leu
    2225                 2230                 2235

Ile Leu  Pro Leu Leu Phe Tyr  Leu Arg Lys Arg Asn  Lys Thr Gly
    2240                 2245                 2250

Lys His  Asp Val Gln Val Leu  Thr Ala Lys Pro Arg  Asn Gly Leu
    2255                 2260                 2265
```

```
Ala Gly  Asp Thr Glu Thr Phe  Arg Lys Val Glu Pro  Gly Gln Ala
    2270                2275                2280

Ile Pro  Leu Thr Ala Val Pro  Gly Gln Gly Pro Pro  Pro Gly Gly
    2285                2290                2295

Gln Pro  Asp Pro Glu Leu Leu  Gln Phe Cys Arg Thr  Pro Asn Pro
    2300                2305                2310

Ala Leu  Lys Asn Gly Gln Tyr  Trp Val
    2315                2320
```

<210> 94
<211> 1210
<212> PRT
<213> Homo sapiens

<400> 94

```
Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1               5                   10                  15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
            20                  25                  30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
        35                  40                  45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
    50                  55                  60

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
                85                  90                  95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
            100                 105                 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
        115                 120                 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
    130                 135                 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145                 150                 155                 160
```

```
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
                165                 170                 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
            180                 185                 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
        195                 200                 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
    210                 215                 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225                 230                 235                 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
                245                 250                 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
            260                 265                 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
        275                 280                 285

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

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305                 310                 315                 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
                325                 330                 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
            340                 345                 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
        355                 360                 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
    370                 375                 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385                 390                 395                 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
```

405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

```
Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
            660                 665                 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
        675                 680                 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
    690                 695                 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705                 710                 715                 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
                725                 730                 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
            740                 745                 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
        755                 760                 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
    770                 775                 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785                 790                 795                 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
                805                 810                 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
            820                 825                 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
        835                 840                 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
    850                 855                 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865                 870                 875                 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
                885                 890                 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
            900                 905                 910
```

```
Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
        915                 920                 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
    930                 935                 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945                 950                 955                 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
                965                 970                 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
            980                 985                 990

Thr Asp Ser Asn Phe Tyr Arg Ala  Leu Met Asp Glu Glu  Asp Met Asp
        995                 1000                1005

Asp Val  Val Asp Ala Asp Glu  Tyr Leu Ile Pro Gln  Gln Gly Phe
    1010                1015                1020

Phe Ser  Ser Pro Ser Thr Ser  Arg Thr Pro Leu Leu  Ser Ser Leu
    1025                1030                1035

Ser Ala  Thr Ser Asn Asn Ser  Thr Val Ala Cys Ile  Asp Arg Asn
    1040                1045                1050

Gly Leu  Gln Ser Cys Pro Ile  Lys Glu Asp Ser Phe  Leu Gln Arg
    1055                1060                1065

Tyr Ser  Ser Asp Pro Thr Gly  Ala Leu Thr Glu Asp  Ser Ile Asp
    1070                1075                1080

Asp Thr  Phe Leu Pro Val Pro  Glu Tyr Ile Asn Gln  Ser Val Pro
    1085                1090                1095

Lys Arg  Pro Ala Gly Ser Val  Gln Asn Pro Val Tyr  His Asn Gln
    1100                1105                1110

Pro Leu  Asn Pro Ala Pro Ser  Arg Asp Pro His Tyr  Gln Asp Pro
    1115                1120                1125

His Ser  Thr Ala Val Gly Asn  Pro Glu Tyr Leu Asn  Thr Val Gln
    1130                1135                1140

Pro Thr  Cys Val Asn Ser Thr  Phe Asp Ser Pro Ala  His Trp Ala
    1145                1150                1155
```

```
Gln Lys  Gly Ser His Gln Ile  Ser Leu Asp Asn Pro  Asp Tyr Gln
    1160                1165                1170


Gln Asp  Phe Phe Pro Lys Glu  Ala Lys Pro Asn Gly  Ile Phe Lys
    1175                1180                1185


Gly Ser  Thr Ala Glu Asn Ala  Glu Tyr Leu Arg Val  Ala Pro Gln
    1190                1195                1200


Ser Ser  Glu Phe Ile Gly Ala
    1205                1210
```

<210> 95
<211> 556
<212> PRT
<213> Homo sapiens

<400> 95

```
Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
1               5                  10                  15


Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
            20                  25                  30


Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
        35                  40                  45


Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
    50                  55                  60


Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
65                  70                  75                  80


Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
                85                  90                  95


Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
            100                 105                 110


Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
        115                 120                 125


Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
    130                 135                 140


Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
145                 150                 155                 160
```

```
Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro
                165                 170                 175

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
            180                 185                 190

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
        195                 200                 205

Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser
    210                 215                 220

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
225                 230                 235                 240

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
                245                 250                 255

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
            260                 265                 270

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
        275                 280                 285

Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu
    290                 295                 300

Cys Ser Leu Val Gly Ile Leu His Leu Gln Arg Ala Leu Val Leu Arg
305                 310                 315                 320

Arg Lys Arg Lys Arg Met Thr Asp Pro Thr Arg Arg Phe Phe Lys Val
                325                 330                 335

Thr Pro Pro Pro Gly Ser Gly Pro Gln Asn Gln Tyr Gly Asn Val Leu
            340                 345                 350

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
        355                 360                 365

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

Val Gln Ala Asp Gly Ala Leu Gly Ser Arg Ser Pro Pro Gly Val Gly
385                 390                 395                 400

Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
```

405 410 415

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
420 425 430

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
435 440 445

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
450 455 460

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
465 470 475 480

Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
485 490 495

Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
500 505 510

Leu Arg Ser Ile Arg Gly Gln Pro Gly Pro Asn His Glu Glu Asp Ala
515 520 525

Asp Ser Tyr Glu Asn Met Asp Asn Pro Asp Gly Pro Asp Pro Ala Trp
530 535 540

Gly Gly Gly Gly Arg Met Gly Thr Trp Ser Thr Arg
545 550 555

<210> 96
<211> 297
<212> PRT
<213> Homo sapiens

<400> 96

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile

65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210 215 220

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

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
290 295

<210> 97
<211> 364
<212> PRT
<213> Homo sapiens

<400> 97

```
Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
1               5                  10                  15

Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln
            20                  25                  30

Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro
        35                  40                  45

Tyr Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly
    50                  55                  60

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

Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro
                85                  90                  95

Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp
            100                 105                 110

Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser
        115                 120                 125

Tyr Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg
    130                 135                 140

Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn
145                 150                 155                 160

Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile
                165                 170                 175

Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr
            180                 185                 190

His Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr
        195                 200                 205

Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu
    210                 215                 220

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr
225                 230                 235                 240
```

```
Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly
                245                 250                 255

Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala
            260                 265                 270

Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys
        275                 280                 285

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

Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr
305                 310                 315                 320

Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu
                325                 330                 335

Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys
            340                 345                 350

Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln
        355                 360
```

<210> 98
<211> 277
<212> PRT
<213> Homo sapiens

<400> 98

```
Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro Cys Ala Ala Leu
1               5                   10                  15

Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val
            20                  25                  30

Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
        35                  40                  45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
    50                  55                  60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
65                  70                  75                  80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
                85                  90                  95
```

```
Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
            100                 105                 110

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

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
    130                 135                 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
145                 150                 155                 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
                165                 170                 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
            180                 185                 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
        195                 200                 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
    210                 215                 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
225                 230                 235                 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
                245                 250                 255

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
            260                 265                 270

Thr Leu Ala Lys Ile
        275


<210>  99
<211>  255
<212>  PRT
<213>  Homo sapiens

<400>  99

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1               5                   10                  15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
            20                  25                  30
```

```
Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
        35                  40                  45

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

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65                  70                  75                  80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
                85                  90                  95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
            100                 105                 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
        115                 120                 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
    130                 135                 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145                 150                 155                 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
                165                 170                 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
            180                 185                 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
        195                 200                 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
    210                 215                 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225                 230                 235                 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
                245                 250                 255
```

<210> 100
<211> 260
<212> PRT
<213> Homo sapiens

<400> 100

```
Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val
1               5                  10                  15

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

Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
        35                  40                  45

Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
    50                  55                  60

Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
65                  70                  75                  80

Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
                85                  90                  95

Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
            100                 105                 110

Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
        115                 120                 125

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
    130                 135                 140

Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
145                 150                 155                 160

Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
                165                 170                 175

His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
            180                 185                 190

Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
        195                 200                 205

Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
    210                 215                 220

Pro Val Glu Pro Ala Glu Pro Cys His Tyr Ser Cys Pro Arg Glu Glu
225                 230                 235                 240

Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
                245                 250                 255
```

```
Ala Cys Ser Pro
            260


<210>  101
<211>  283
<212>  PRT
<213>  Homo sapiens

<400>  101

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
1               5                   10                  15


Lys Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
            20                  25                  30


Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
        35                  40                  45


Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
    50                  55                  60


Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
65                  70                  75                  80


Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
                85                  90                  95


Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
            100                 105                 110


Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
        115                 120                 125


Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
    130                 135                 140


Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
145                 150                 155                 160


Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
                165                 170                 175


Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
            180                 185                 190


Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
        195                 200                 205
```

```
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
    210                 215                 220

Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
225                 230                 235                 240

Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
                245                 250                 255

Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
            260                 265                 270

Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
        275                 280
```

<210> 102
<211> 595
<212> PRT
<213> Homo sapiens

<400> 102

```
Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
1               5                   10                  15

Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn
            20                  25                  30

Pro Ser His Tyr Tyr Asp Lys Ala Val Arg Arg Cys Cys Tyr Arg Cys
        35                  40                  45

Pro Met Gly Leu Phe Pro Thr Gln Gln Cys Pro Gln Arg Pro Thr Asp
    50                  55                  60

Cys Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Asp Arg
65                  70                  75                  80

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

Pro Cys Ala Trp Asn Ser Ser Arg Val Cys Glu Cys Arg Pro Gly Met
            100                 105                 110

Phe Cys Ser Thr Ser Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His
        115                 120                 125

Ser Val Cys Pro Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln
    130                 135                 140
```

```
Lys Asn Thr Val Cys Glu Pro Ala Ser Pro Gly Val Ser Pro Ala Cys
145                 150                 155                 160

Ala Ser Pro Glu Asn Cys Lys Glu Pro Ser Ser Gly Thr Ile Pro Gln
                165                 170                 175

Ala Lys Pro Thr Pro Val Ser Pro Ala Thr Ser Ser Ala Ser Thr Met
            180                 185                 190

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

Thr Arg Ala Pro Asp Ser Pro Ser Ser Val Gly Arg Pro Ser Ser Asp
    210                 215                 220

Pro Gly Leu Ser Pro Thr Gln Pro Cys Pro Glu Gly Ser Gly Asp Cys
225                 230                 235                 240

Arg Lys Gln Cys Glu Pro Asp Tyr Tyr Leu Asp Glu Ala Gly Arg Cys
                245                 250                 255

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

Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile
        275                 280                 285

Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro
    290                 295                 300

Ile Cys Ala Ala Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys
305                 310                 315                 320

Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn
                325                 330                 335

Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln
            340                 345                 350

Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr
        355                 360                 365

Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala
    370                 375                 380

Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Val Gly
385                 390                 395                 400
```

```
Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
                405                 410                 415

Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
            420                 425                 430

Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
        435                 440                 445

Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
    450                 455                 460

Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
465                 470                 475                 480

Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
                485                 490                 495

Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
            500                 505                 510

Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
        515                 520                 525

Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
    530                 535                 540

Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
545                 550                 555                 560

Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
                565                 570                 575

Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
            580                 585                 590

Ser Gly Lys
        595


<210>  103
<211>  241
<212>  PRT
<213>  Homo sapiens

<400>  103

Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1               5                   10                  15
```

```
Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
            20                  25                  30

Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
        35                  40                  45

Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
    50                  55                  60

Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65                  70                  75                  80

Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
                85                  90                  95

Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
            100                 105                 110

Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
        115                 120                 125

Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
    130                 135                 140

Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145                 150                 155                 160

Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
                165                 170                 175

Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
            180                 185                 190

Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
        195                 200                 205

Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
    210                 215                 220

Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
225                 230                 235                 240

Val
```

<210> 104

<211> 272
<212> PRT
<213> Mus musculus

<400> 104

```
Met Tyr Val Trp Val Gln Gln Pro Thr Ala Leu Leu Leu Leu Ala Leu
1               5                  10                  15

Thr Leu Gly Val Thr Ala Arg Arg Leu Asn Cys Val Lys His Thr Tyr
            20                  25                  30

Pro Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met
        35                  40                  45

Val Ser Arg Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu
    50                  55                  60

Thr Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys
65                  70                  75                  80

Thr Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr
                85                  90                  95

Pro Thr Gln Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg
            100                 105                 110

Gln Asp Ser Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro
        115                 120                 125

Gly His Phe Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn
    130                 135                 140

Cys Thr Leu Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu
145                 150                 155                 160

Asp Ala Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu
                165                 170                 175

Thr Gln Arg Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val
            180                 185                 190

Trp Pro Arg Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro
        195                 200                 205

Glu Gly Pro Ala Phe Ala Val Leu Leu Gly Leu Gly Leu Gly Leu Leu
    210                 215                 220

Ala Pro Leu Thr Val Leu Leu Ala Leu Tyr Leu Leu Arg Lys Ala Trp
```

225 230 235 240

Arg Leu Pro Asn Thr Pro Lys Pro Cys Trp Gly Asn Ser Phe Arg Thr
245 250 255

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

<210> 105
<211> 256
<212> PRT
<213> Mus musculus

<400> 105

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val
1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln
20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
130 135 140

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

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala

180 185 190

Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe
195 200 205

Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
210 215 220

Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
225 230 235 240

Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu
245 250 255

<210> 106
<211> 254
<212> PRT
<213> cynomolgus

<400> 106

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Leu Cys Ser Asn Cys Pro
20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Ser Gln Ile Cys Ser Pro Cys
35 40 45

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

Cys Arg Gln Cys Lys Gly Val Phe Lys Thr Arg Lys Glu Cys Ser Ser
65 70 75 80

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

Ala Glu Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
130 135 140

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

145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Ala Thr Pro Pro Ala
165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Phe Phe Leu Ala
180 185 190

Leu Thr Ser Thr Val Val Leu Phe Leu Leu Phe Phe Leu Val Leu Arg
195 200 205

Phe Ser Val Val Lys Arg Ser Arg Lys Lys Leu Leu Tyr Ile Phe Lys
210 215 220

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
225 230 235 240

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
245 250

<210> 107
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 107

Gly Gly Gly Gly Ser
1 5

<210> 108
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 108

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

<210> 109
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 109

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

<210> 110
<211> 14
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 110

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

<210> 111
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 111

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

<210> 112
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 112

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

<210> 113
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 113

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

Gly Gly Gly Ser

<210> 114
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 114

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 115
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 115

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

<210> 116
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 116

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 117
<211> 6
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 117

Gly Gly Ser Gly Ser Gly
1 5

<210> 118
<211> 4
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 118

Gly Gly Ser Gly
1

<210> 119
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 119

Gly Gly Ser Gly Asn Gly Ser Gly
1   5

<210> 120
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador peptídico

<400> 120

Gly Gly Asn Gly Ser Gly Ser Gly
1   5

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

<220>
<223> Enlazador peptídico

<400> 121

Gly Gly Asn Gly Ser Gly
1   5

<210> 122
<211> 186
<212> PRT
<213> cynomolgus

<400> 122

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys Gln
1   5   10   15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Asn Arg Ser Gln
20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
35 40 45

Ser Ala Lys Pro Cys Lys Ala Cys Thr Trp Cys Asn Leu Arg Ser Gly
50 55 60

Ser Glu Arg Lys Gln Pro Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
65 70 75 80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
100 105 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
115 120 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
130 135 140

Pro Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Thr Thr
145 150 155 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Arg Pro Ser Thr
165 170 175

Arg Pro Val Glu Val Pro Arg Gly Pro Ala
180 185

<210> 123
<211> 192
<212> PRT
<213> Mus musculus

<400> 123

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

His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg
20 25 30

Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu Thr Gly Phe
35 40 45

Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr Gln Cys
50 55 60

Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro Thr Gln
65 70 75 80

Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg Gln Asp Ser
85 90 95

Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly His Phe
100 105 110

Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu
115 120 125

Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu Asp Ala Val
130 135 140

Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg
145 150 155 160

Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val Trp Pro Arg
165 170 175

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

<210> 124
<211> 681
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nuecleotídica de la cadena del agujero de Fc

<400> 124
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 420

aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggtaa a 681

<210> 125
<211> 1335
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nuecleotídica de la cadena humana del pomo Fc antígeno OX40

<400> 125
ctgcactgcg tgggcgacac ctaccccagc aacgaccggt gctgccacga gtgcagaccc 60

ggcaacggca tggtgtcccg gtgcagccgg tcccagaaca ccgtgtgcag accttgcggc 120

cctggcttct acaacgacgt ggtgtccagc aagccctgca agccttgtac ctggtgcaac 180

ctgcggagcg gcagcgagcg gaagcagctg tgtaccgcca cccaggatac cgtgtgccgg 240

tgtagagccg gcacccagcc cctggacagc tacaaacccg gcgtggactg cgccccttgc 300

cctcctggcc acttcagccc tggcgacaac caggcctgca agccttggac caactgcacc 360

ctggccggca agcacaccct gcagcccgcc agcaatagca gcgacgccat ctgcgaggac 420

cgggatcctc ctgccaccca gcctcaggaa acccagggcc ctcccgccag acccatcacc 480

gtgcagccta cagaggcctg gcccagaacc agccaggggc ctagcaccag acccgtggaa 540

gtgcctggcg gcagagccgt cgacgaacag ttatattttc agggcggctc acccaaatct 600

gcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 660

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 720

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 780

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 840

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 900

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 960

aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc 1020

aagaaccagg tcagcctgtg gtgcctggtc aaaggcttct atcccagcga catcgccgtg 1080

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1140

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1200

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1260

agcctctccc tgtctccggg taaatccgga ggcctgaacg acatcttcga ggcccagaag 1320

attgaatggc acgag 1335

<210> 126
<211> 1335
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nuecleotídica de la cadena de macaco del pomo Fc antígeno OX40

<400> 126
ctccactgtg tcggggacac ctaccccagc aacgaccggt gctgtcagga gtgcaggcca 60

ggcaacggga tggtgagccg ctgcaaccgc tcccagaaca cggtgtgccg tccgtgcggg 120

cccggcttct acaacgacgt ggtcagcgcc aagccctgca aggcctgcac atggtgcaac 180

ctcagaagtg ggagtgagcg gaaacagccg tgcacggcca cacaggacac agtctgccgc 240

tgccgggcgg gcacccagcc cctggacagc tacaagcctg gagttgactg tgcccctgc 300

cctccagggc acttctcccc gggcgacaac caggcctgca agccctggac caactgcacc 360

ttggccggga agcacaccct gcagccagcc agcaatagct cggacgccat ctgtgaggac 420

agggaccccc cacccacaca gccccaggag acccagggcc ccccggccag gcccaccact 480

gtccagccca ctgaagcctg gcccagaacc tcacagagac cctccacccg gcccgtggag 540

gtccccaggg gccctgcggt cgacgaacag ttatattttc agggcggctc acccaaatct 600

gcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 660

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 720

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 780

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 840

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 900

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 960

aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc 1020

aagaaccagg tcagcctgtg gtgcctggtc aaaggcttct atcccagcga catcgccgtg 1080

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1140

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1200

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1260

agcctctccc tgtctccggg taaatccgga ggcctgaacg acatcttcga ggcccagaag 1320

attgaatggc acgag 1335

<210> 127
<211> 1353
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nuecleotídica de la cadena de murino del pomo Fc antígeno OX40

<400> 127
gtgaccgcca gacggctgaa ctgcgtgaag cacacctacc ccagcggcca caagtgctgc 60

agagagtgcc agcccggcca cggcatggtg tccagatgcg accacacacg ggacaccctg 120

tgccaccctt gcgagacagg cttctacaac gaggccgtga actacgatac ctgcaagcag 180

tgcacccagt gcaaccacag aagcggcagc gagctgaagc agaactgcac ccccacccag 240

gataccgtgt gcagatgcag acccggcacc cagcccagac aggacagcgg ctacaagctg 300

ggcgtggact gcgtgccctg ccctcctggc cacttcagcc ccggcaacaa ccaggcctgc 360

aagccctgga ccaactgcac cctgagcggc aagcagacca gacaccccgc cagcgacagc 420

ctggatgccg tgtgcgagga cagaagcctg ctggccaccc tgctgtggga gacacagcgg 480

cccaccttca gacccaccac cgtgcagagc accaccgtgt ggcccagaac cagcgagctg 540

cccagtcctc ctaccctcgt gacacctgag ggccccgtcg acgaacagtt atattttcag 600

ggcggctcac ccaaatctgc agacaaaact cacacatgcc caccgtgccc agcacctgaa 660

ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 720

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 780

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 840

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 900

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 960

aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1020

tgccgggatg agctgaccaa gaaccaggtc agcctgtggt gcctggtcaa aggcttctat 1080

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1140

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1200

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1260

aaccactaca cgcagaagag cctctccctg tctccgggta aatccggagg cctgaacgac 1320

atcttcgagg cccagaagat tgaatggcac gag 1353

<210> 128
<211> 227
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena Fc del agujero

<400> 128

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 129
<211> 445
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena del pomo de Fc del antígeno humano OX40

<400> 129

```
Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
1               5                  10                  15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
            20                  25                  30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
        35                  40                  45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
    50                  55                  60

Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
65                  70                  75                  80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
                85                  90                  95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
            100                 105                 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
        115                 120                 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
    130                 135                 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
145                 150                 155                 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
                165                 170                 175

Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Asp Glu Gln Leu Tyr
            180                 185                 190

Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
        195                 200                 205

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
    210                 215                 220

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
225                 230                 235                 240
```

```
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                245                 250                 255

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            260                 265                 270

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
        275                 280                 285

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    290                 295                 300

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
305                 310                 315                 320

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
                325                 330                 335

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
            340                 345                 350

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
        355                 360                 365

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    370                 375                 380

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
385                 390                 395                 400

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                405                 410                 415

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu
            420                 425                 430

Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
        435                 440                 445


<210>  130
<211>  445
<212>  PRT
<213>  Secuencia artificial

<220>
<223>  Cadena del pomo de Fc del antígeno de macaco OX40

<400>  130

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys Gln
```

```
1               5                   10                  15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Asn Arg Ser Gln
            20                  25                  30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
        35                  40                  45

Ser Ala Lys Pro Cys Lys Ala Cys Thr Trp Cys Asn Leu Arg Ser Gly
    50                  55                  60

Ser Glu Arg Lys Gln Pro Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
65                  70                  75                  80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
                85                  90                  95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
            100                 105                 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
        115                 120                 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
    130                 135                 140

Pro Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Thr Thr
145                 150                 155                 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Arg Pro Ser Thr
                165                 170                 175

Arg Pro Val Glu Val Pro Arg Gly Pro Ala Val Asp Glu Gln Leu Tyr
            180                 185                 190

Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
        195                 200                 205

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
    210                 215                 220

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
225                 230                 235                 240

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                245                 250                 255
```

```
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            260                 265                 270

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
        275                 280                 285

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    290                 295                 300

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
305                 310                 315                 320

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg
                325                 330                 335

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly
            340                 345                 350

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
        355                 360                 365

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    370                 375                 380

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
385                 390                 395                 400

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                405                 410                 415

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu
            420                 425                 430

Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
        435                 440                 445
```

<210> 131
<211> 451
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena del pomo de Fc del antígeno murino OX40

<400> 131

```
Val Thr Ala Arg Arg Leu Asn Cys Val Lys His Thr Tyr Pro Ser Gly
1               5                   10                  15

His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg
```

```
            20                  25                  30

Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu Thr Gly Phe
        35                  40                  45

Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr Gln Cys
    50                  55                  60

Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro Thr Gln
65                  70                  75                  80

Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg Gln Asp Ser
                85                  90                  95

Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly His Phe
            100                 105                 110

Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu
        115                 120                 125

Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu Asp Ala Val
    130                 135                 140

Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg
145                 150                 155                 160

Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val Trp Pro Arg
                165                 170                 175

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

Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp
        195                 200                 205

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
    210                 215                 220

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
225                 230                 235                 240

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
                245                 250                 255

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
            260                 265                 270
```

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
275 280 285

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
305 310 315 320

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
325 330 335

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
340 345 350

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
355 360 365

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
370 375 380

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
385 390 395 400

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
405 410 415

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
420 425 430

Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
435 440 445

Trp His Glu
450

<210> 132
<211> 1613
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de la biblioteca DP88-4

<400> 132
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tggccgacat ccagatgacc cagtctcctt ccaccctgtc tgcatctgta ggagaccgtg 120

tcaccatcac ttgccgtgcc agtcagagta ttagtagctg gttggcctgg tatcagcaga 180

aaccagggaa agcccctaag ctcctgatct atgatgcctc cagtttggaa agtggggtcc 240

catcacgttt cagcggcagt ggatccggga cagaattcac tctcaccatc agcagcttgc 300

agcctgatga ttttgcaact tattactgcc aacagtataa tagttattct acgtttggcc 360

agggcaccaa agtcgagatc aagcgtacgg tggctgcacc atctgtcttc atcttcccgc 420

catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg aataacttct 480

atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg ggtaactccc 540

aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc agcaccctga 600

cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc acccatcagg 660

gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgtggagcc gcagaacaaa 720

aactcatctc agaagaggat ctgaatggag ccgcagacta caaggacgac gacgacaagg 780

gtgccgcata ataaggcgcg ccaattctat ttcaaggaga cagtcatatg aaatacctgc 840

tgccgaccgc tgctgctggt ctgctgctcc tcgctgccca gccggcgatg gcccaggtgc 900

aattggtgca gtctggggct gaggtgaaga agcctgggtc ctcggtgaag gtctcctgca 960

aggcctccgg aggcacattc agcagctacg ctataagctg ggtgcgacag gcccctggac 1020

aagggctcga gtggatggga gggatcatcc ctatctttgg tacagcaaac tacgcacaga 1080

agttccaggg cagggtcacc attactgcag acaaatccac gagcacagcc tacatggagc 1140

tgagcagcct gagatctgag gacaccgccg tgtattactg tgcgagacta tccccaggcg 1200

gttactatgt tatggatgcc tggggccaag ggaccaccgt gaccgtctcc tcagctagca 1260

ccaaaggccc atcggtcttc cccctggcac cctcctccaa gagcacctct gggggcacag 1320

cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg tcgtggaact 1380

caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc tcaggactct 1440

actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag acctacatct 1500

gcaacgtgaa tcacaagccc agcaacacca aagtggacaa gaaagttgag cccaaatctt 1560

gtgacgcggc cgcaagcact agtgcccatc accatcacca tcacgccgcg gca 1613

<210> 133
<211> 723
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de la cadena ligera de Fab Vk1_5

<400> 133
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctacgtt tggccagggc 300

accaaagtcg agatcaagcg tacggtggct gcaccatctg tcttcatctt cccgccatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600

agctcgcccg tcacaaagag cttcaacagg ggagagtgtg gagccgcaga acaaaaactc 660

atctcagaag aggatctgaa tggagccgca gactacaagg acgacgacga caagggtgcc 720

gca 723

<210> 134
<211> 241
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera de Fab Vk1_5

<400> 134

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Asn Arg Gly Glu Cys Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
    210                 215                 220

Asp Leu Asn Gly Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala
225                 230                 235                 240

Ala
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<210> 135
<211> 720
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de la cadena pesada de Fab VH1_69

<400> 135

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caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactatcc      300

ccaggcggtt actatgttat ggatgcctgg ggccaaggga ccaccgtgac cgtctcctca      360

gctagcacca aaggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg      480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc      600

tacatctgca acgtgaatca caagcccagc aacaccaaag tggacaagaa agttgagccc      660
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aaatcttgtg acgcggccgc aagcactagt gcccatcacc atcaccatca cgccgcggca 720

<210> 136
<211> 240
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada de Fab VH1_69

<400> 136

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

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

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

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

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

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

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

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

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

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

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

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

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

195 200 205

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

Ala Ala Ala Ser Thr Ser Ala His His His His His His Ala Ala Ala
225 230 235 240

<210> 137
<211> 26
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador LMB3

<400> 137
caggaaacag ctatgaccat gattac 26

<210> 138
<211> 71
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador Vk1_5_L3r_S

<400> 138
ctcgactttg gtgccctggc caaacgtsba atacgaatta tactgttggc agtaataagt 60

tgcaaaatca t 71

<210> 139
<211> 74
<212> ADN
<213> Secuencia artificial

<220>
<223> Vk1_5_L3r_SY Primer

<400> 139
ctcgactttg gtgccctggc caaacgtmhr sgratacgaa ttatactgtt ggcagtaata 60

agttgcaaaa tcat 74

<210> 140
<211> 77
<212> ADN
<213> Secuencia artificial

<220>
<223> Vk1_5_L3r_SPY

<400> 140
ctcgactttg gtgccctggc caaacgtmhh msssgratac gaattatact gttggcagta 60

ataagttgca aaatcat 77

<210> 141
<211> 27
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador RJH31

<400> 141
acgtttggcc agggcaccaa agtcgag 27

<210> 142
<211> 28
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador RJH32

<400> 142
tctcgcacag taatacacgg cggtgtcc 28

<210> 143
<211> 64
<212> ADN
<213> Secuencia artificial

<220>
<223> DP88-v4-4

<400> 143
ggacaccgcc gtgtattact gtgcgagaga ctactggggc caagggacca ccgtgaccgt 60

ctcc 64

<210> 144
<211> 64
<212> ADN
<213> Secuencia artificial

<220>
<223> DP88-v4-6

<400> 144
ggacaccgcc gtgtattact gtgcgagaga ctactggggc caagggacca ccgtgaccgt 60

ctcc 64

<210> 145
<211> 64
<212> ADN
<213> Secuencia artificial

<220>
<223> DP88-v4-8

<400> 145

ggacaccgcc gtgtattact gtgcgagaga ctactggggc caagggacca ccgtgaccgt 60

ctcc 64

<210> 146
<211> 30
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador fdseqlong

<400> 146
gacgttagta aatgaatttt ctgtatgagg 30

<210> 147
<211> 1596
<212> ADN
<213> Secuencia artificial

<220>
<223> Molde (Vk3_20/VH3_23)

<400> 147
atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60

atggccgaaa tcgtgttaac gcagtctcca ggcaccctgt ctttgtctcc aggggaaaga 120

gccaccctct cttgcagggc cagtcagagt gttagcagca gctacttagc ctggtaccag 180

cagaaacctg gccaggctcc caggctcctc atctatggag catccagcag ggccactggc 240

atcccagaca ggttcagtgg cagtggatcc gggacagact tcactctcac catcagcaga 300

ctggagcctg aagattttgc agtgtattac tgtcagcagt atggtagctc accgctgacg 360

ttcggccagg ggaccaaagt ggaaatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 420

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 480

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 540

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 600

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 660

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg tggagccgca 720

catcaccatc accatcacgg agccgcagac tacaaggacg acgacgacaa gggtgccgca 780

taataaggcg cgccaattct atttcaagga gacagtcata tgaaatacct gctgccgacc 840

gctgctgctg gtctgctgct cctcgctgcc cagccggcga tggccgaggt gcaattgctg 900

gagtctgggg gaggcttggt acagcctggg gggtccctga gactctcctg tgcagcctcc 960

ggattcacct ttagcagtta tgccatgagc tgggtccgcc aggctccagg gaaggggctg 1020

gagtgggtct cagctattag tggtagtggt ggtagcacat actacgcaga ctccgtgaag 1080

ggccggttca ccatctccag agacaattcc aagaacacgc tgtatctgca gatgaacagc 1140

ctgagagccg aggacacggc cgtatattac tgtgcgaaac cgtttccgta ttttgactac 1200

tggggccaag gaaccctggt caccgtctcg agtgctagca ccaaaggccc atcggtcttc 1260

cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1320

aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1380

gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg 1440

accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc 1500

agcaacacca aagtggacaa gaaagttgag cccaaatctt gtgacgcggc cgcagaacaa 1560

aaactcatct cagaagagga tctgaatgcc gcggca 1596

<210> 148
<211> 714
<212> ADN
<213> Secuencia artificial

<220>
<223> Cadena ligera de Fab Vk3_20

<400> 148
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct gacgttcggc 300

caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgtggagc cgcacatcac 660

catcaccatc acggagccgc agactacaag gacgacgacg acaagggtgc cgca 714

<210> 149
<211> 238
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera de Fab Vk3_20

<400> 149

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

1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys Gly Ala Ala His His His His His His
210 215 220

Gly Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala
225 230 235

<210> 150
<211> 711
<212> ADN
<213> Secuencia artificial

<220>
<223> Cadena pesada de Fab VH3_23

<400> 150
gaggtgcaat tgctggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt 300

ccgtattttg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaaa 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaagtg gacaagaaag ttgagcccaa atcttgtgac 660

gcggccgcag aacaaaaact catctcagaa gaggatctga atgccgcggc a 711

<210> 151
<211> 237
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada de Fab VH3_23 (DP47)

<400> 151

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Ala Ala
225 230 235

<210> 152
<211> 25
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador MS64

<400> 152
acgttcggcc aggggaccaa agtgg 25

<210> 153
<211> 25
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador DP47CDR3_ba

<400> 153
cgcacagtaa tatacggccg tgtcc 25

<210> 154
<211> 64

<212> ADN
<213> Secuencia artificial

<220>
<223> DP47-v4-4

<400> 154
cgaggacacg gccgtatatt actgtgcgga ctactggggc caaggaaccc tggtcaccgt 60

ctcg 64

<210> 155
<211> 64
<212> ADN
<213> Secuencia artificial

<220>
<223> DP47-v4-6

<400> 155
cgaggacacg gccgtatatt actgtgcgga ctactggggc caaggaaccc tggtcaccgt 60

ctcg 64

<210> 156
<211> 64
<212> ADN
<213> Secuencia artificial

<220>
<223> DP47-v4-8

<400> 156
cgaggacacg gccgtatatt actgtgcgga ctactggggc caaggaaccc tggtcaccgt 60

ctcg 64

<210> 157
<211> 30
<212> ADN
<213> Secuencia artificial

<220>
<223> fdseqlong

<400> 157
gacgttagta aatgaatttt ctgtatgagg 30

<210> 158
<211> 1605
<212> ADN
<213> Secuencia artificial

<220>
<223> Molde de biblioteca Vl3_19/VH3_23

<400> 158
atgaaatacc tattgcctac ggcagccgct ggattgttat tactcgcggc ccagccggcc 60

atggcctcgt ctgagctgac tcaggaccct gctgtgtctg tggccttggg acagacagtc 120

aggatcacat gccaaggaga cagcctcaga agttattatg caagctggta ccagcagaag 180

ccaggacagg cccctgtact tgtcatctat ggtaaaaaca accggccctc agggatccca 240

gaccgattct ctggctccag ctcaggaaac acagcttcct tgaccatcac tggggctcag 300

gcggaagatg aggctgacta ttactgtaac tcccgtgata gtagcggtaa tcatgtggta 360

ttcggcggag ggaccaagct gaccgtccta ggacaaccca aggctgcccc cagcgtgacc 420

ctgttccccc ccagcagcga ggaattgcag gccaacaagg ccaccctggt ctgcctgatc 480

agcgacttct acccaggcgc cgtgaccgtg gcctggaagg ccgacagcag ccccgtgaag 540

gccggcgtgg agaccaccac ccccagcaag cagagcaaca acaagtacgc cgccagcagc 600

tacctgagcc tgaccccga gcagtggaag agccacaggt cctacagctg ccaggtgacc 660

cacgagggca gcaccgtgga gaaaaccgtg gcccccaccg agtgcagcgg agccgcagaa 720

caaaaactca tctcagaaga ggatctgaat ggagccgcag actacaagga cgacgacgac 780

aagggtgccg cataataagg cgcgccaatt ctatttcaag gagacagtca tatgaaatac 840

ctgctgccga ccgctgctgc tggtctgctg ctcctcgctg cccagccggc gatggccgag 900

gtgcaattgc tggagtctgg gggaggcttg gtacagcctg gggggtccct gagactctcc 960

tgtgcagcct ccggattcac ctttagcagt tatgccatga gctgggtccg ccaggctcca 1020

gggaaggggc tggagtgggt ctcagctatt agtggtagtg gtggtagcac atactacgca 1080

gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 1140

cagatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgaa accgtttccg 1200

tattttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaaaggc 1260

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 1320

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 1380

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 1440

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 1500

aatcacaagc ccagcaacac caaagtggac aagaaagttg agcccaaatc ttgtgacgcg 1560

gccgcaagca ctagtgccca tcaccatcac catcacgccg cggca 1605

<210> 159
<211> 726
<212> ADN
<213> Secuencia artificial

<220>
<223> Cadena ligera de Fab Vl3_19

<400> 159
tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactcccgt gatagtagcg gtaatcatgt ggtattcggc 300

ggagggacca agctgaccgt cctaggacaa cccaaggctg cccccagcgt gaccctgttc 360

ccccccagca gcgaggaatt gcaggccaac aaggccaccc tggtctgcct gatcagcgac 420

ttctacccag gcgccgtgac cgtggcctgg aaggccgaca gcagccccgt gaaggccggc 480

gtggagacca ccacccccag caagcagagc aacaacaagt acgccgccag cagctacctg 540

agcctgaccc ccgagcagtg gaagagccac aggtcctaca gctgccaggt gacccacgag 600

ggcagcaccg tggagaaaac cgtggccccc accgagtgca gcggagccgc agaacaaaaa 660

ctcatctcag aagaggatct gaatggagcc gcagactaca aggacgacga cgacaagggt 720

gccgca 726

<210> 160
<211> 242
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera de Fab Vl3_19

<400> 160

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

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

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

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

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

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

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

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

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

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145   150   155   160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
                165   170   175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
            180   185   190

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

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

Glu Asp Leu Asn Gly Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Gly
225   230   235   240

Ala Ala

<210> 161
<211> 26
<212> ADN
<213> Secuencia artificial

<220>
<223> Biblioteca LMB3 lambda-DP47

<400> 161
caggaaacag ctatgaccat gattac   26

<210> 162
<211> 85
<212> ADN
<213> Secuencia artificial

<220>
<223> Biblioteca Vl_3_19_L3r_V lambda-DP47

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agtaatagtc agcctcatct tccgc   85

<210> 163
<211> 88
<212> ADN
<213> Secuencia artificial

<220>
<223> Vl_3_19_L3r_HV lambda-DP47

<400> 163
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tacagtaata gtcagcctca tcttccgc 88

<210> 164
<211> 91
<212> ADN
<213> Secuencia artificial

<220>
<223> Vl_3_19_L3r_HLV lambda-DP47

<400> 164
ggacggtcag cttggtccct ccgccgaata crhmvwgatg attaccgcta ctatcacggg 60

agttacagta atagtcagcc tcatcttccg c 91

<210> 165
<211> 28
<212> ADN
<213> Secuencia artificial

<220>
<223> RJH80 lambda-DP47

<400> 165
ttcggcggag ggaccaagct gaccgtcc 28

<210> 166
<211> 318
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (8H9) VL

<400> 166
tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactcccgt gttatgcctc ataatcgcgt attcggcgga 300

gggaccaagc tgaccgtc 318

<210> 167

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

<220>
<223> ADN (8H9) VH

<400> 167
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttttc 300

taccgtggtg gtgtttctat ggactactgg ggccaaggaa ccctggtcac cgtctcgagt 360

<210> 168
<211> 321
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (49B4) VL

<400> 168
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atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatagttcgc agccgtatac gtttggccag 300

ggcaccaaag tcgagatcaa g 321

<210> 169
<211> 354
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (49B4) VH

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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctca 354

<210> 170
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (1G4) VL

<400> 170
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atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatatttcgt attccatgtt gacgtttggc 300

cagggcacca aagtcgagat caag 324

<210> 171
<211> 348
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (1G4) VH

<400> 171
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctca 348

<210> 172
<211> 321
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (20B7) VL

<400> 172
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atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatcaggctt tttcgcttac gtttggccag 300

ggcaccaaag tcgagatcaa g 321

<210> 173
<211> 366
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (20B7) VH

<400> 173
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac 300

tacccgtact cttactgggg tgacttcgac tactggggcc aagggaccac cgtgaccgtc 360

tcctca 366

<210> 174
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-563) VL

<400> 174
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ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag 120

ccaggacaag ccccccgcct cctgatttac ggcgcttcct ctcgggcaac tggtatccct 180

gacaggttct cagggagcgg aagcggaaca gattttacct tgactatttc tagactggag 240

ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagcccccc caccttggc 300

caggggacaa aagtcgaaat caag 324

<210> 175
<211> 348
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-563) VH

<400> 175
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcttgacgtt 300

ggtgctttcg actactgggg ccaaggagcc ctggtcaccg tctcgagt 348

<210> 176
<211> 324
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-564) VL

<400> 176
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ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag 120

ccaggacaag ccccccgcct cctgatttac ggcgcttcct ctcgggcaac tggtatccct 180

gacaggttct cagggagcgg aagcggaaca gattttacct tgactatttc tagactggag 240

ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagcccccc caccttggc 300

caggggacaa aagtcgaaat caag 324

<210> 177
<211> 348
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-564) VH

<400> 177
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

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ggtccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagt 348

<210> 178
<211> 318
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (17A9) VL

<400> 178

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acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactcccgt gttatgcctc ataatcgcgt attcggcgga 300

gggaccaagc tgaccgtc 318

<210> 179
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (17A9) VH

<400> 179
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttttc 300

taccgtggtg gtgtttctat ggactactgg ggccaaggaa ccctggtcac cgtctcgagt 360

<210> 180
<211> 645
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 8H9 P329GLALA IgG1

<400> 180
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatttgacgt attcgcggtt tacgtttggc 300

cagggcacca aagtcgagat caagcgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 181
<211> 1338
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 8H9 P329GLALA IgG1

<400> 181
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

ggttggatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 182
<211> 215
<212> PRT

<213> Secuencia artificial

<220>
<223> Cadena ligera 8H9 P329GLALA IgG1

<400> 182

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

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 183
<211> 446
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 8H9 P329GLALA IgG1

<400> 183

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


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


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


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


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


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


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


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


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


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


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


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


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


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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 184
<211> 642
<212> ADN
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<220>
<223> ADN cadena ligera 49B4 P329GLALA IgG1

<400> 184
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atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatagttcgc agccgtatac gtttggccag 300

ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

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ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 185
<211> 1344
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 49B4 P329GLALA IgG1

<400> 185
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg taaa 1344

<210> 186
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera 49B4 P329GLALA IgG1

<400> 186

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 187
<211> 448
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 49B4

<400> 187

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

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

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

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

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

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

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

115 120 125

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

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

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 188
<211> 645
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 1G4 P329GLALA IgG1

<400> 188
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atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatatttcgt attccatgtt gacgtttggc 300

cagggcacca aagtcgagat caagcgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 189
<211> 1338
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 1G4 P329GLALA IgG1

<400> 189
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 190
<211> 215
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera 1G4 P329GLALA IgG1

<400> 190

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 191
<211> 446
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 1G4 P329GLALA IgG1

<400> 191

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

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

```
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270
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Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

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

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

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

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

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

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

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

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

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

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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<210> 192
<211> 642
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 20B7 P329GLALA IgG1

<400> 192

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gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc       60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca      120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca      180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct      240

gatgattttg caacttatta ctgccaacag tatcaggctt tttcgcttac gtttggccag      300
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ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 193
<211> 1356
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 20B7 P329GLALA IgG1

<400> 193
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac 300

tacccgtact cttactgggg tgacttcgac tactggggcc aagggaccac cgtgaccgtc 360

tcctcagcta gcaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaagctgca 720

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcg gcgccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

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tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 194
<211> 214
<212> PRT
<213> Artificial

<220>
<223> Cadena ligera 20B7 P329GLALA IgG1

<400> 194

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

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

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

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

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

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

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


Phe Asn Arg Gly Glu Cys
    210


<210>  195
<211>  452
<212>  PRT
<213>  Artificial

<220>
<223>  Cadena pesada 20B7 P329GLALA IgG1

<400>  195

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


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


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


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


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


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


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


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


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


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


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

```
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
450

<210> 196
<211> 645
<212> ADN
<213> Artificial

<220>
<223> ADN cadena ligera CLC-563 P329GLALA IgG1

<400> 196
gagatcgtgc tgacccagag ccccggcaca ctctccctgt ctcctgggga aagggccacc 60

ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag 120

ccaggacaag ccccccgcct cctgatttac ggcgcttcct ctcgggcaac tggtatccct 180

gacaggttct cagggagcgg aagcggaaca gattttacct tgactatttc tagactggag 240

ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagcccccc caccttggc 300

caggggacaa aagtcgaaat caagcgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 197
<211> 1338
<212> ADN
<213> Artificial

<220>
<223> ADN cadena pesada CLC-563 P329GLALA IgG1

<400> 197
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcttgacgtt 300

ggtgctttcg actactgggg ccaaggagcc ctggtcaccg tctcgagtgc tagcaccaag 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 198
<211> 215
<212> PRT
<213> Artificial

<220>
<223> Cadena ligera CLC-563 P329GLALA IgG1

<400> 198

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 199
<211> 446
<212> PRT
<213> Artificial

<220>
<223> Cadena pesada CLC-563 P329GLALA IgG1

<400> 199

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 200
<211> 645
<212> ADN
<213> Artificial

<220>
<223> ADN cadena ligera CLC-564 P329GLALA IgG1

<400> 200
gagatcgtgc tgacccagag ccccggcaca ctctccctgt ctcctgggga aagggccacc 60

ctttcatgca gagccagcca gtccgtctct agtagctacc tggcatggta tcagcagaag 120

ccaggacaag ccccccgcct cctgatttac ggcgcttcct ctcgggcaac tggtatccct 180

gacaggttct cagggagcgg aagcggaaca gattttacct tgactatttc tagactggag 240

ccagaggact tcgccgtgta ttactgtcag cagtacggta gtagcccccc caccttttggc 300

caggggacaa aagtcgaaat caagcgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 201
<211> 1338
<212> ADN
<213> Artificial

<220>
<223> ADN cadena pesada CLC-564 P329GLALA IgG1

<400> 201
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gttcgacgtt 300

ggtccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaag 360

ggcccatcgg tcttcccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 202
<211> 215
<212> PRT
<213> Artificial

<220>
<223> Cadena ligera CLC-564 P329GLALA IgG1

<400> 202

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 203
<211> 446

<212> PRT
<213> Artificial

<220>
<223> Cadena pesada CLC-564 P329GLALA IgG1

<400> 203

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 204
<211> 639
<212> ADN
<213> Artificial

<220>

<223> ADN cadena ligera 17A9 P329GLALA IgG1

<400> 204
tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactcccgt gttatgcctc ataatcgcgt attcggcgga 300

gggaccaagc tgaccgtcct aggtcaaccc aaggctgccc ccagcgtgac cctgttcccc 360

cccagcagcg aggaactgca ggccaacaag gccaccctgg tctgcctgat cagcgacttc 420

tacccaggcg ccgtgaccgt ggcctggaag gccgacagca gccccgtgaa ggccggcgtg 480

gagaccacca cccccagcaa gcagagcaac aacaagtacg ccgccagcag ctacctgagc 540

ctgacccccg agcagtggaa gagccacagg tcctacagct gccaggtgac ccacgagggc 600

agcaccgtgg agaaaaccgt ggcccccacc gagtgcagc 639

<210> 205
<211> 1350
<212> ADN
<213> Artificial

<220>
<223> ADN cadena pesada 17A9 P329GLALA IgG1

<400> 205
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgttttc 300

taccgtggtg gtgtttctat ggactactgg ggccaaggaa ccctggtcac cgtctcgagt 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 206
<211> 213
<212> PRT
<213> Artificial

<220>
<223> Cadena ligera 17A9 P329GLALA IgG1

<400> 206

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

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

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

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

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

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

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

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

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

```
Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
145                 150                 155                 160


Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
                165                 170                 175


Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
            180                 185                 190


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


Pro Thr Glu Cys Ser
    210


<210>  207
<211>  450
<212>  PRT
<213>  Artificial

<220>
<223>  Cadena pesada 17A9 P329GLALA IgG1

<400>  207

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


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


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


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


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


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


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


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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
    450
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<210> 208
<211> 663
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica His de OX40 humano

<400> 208

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ctgcactgcg tgggcgacac ctaccccagc aacgaccggt gctgccacga gtgcagaccc       60

ggcaacggca tggtgtcccg gtgcagccgg tcccagaaca ccgtgtgcag accttgcggc      120

cctggcttct acaacgacgt ggtgtccagc aagccctgca agccttgtac ctggtgcaac      180

ctgcggagcg gcagcgagcg gaagcagctg tgtaccgcca cccaggatac cgtgtgccgg      240

tgtagagccg gcacccagcc cctggacagc tacaaacccg gcgtggactg cgccccttgc      300

cctcctggcc acttcagccc tggcgacaac caggcctgca agccttggac caactgcacc      360

ctggccggca agcacaccct gcagcccgcc agcaatagca gcgacgccat ctgcgaggac      420

cgggatcctc ctgccaccca gcctcaggaa acccagggcc ctcccgccag acccatcacc      480

gtgcagccta cagaggcctg gcccagaacc agccaggggc ctagcaccag acccgtggaa      540

gtgcctggcg gcagagccgt cgacgaacag ttatattttc agggcggctc aggcctgaac      600

gacatcttcg aggcccagaa gatcgagtgg cacgaggctc gagctcacca ccatcaccat      660

cac                                                                    663
```

<210> 209
<211> 221
<212> PRT
<213> Secuencia artificial

<220>
<223> His de OX40 humano

<400> 209

```
Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
1               5                   10                  15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
            20                  25                  30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
        35                  40                  45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
    50                  55                  60

Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
65                  70                  75                  80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
                85                  90                  95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala
            100                 105                 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
        115                 120                 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
    130                 135                 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
145                 150                 155                 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
                165                 170                 175

Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Asp Glu Gln Leu Tyr
            180                 185                 190

Phe Gln Gly Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile
        195                 200                 205

Glu Trp His Glu Ala Arg Ala His His His His His His
    210                 215                 220
```

<210> 210
<211> 681
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN OX40 His murino

<400> 210
gtgaccgcca gacggctgaa ctgcgtgaag cacacctacc ccagcggcca caagtgctgc 60

agagagtgcc agcccggcca cggcatggtg tccagatgcg accacacacg ggacaccctg 120

tgccaccctt gcgagacagg cttctacaac gaggccgtga actacgatac ctgcaagcag 180

tgcacccagt gcaaccacag aagcggcagc gagctgaagc agaactgcac ccccacccag 240

gataccgtgt gcagatgcag acccggcacc cagcccagac aggacagcgg ctacaagctg 300

ggcgtggact gcgtgccctg ccctcctggc cacttcagcc ccggcaacaa ccaggcctgc 360

aagccctgga ccaactgcac cctgagcggc aagcagacca gacaccccgc cagcgacagc 420

ctggatgccg tgtgcgagga cagaagcctg ctggccaccc tgctgtggga gacacagcgg 480

cccaccttca gacccaccac cgtgcagagc accaccgtgt ggcccagaac cagcgagctg 540

cccagtcctc ctaccctcgt gacacctgag ggccccgtcg acgaacagtt atattttcag 600

ggcggctcag gcctgaacga catcttcgag gcccagaaga tcgagtggca cgaggctcga 660

gctcaccacc atcaccatca c 681

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

<220>
<223> His de OX40 murino

<400> 211

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

Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val Ser Arg Cys
            20   25   30

Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu Thr Gly Phe Tyr
        35   40   45

Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr Gln Cys Asn
    50   55   60

His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro Thr Gln Asp
65   70   75   80

Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg Gln Asp Ser Gly
                85   90   95

Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly His Phe Ser
100 105 110

Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu Ser
115 120 125

Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu Asp Ala Val Cys
130 135 140

Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg Pro
145 150 155 160

Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val Trp Pro Arg Thr
165 170 175

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

Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Gly Leu Asn Asp Ile Phe
195 200 205

Glu Ala Gln Lys Ile Glu Trp His Glu Ala Arg Ala His His His His
210 215 220

His His
225

<210> 212
<211> 1317
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica Fc antígeno OX40 dimérico humano

<400> 212
ctgcactgcg tgggcgacac ctaccccagc aacgaccggt gctgccacga gtgcagaccc 60

ggcaacggca tggtgtcccg gtgcagccgg tcccagaaca ccgtgtgcag accttgcggc 120

cctggcttct acaacgacgt ggtgtccagc aagccctgca agccttgtac ctggtgcaac 180

ctgcggagcg gcagcgagcg gaagcagctg tgtaccgcca cccaggatac cgtgtgccgg 240

tgtagagccg gcacccagcc cctggacagc tacaaacccg gcgtggactg cgccccttgc 300

cctcctggcc acttcagccc tggcgacaac caggcctgca agccttggac caactgcacc 360

ctggccggca agcacaccct gcagcccgcc agcaatagca gcgacgccat ctgcgaggac 420

cgggatcctc ctgccaccca gcctcaggaa acccagggcc ctcccgccag acccatcacc 480

gtgcagccta cagaggcctg gcccagaacc agccaggggc ctagcaccag acccgtggaa 540

gtgcctggcg gcagagccgt cgacgaacag ttatattttc agggcggctc acccaaatct 600

gcagacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 660

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 720

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 780

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 840

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 900

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 960

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1020

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1080

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1140

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1200

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1260

agcctctccc tgtctccggg taaatccggc tacccatacg atgttccaga ttacgct 1317

<210> 213
<211> 439
<212> PRT
<213> Secuencia artificial

<220>
<223> Fc antígeno OX40 dimérico humano

<400> 213

Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
1 5 10 15

Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln
20 25 30

Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val
35 40 45

Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly
50 55 60

Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg
65 70 75 80

Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp
85 90 95

Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala

```
            100                 105                 110

Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln
        115                 120                 125

Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro
    130                 135                 140

Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr
145                 150                 155                 160

Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr
                165                 170                 175

Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Asp Glu Gln Leu Tyr
            180                 185                 190

Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro
        195                 200                 205

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
    210                 215                 220

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
225                 230                 235                 240

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                245                 250                 255

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            260                 265                 270

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
        275                 280                 285

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    290                 295                 300

Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
305                 310                 315                 320

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                325                 330                 335

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
            340                 345                 350
```

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
355 360 365

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
370 375 380

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
385 390 395 400

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
405 410 415

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Tyr Pro
420 425 430

Tyr Asp Val Pro Asp Tyr Ala
435

<210> 214
<211> 2064
<212> ADN
<213> Secuencia artificial

<220>
<223> (8B9) VHCH1-Cadena pesada-(28H1) VHCL

<400> 214
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

ggttggatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360

ggcccatccg tgttccctct ggcccccttcc agcaagtcta cctctggcgg cacagccgct 420

ctgggctgcc tcgtgaagga ctacttcccc gagcctgtga cagtgtcctg gaactctggc 480

gccctgacat ccggcgtgca cacctttcca gctgtgctgc agtcctccgg cctgtactcc 540

ctgtcctccg tcgtgacagt gccctccagc tctctgggca cccagaccta catctgcaac 600

gtgaaccaca agccctccaa caccaaggtg gacaagaagg tggaacccaa gtcctgcgac 660

aagacccaca cctgtccccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc 720

ctgttccccc caaagcccaa ggacaccctg atgatctccc ggacccccga agtgacctgc 780

gtggtggtgg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840

gtggaagtgc acaatgccaa gaccaagcct agagaggaac agtacaactc cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaaaga gtacaagtgc 960

aaggtgtcca acaaggccct gggagccccc atcgaaaaga ccatctccaa ggccaagggc 1020

cagcctcgcg agcctcaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgtct cgtgaaaggc ttctaccct ccgatatcgc cgtggaatgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgac 1200

ggctcattct tcctgtactc taagctgaca gtggacaagt cccggtggca gcagggcaac 1260

gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 1320

tccctgtctc ccgggggagg cggaggatct ggcggaggcg gatccggtgg tggcggatct 1380

gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc 1440

ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt 1500

tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggcctccggc 1560

gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcggga taacagcaag 1620

aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc 1680

gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg 1740

agcgcttctg tggccgctcc ctccgtgttc atcttcccac cttccgacga gcagctgaag 1800

tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcggga agccaaggtg 1860

cagtggaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag 1920

gactccaagg acagcaccta ctccctgagc agcaccctga ccctgtccaa ggccgactac 1980

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aagtccttca accggggcga gtgc 2064

<210> 215
<211> 642
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN VLCH1-Cadena ligera 2 (28H1)

<400> 215
gagatcgtgc tgacccagtc tcccggcacc ctgagcctga gccctggcga gagagccacc 60

ctgagctgca gagccagcca gagcgtgagc cggagctacc tggcctggta tcagcagaag 120

cccggccagg cccccagact gctgatcatc ggcgccagca cccgggccac cggcatcccc 180

gatagattca gcggcagcgg ctccggcacc gacttcaccc tgaccatcag ccggctggaa 240

cccgaggact tcgccgtgta ctactgccag cagggccagg tgatcccccc caccttcggc 300

cagggcacca aggtggaaat caagagctcc gctagcacca agggcccctc cgtgtttcct 360

ctggccccca gcagcaagag cacctctggc ggaacagccg ccctgggctg cctggtgaaa 420

gactacttcc ccgagcccgt gaccgtgtcc tggaactctg gcgccctgac cagcggcgtg 480

cacacctttc cagccgtgct gcagagcagc ggcctgtact ccctgagcag cgtggtgaca 540

gtgccctcca gcagcctggg cacccagacc tacatctgca acgtgaacca caagcccagc 600

aacaccaaag tggacaagaa ggtggaaccc aagagctgcg ac 642

<210> 216
<211> 688
<212> PRT
<213> Secuencia artificial

<220>
<223> (8B9) VHCH1-Cadena pesada-(28H1) VHCL

<400> 216

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
465                 470                 475                 480

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                485                 490                 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            500                 505                 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
        515                 520                 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
    530                 535                 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
545                 550                 555                 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
                565                 570                 575

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

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
        595                 600                 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
    610                 615                 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
625                 630                 635                 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                645                 650                 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
            660                 665                 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
```

675 680 685

<210> 217
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> VLCH1-Cadena ligera 2 (28H1)

<400> 217

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

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

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

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

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

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

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

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

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
145 150 155 160

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

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

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
195 200 205

Glu Pro Lys Ser Cys Asp
210

<210> 218
<211> 2070
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (49B4) VHCH1-Cadena pesada-(28H1) VHCL

<400> 218
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360

accaagggcc catccgtgtt ccctctggcc ccttccagca agtctacctc tggcggcaca 420

gccgctctgg gctgcctcgt gaaggactac ttccccgagc ctgtgacagt gtcctggaac 480

tctggcgccc tgacatccgg cgtgcacacc tttccagctg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtcgt gacagtgccc tccagctctc tgggcaccca gacctacatc 600

tgcaacgtga accacaagcc ctccaacacc aaggtggaca agaaggtgga acccaagtcc 660

tgcgacaaga cccacacctg tccccccttgt cctgcccctg aagctgctgg cggccctagc 720

gtgttcctgt tccccccaaa gcccaaggac accctgatga tctcccggac ccccgaagtg 780

acctgcgtgg tggtggatgt gtcccacgag gaccctgaag tgaagttcaa ttggtacgtg 840

gacggcgtgg aagtgcacaa tgccaagacc aagcctagag aggaacagta caactccacc 900

taccgggtgg tgtccgtgct gaccgtgctg caccaggatt ggctgaacgg caaagagtac 960

aagtgcaagg tgtccaacaa ggccctggga gcccccatcg aaaagaccat ctccaaggcc 1020

aagggccagc ctcgcgagcc tcaggtgtac accctgcccc ctagcagaga tgagctgacc 1080

aagaaccagg tgtccctgac ctgtctcgtg aaaggcttct acccctccga tatcgccgtg 1140

gaatgggaga gcaacggcca gcccgagaac aactacaaga ccacccccccc tgtgctggac 1200

tccgacggct cattcttcct gtactctaag ctgacagtgg acaagtcccg gtggcagcag 1260

ggcaacgtgt tctcctgctc cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgtccc tgtctcccgg gggaggcgga ggatctggcg gaggcggatc cggtggtggc 1380

ggatctgggg gcggtggatc tgaggtgcag ctgctggaat ctgggggagg actggtgcag 1440

ccaggcggat ctctgaggct gtcctgcgct gcttccggct ttaccttctc cagccacgcc 1500

atgagttggg tgcgccaggc acccggaaaa ggactggaat gggtgtcagc catctgggcc 1560

tccggcgagc agtactacgc cgatagcgtg aagggccggt tcaccatctc tcgggataac 1620

agcaagaata ctctgtacct gcagatgaac tccctgcgcg ctgaagatac cgctgtgtat 1680

tactgcgcca agggctggct gggcaacttc gattactggg gccagggaac cctcgtgact 1740

gtctcgagcg cttctgtggc cgctccctcc gtgttcatct tcccaccttc cgacgagcag 1800

ctgaagtccg gcactgcctc tgtcgtgtgc ctgctgaaca acttctaccc tcgggaagcc 1860

aaggtgcagt ggaaagtgga taacgccctg cagtccggca actcccagga atccgtgacc 1920

gagcaggact ccaaggacag cacctactcc ctgagcagca ccctgaccct gtccaaggcc 1980

gactacgaga agcacaaggt gtacgcctgt gaagtgaccc accagggcct gtccagcccc 2040

gtgaccaagt ccttcaaccg gggcgagtgc 2070

<210> 219
<211> 690
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1-Cadena pesada-(28H1) VHCL

<400> 219

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

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

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

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

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

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

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

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

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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    370                 375                 380

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

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

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

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    450                 455                 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
465                 470                 475                 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                485                 490                 495

Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            500                 505                 510

Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp
        515                 520                 525

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
    530                 535                 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
545                 550                 555                 560

Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly
                565                 570                 575

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

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
        595                 600                 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
    610                 615                 620
```

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
625 630 635 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
645 650 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
660 665 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
675 680 685

Glu Cys
690

<210> 220
<211> 2064
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (1G4) VHCH1-Cadena pesada-(28H1) VHCL

<400> 220
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360

ggcccatccg tgttccctct ggccccttcc agcaagtcta cctctggcgg cacagccgct 420

ctgggctgcc tcgtgaagga ctacttcccc gagcctgtga cagtgtcctg gaactctggc 480

gccctgacat ccggcgtgca cacctttcca gctgtgctgc agtcctccgg cctgtactcc 540

ctgtcctccg tcgtgacagt gccctccagc tctctgggca cccagaccta catctgcaac 600

gtgaaccaca agccctccaa caccaaggtg gacaagaagg tggaacccaa gtcctgcgac 660

aagacccaca cctgtccccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc 720

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gtggtggtgg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840

gtggaagtgc acaatgccaa gaccaagcct agagaggaac agtacaactc cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaaaga gtacaagtgc 960

aaggtgtcca acaaggccct gggagccccc atcgaaaaga ccatctccaa ggccaagggc 1020

cagcctcgcg agcctcaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgtct cgtgaaaggc ttctacccct ccgatatcgc cgtggaatgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgac 1200

ggctcattct tcctgtactc taagctgaca gtggacaagt cccggtggca gcagggcaac 1260

gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 1320

tccctgtctc ccgggggagg cggaggatct ggcggaggcg gatccggtgg tggcggatct 1380

gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc 1440

ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt 1500

tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggcctccggc 1560

gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcggga taacagcaag 1620

aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc 1680

gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg 1740

agcgcttctg tggccgctcc ctccgtgttc atcttcccac cttccgacga gcagctgaag 1800

tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcggga agccaaggtg 1860

cagtggaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag 1920

gactccaagg acagcaccta ctccctgagc agcaccctga ccctgtccaa ggccgactac 1980

gagaagcaca aggtgtacgc ctgtgaagtg acccaccagg gcctgtccag ccccgtgacc 2040

aagtccttca accggggcga gtgc 2064

<210> 221
<211> 688
<212> PRT
<213> Secuencia artificial

<220>
<223> (1G4) VHCH1-Cadena pesada-(28H1) VHCL

<400> 221

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
465                 470                 475                 480

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                485                 490                 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            500                 505                 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
        515                 520                 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
    530                 535                 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
545                 550                 555                 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
                565                 570                 575
```

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

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
595 600 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
610 615 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
625 630 635 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
645 650 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
660 665 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
675 680 685

<210> 222
<211> 2082
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (20B7) VHCH1-Cadena pesada-(28H1) VHCL

<400> 222
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac 300

tacccgtact cttactgggg tgacttcgac tactggggcc aagggaccac cgtgaccgtc 360

tcctcagcta gcaccaaggg cccatccgtg ttccctctgg ccccttccag caagtctacc 420

tctggcggca cagccgctct gggctgcctc gtgaaggact acttccccga gcctgtgaca 480

gtgtcctgga actctggcgc cctgacatcc ggcgtgcaca cctttccagc tgtgctgcag 540

tcctccggcc tgtactccct gtcctccgtc gtgacagtgc cctccagctc tctgggcacc 600

cagacctaca tctgcaacgt gaaccacaag ccctccaaca ccaaggtgga caagaaggtg 660

gaacccaagt cctgcgacaa gacccacacc tgtccccctt gtcctgcccc tgaagctgct 720

ggcggcccta gcgtgttcct gttcccccca aagcccaagg acaccctgat gatctcccgg 780

accccgaag tgacctgcgt ggtggtggat gtgtcccacg aggaccctga agtgaagttc 840

aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagcctag agaggaacag 900

tacaactcca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac 960

ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgg gagcccccat cgaaaagacc 1020

atctccaagg ccaagggcca gcctcgcgag cctcaggtgt acaccctgcc ccctagcaga 1080

gatgagctga ccaagaacca ggtgtccctg acctgtctcg tgaaaggctt ctacccctcc 1140

gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200

cctgtgctgg actccgacgg ctcattcttc ctgtactcta agctgacagt ggacaagtcc 1260

cggtggcagc agggcaacgt gttctcctgc tccgtgatgc acgaggccct gcacaaccac 1320

tacacccaga agtccctgtc cctgtctccc gggggaggcg gaggatctgg cggaggcgga 1380

tccggtggtg gcggatctgg gggcggtgga tctgaggtgc agctgctgga atctggggga 1440

ggactggtgc agccaggcgg atctctgagg ctgtcctgcg ctgcttccgg ctttaccttc 1500

tccagccacg ccatgagttg ggtgcgccag gcacccggaa aaggactgga atgggtgtca 1560

gccatctggg cctccggcga gcagtactac gccgatagcg tgaagggccg gttcaccatc 1620

tctcgggata acagcaagaa tactctgtac ctgcagatga actccctgcg cgctgaagat 1680

accgctgtgt attactgcgc caagggctgg ctgggcaact tcgattactg gggccaggga 1740

accctcgtga ctgtctcgag cgcttctgtg gccgctccct ccgtgttcat cttcccacct 1800

tccgacgagc agctgaagtc cggcactgcc tctgtcgtgt gcctgctgaa caacttctac 1860

cctcgggaag ccaaggtgca gtggaaagtg gataacgccc tgcagtccgg caactcccag 1920

gaatccgtga ccgagcagga ctccaaggac agcacctact ccctgagcag caccctgacc 1980

ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gtgaagtgac ccaccagggc 2040

ctgtccagcc ccgtgaccaa gtccttcaac cggggcgagt gc 2082

<210> 223
<211> 694
<212> PRT
<213> Secuencia artificial

<220>
<223> (20B7) VHCH1-Cadena pesada-(28H1) VHCL

<400> 223

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

275 280 285

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
450 455 460

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
465 470 475 480

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
485 490 495

Gly Phe Thr Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro
500 505 510

Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln
515 520 525

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
530 535 540

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
545 550 555 560

Thr Ala Val Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr
565 570 575

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala
580 585 590

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
595 600 605

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
610 615 620

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
625 630 635 640

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
645 650 655

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
660 665 670

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
675 680 685

Phe Asn Arg Gly Glu Cys
690

<210> 224
<211> 2064
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-563) VHCH1-Cadena pesada-(28H1) VHCL

<400> 224
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

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gtgaaccaca agccctccaa caccaaggtg gacaagaagg tggaacccaa gtcctgcgac 660

aagacccaca cctgtccccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc 720

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caggtgtccc tgacctgtct cgtgaaaggc ttctacccct ccgatatcgc cgtggaatgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgac 1200

ggctcattct tcctgtactc taagctgaca gtggacaagt cccggtggca gcagggcaac 1260

gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 1320

tccctgtctc ccgggggagg cggaggatct ggcggaggcg gatccggtgg tggcggatct 1380

gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc 1440

ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt 1500

tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggcctccggc 1560

gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcggga taacagcaag 1620

aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc 1680

gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg 1740

agcgcttctg tggccgctcc ctccgtgttc atcttcccac cttccgacga gcagctgaag 1800

tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcggga agccaaggtg 1860

cagtggaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag 1920

gactccaagg acagcaccta ctccctgagc agcaccctga ccctgtccaa ggccgactac 1980

gagaagcaca aggtgtacgc ctgtgaagtg acccaccagg gcctgtccag ccccgtgacc 2040

aagtccttca accggggcga gtgc 2064

<210> 225
<211> 688

<212> PRT
<213> Secuencia artificial

<220>
<223> (CLC-563) VHCH1-Cadena pesada-(28H1) VHCL

<400> 225

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

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

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Leu Asp Val Gly Ala Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

```
Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        435                 440                 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
465                 470                 475                 480
```

```
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                485                 490                 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            500                 505                 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
        515                 520                 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
    530                 535                 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
545                 550                 555                 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
                565                 570                 575

Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
            580                 585                 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
        595                 600                 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
    610                 615                 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
625                 630                 635                 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                645                 650                 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
            660                 665                 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
        675                 680                 685
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<210> 226
<211> 2064
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-564) VHCH1-Cadena pesada-(28H1) VHCL

<400> 226

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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gttcgacgtt 300

ggtccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaag 360

ggcccatccg tgttccctct ggccccttcc agcaagtcta cctctggcgg cacagccgct 420

ctgggctgcc tcgtgaagga ctacttcccc gagcctgtga cagtgtcctg gaactctggc 480

gccctgacat ccggcgtgca cacctttcca gctgtgctgc agtcctccgg cctgtactcc 540

ctgtcctccg tcgtgacagt gccctccagc tctctgggca cccagaccta catctgcaac 600

gtgaaccaca agccctccaa caccaaggtg gacaagaagg tggaacccaa gtcctgcgac 660

aagacccaca cctgtccccc ttgtcctgcc cctgaagctg ctggcggccc tagcgtgttc 720

ctgttccccc caaagcccaa ggacaccctg atgatctccc ggacccccga agtgacctgc 780

gtggtggtgg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840

gtggaagtgc acaatgccaa gaccaagcct agagaggaac agtacaactc cacctaccgg 900

gtggtgtccg tgctgaccgt gctgcaccag gattggctga acggcaaaga gtacaagtgc 960

aaggtgtcca acaaggccct gggagccccc atcgaaaaga ccatctccaa ggccaagggc 1020

cagcctcgcg agcctcaggt gtacaccctg ccccctagca gagatgagct gaccaagaac 1080

caggtgtccc tgacctgtct cgtgaaaggc ttctacccct ccgatatcgc cgtggaatgg 1140

gagagcaacg gccagcccga gaacaactac aagaccaccc cccctgtgct ggactccgac 1200

ggctcattct tcctgtactc taagctgaca gtggacaagt cccggtggca gcagggcaac 1260

gtgttctcct gctccgtgat gcacgaggcc ctgcacaacc actacaccca gaagtccctg 1320

tccctgtctc ccgggggagg cggaggatct ggcggaggcg gatccggtgg tggcggatct 1380

gggggcggtg gatctgaggt gcagctgctg gaatctgggg gaggactggt gcagccaggc 1440

ggatctctga ggctgtcctg cgctgcttcc ggctttacct tctccagcca cgccatgagt 1500

tgggtgcgcc aggcacccgg aaaaggactg gaatgggtgt cagccatctg ggcctccggc 1560

gagcagtact acgccgatag cgtgaagggc cggttcacca tctctcggga taacagcaag 1620

aatactctgt acctgcagat gaactccctg cgcgctgaag ataccgctgt gtattactgc 1680

gccaagggct ggctgggcaa cttcgattac tggggccagg gaaccctcgt gactgtctcg 1740

agcgcttctg tggccgctcc ctccgtgttc atcttcccac cttccgacga gcagctgaag 1800

tccggcactg cctctgtcgt gtgcctgctg aacaacttct accctcggga agccaaggtg 1860

cagtggaaag tggataacgc cctgcagtcc ggcaactccc aggaatccgt gaccgagcag 1920

gactccaagg acagcaccta ctccctgagc agcaccctga ccctgtccaa ggccgactac 1980

gagaagcaca aggtgtacgc ctgtgaagtg acccaccagg gcctgtccag ccccgtgacc 2040

aagtccttca accggggcga gtgc 2064

<210> 227
<211> 688
<212> PRT
<213> Secuencia artificial

<220>
<223> (CLC-564) VHCH1-Cadena pesada-(28H1) VHCL

<400> 227

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Phe Asp Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu

```
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
```

```
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
        435                 440                 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    450                 455                 460

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
465                 470                 475                 480

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
                485                 490                 495

His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            500                 505                 510

Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val
        515                 520                 525

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
    530                 535                 540

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
545                 550                 555                 560

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
                565                 570                 575

Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe
            580                 585                 590

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
        595                 600                 605

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
    610                 615                 620

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
625                 630                 635                 640

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                645                 650                 655

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
            660                 665                 670

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
        675                 680                 685
```

<210> 228
<211> 1350
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (28H1) VHCL-agujero de la cadena pesada

<400> 228
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60

tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct 120

cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180

gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240

cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgccaa gggctggctg 300

ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcgtggcc 360

gctcccagcg tgttcatctt cccacccagc gacgagcagc tgaagtccgg cacagccagc 420

gtggtgtgcc tgctgaacaa cttctacccc cgcgaggcca aggtgcagtg gaaggtggac 480

aacgccctgc agagcggcaa cagccaggaa tccgtgaccg agcaggacag caaggactcc 540

acctacagcc tgagcagcac cctgaccctg agcaaggccg actacgagaa gcacaaggtg 600

tacgcctgcg aagtgaccca ccagggcctg tccagccccg tgaccaagag cttcaaccgg 660

ggcgagtgcg acaagaccca cacctgtccc ccttgccctg cccctgaagc tgctggtggc 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc 780

gaagtgacct gcgtggtggt cgatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 229
<211> 450
<212> PRT
<213> Secuencia artificial

<220>

<223> (28H1) VHCL-agujero de la cadena pesada

<400> 229

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe Ile Phe Pro
        115                 120                 125

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
    130                 135                 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145                 150                 155                 160

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                165                 170                 175

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
            180                 185                 190

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
        195                 200                 205

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240
```

```
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 230
<211> 1343
<212> ADN
<213> Secuencia artificial

<220>

<223> ADN (49B4) VHCH1-pomo de la cadena pesada

<400> 230
aggtgcaatt ggtgcagtct ggggctgagg tgaagaagcc tgggtcctcg gtgaaggtct 60

cctgcaaggc ctccggaggc acattcagca gctacgctat aagctgggtg cgacaggccc 120

ctggacaagg gctcgagtgg atgggaggga tcatccctat ctttggtaca gcaaactacg 180

cacagaagtt ccagggcagg gtcaccatta ctgcagacaa atccacgagc acagcctaca 240

tggagctgag cagcctgaga tctgaggaca ccgccgtgta ttactgtgcg agagaatact 300

accgtggtcc gtacgactac tggggccaag ggaccaccgt gaccgtctcc tcagctagca 360

ccaagggccc tagcgtgttc cctctggccc ctagcagcaa gagcacaagt ggaggaacag 420

ccgccctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg tcctggaatt 480

ctggcgccct gacaagcggc gtgcacacat ttccagccgt gctgcagagc agcggcctgt 540

actctctgag cagcgtcgtg accgtgccct ctagctctct gggcacccag acctacatct 600

gcaacgtgaa ccacaagccc agcaacacca aagtggacaa gaaggtggaa cccaagagct 660

gcgacaagac ccacacctgt ccccccttgcc ctgcccctga agctgctggt ggcccttccg 720

tgttcctgtt ccccccaaag cccaaggaca ccctgatgat cagccggacc cccgaagtga 780

cctgcgtggt ggtcgatgtg tcccacgagg accctgaagt gaagttcaat tggtacgtgg 840

acggcgtgga agtgcacaat gccaagacca agccgcggga ggagcagtac aacagcacgt 900

accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc aaggagtaca 960

agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc tccaaagcca 1020

aagggcagcc ccgagaacca caggtgtaca ccctgccccc atgccgggat gagctgacca 1080

agaaccaggt cagcctgtgg tgcctggtca aaggcttcta tcccagcgac atcgccgtgg 1140

agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact 1200

ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg tggcagcagg 1260

ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac acgcagaaga 1320

gcctctccct gtctccgggt aaa 1343

<210> 231
<211> 448
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1-pomo de la cadena pesada

<400> 231

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270
```

```
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 232
<211> 1338
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (1G4) VHCH1-pomo de la cadena pesada

<400> 232
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

ggttctatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360

ggccctagcg tgttccctct ggcccctagc agcaagagca caagtggagg aacagccgcc 420

ctgggctgcc tggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaattctggc 480

gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct 540

ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac 600

gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac 660

aagacccaca cctgtccccc ttgccctgcc cctgaagctg ctggtggccc ttccgtgttc 720

ctgttccccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc 780

gtggtggtcg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840

gtggaagtgc acaatgccaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 1080

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 233
<211> 446
<212> PRT
<213> Secuencia artificial

<220>
<223> (1G4) VHCH1-pomo de la cadena pesada

<400> 233

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

```
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Tyr Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
            100                 105                 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
```

305 310 315 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 234
<211> 1356
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (20B7) VHCH1-pomo de la cadena pesada

<400> 234
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagttaac 300

tacccgtact cttactgggg tgacttcgac tactggggcc aagggaccac cgtgaccgtc 360

tcctcagcta gcaccaaggg ccctagcgtg ttccctctgg cccctagcag caagagcaca 420

agtggaggaa cagccgccct gggctgcctg gtcaaggact acttccccga gcccgtgacc 480

gtgtcctgga attctggcgc cctgacaagc ggcgtgcaca catttccagc cgtgctgcag 540

agcagcggcc tgtactctct gagcagcgtc gtgaccgtgc cctctagctc tctgggcacc 600

cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaagtgga caagaaggtg 660

gaacccaaga gctgcgacaa gacccacacc tgtccccctt gccctgcccc tgaagctgct 720

ggtggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780

acccccgaag tgacctgcgt ggtggtcgat gtgtcccacg aggaccctga agtgaagttc 840

aattggtacg tggacggcgt ggaagtgcac aatgccaaga ccaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcg gcgccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1080

gatgagctga ccaagaacca ggtcagcctg tggtgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggtaaa 1356

<210> 235
<211> 452
<212> PRT
<213> Secuencia artificial

<220>
<223> (20B7) VHCH1-pomo de la cadena pesada

<400> 235

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Asn Tyr Pro Tyr Ser Tyr Trp Gly Asp Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 236
<211> 1338
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-563) VHCH1-pomo de la cadena pesada

<400> 236
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcttgacgtt 300

ggtgctttcg actactgggg ccaaggagcc ctggtcaccg tctcgagtgc tagcaccaag 360

ggccctagcg tgttccctct ggcccctagc agcaagagca caagtggagg aacagccgcc 420

ctgggctgcc tggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaattctggc 480

gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct 540

ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac 600

gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac 660

aagacccaca cctgtccccc ttgccctgcc cctgaagctg ctggtggccc ttccgtgttc 720

ctgttccccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc 780

gtggtggtcg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840

gtggaagtgc acaatgccaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 1080

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 237
<211> 446
<212> PRT
<213> Secuencia artificial

<220>
<223> (CLC-563) VHCH1-pomo de la cadena pesada

<400> 237

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Leu Asp Val Gly Ala Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

```
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380
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Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 238
<211> 1338
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (CLC-564) VHCH1-pomo de la cadena pesada

<400> 238
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gttcgacgtt 300

ggtccgttcg actactgggg ccaaggaacc ctggtcaccg tctcgagtgc tagcaccaag 360

ggccctagcg tgttccctct ggcccctagc agcaagagca caagtggagg aacagccgcc 420

ctgggctgcc tggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaattctggc 480

gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct 540

ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac 600

gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac 660

aagacccaca cctgtccccc ttgccctgcc cctgaagctg ctggtggccc ttccgtgttc 720

ctgttccccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc 780

gtggtggtcg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840

gtggaagtgc acaatgccaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 1080

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 239
<211> 446
<212> PRT
<213> Secuencia artificial

<220>
<223> (CLC-564) VHCH1-pomo de la cadena pesada

<400> 239

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Phe Asp Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

```
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430
```

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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445


<210>  240
<211>  163
<212>  PRT
<213>  cynomolgus

<400>  240

Leu Gln Asp Leu Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1               5                   10                  15


Asn Arg Ser Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
            20                  25                  30


Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
        35                  40                  45


Phe Lys Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
    50                  55                  60


Cys Ile Ser Gly Tyr His Cys Leu Gly Ala Glu Cys Ser Met Cys Glu
65                  70                  75                  80


Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
                85                  90                  95


Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
            100                 105                 110


Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
        115                 120                 125


Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
    130                 135                 140


Gly Ala Ser Ser Ala Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145                 150                 155                 160


Ser Pro Gln



<210>  241
<211>  164
<212>  PRT
<213>  Mus musculus

<400>  241
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Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
1               5                  10                  15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
            20                  25                  30

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
        35                  40                  45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
    50                  55                  60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
65                  70                  75                  80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys
                85                  90                  95

Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro
            100                 105                 110

Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr
        115                 120                 125

Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe Ser Pro
    130                 135                 140

Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly His Ser
145                 150                 155                 160

Leu Gln Val Leu
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<210> 242
<211> 1266
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena del pomo de Fc del antígeno 4-1BB humano

<400> 242

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ctgcaggacc cctgcagcaa ctgccctgcc ggcaccttct gcgacaacaa ccggaaccag       60

atctgcagcc cctgcccccc caacagcttc agctctgccg gcggacagcg gacctgcgac      120

atctgcagac agtgcaaggg cgtgttcaga acccggaaag agtgcagcag caccagcaac      180

gccgagtgcg actgcacccc cggcttccat tgtctgggag ccggctgcag catgtgcgag      240

caggactgca agcagggcca ggaactgacc aagaagggct gcaaggactg ctgcttcggc      300
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accttcaacg accagaagcg gggcatctgc cggccctgga ccaactgtag cctggacggc 360

aagagcgtgc tggtcaacgg caccaaagaa cgggacgtcg tgtgcggccc cagccctgct 420

gatctgtctc ctggggccag cagcgtgacc cctcctgccc ctgccagaga gcctggccac 480

tctcctcagg tcgacgaaca gttatatttt cagggcggct cacccaaatc tgcagacaaa 540

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 600

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 660

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 720

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 780

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 840

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 900

ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 960

gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1020

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1080

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1140

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1200

ctgtctccgg gtaaatccgg aggcctgaac gacatcttcg aggcccagaa gattgaatgg 1260

cacgag 1266

<210> 243
<211> 1266
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena del pomo de Fc del antígeno 4-1BB de macaco

<400> 243
ttgcaggatc tgtgtagtaa ctgcccagct ggtacattct gtgataataa caggagtcag 60

atttgcagtc cctgtcctcc aaatagtttc tccagcgcag gtggacaaag gacctgtgac 120

atatgcaggc agtgtaaagg tgttttcaag accaggaagg agtgttcctc caccagcaat 180

gcagagtgtg actgcatttc agggtatcac tgcctggggg cagagtgcag catgtgtgaa 240

caggattgta aacaaggtca agaattgaca aaaaaaggtt gtaaagactg ttgctttggg 300

acatttaatg accagaaacg tggcatctgt cgcccctgga caaactgttc tttggatgga 360

aagtctgtgc ttgtgaatgg gacgaaggag agggacgtgg tctgcggacc atctccagcc 420

gacctctctc caggagcatc ctctgcgacc ccgcctgccc ctgcgagaga gccaggacac 480

tctccgcagg tcgacgaaca gttatatttt cagggcggct cacccaaatc tgcagacaaa 540

actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc 600

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 660

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 720

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 780

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 840

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 900

ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 960

gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1020

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1080

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1140

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1200

ctgtctccgg gtaaatccgg aggcctgaac gacatcttcg aggcccagaa gattgaatgg 1260

cacgag 1266

<210> 244
<211> 1269
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena del pomo de Fc del antígeno 4-1BB murino

<400> 244
gtgcagaaca gctgcgacaa ctgccagccc ggcaccttct gccggaagta caaccccgtg 60

tgcaagagct gccccccccag caccttcagc agcatcggcg gccagcccaa ctgcaacatc 120

tgcagagtgt gcgccggcta cttccggttc aagaagttct gcagcagcac ccacaacgcc 180

gagtgcgagt gcatcgaggg cttccactgc ctgggccccc agtgcaccag atgcgagaag 240

gactgcagac ccggccagga actgaccaag cagggctgta agacctgcag cctgggcacc 300

ttcaacgacc agaacgggac cggcgtgtgc cggccttgga ccaattgcag cctggacggg 360

agaagcgtgc tgaaaaccgg caccaccgag aaggacgtcg tgtgcggccc tcccgtggtg 420

tccttcagcc ctagcaccac catcagcgtg acccctgaag gcggccctgg cggacactct 480

ctgcaggtcc tggtcgacga acagttatat tttcagggcg gctcacccaa atctgcagac 540

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 600

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 660

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gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 840

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 900

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 960

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1020

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1080

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1140

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1200

tccctgtctc cgggtaaatc cggaggcctg aacgacatct tcgaggccca gaagattgaa 1260

tggcacgag 1269

<210> 245
<211> 422
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena del pomo de Fc del antígeno 4-1BB humano

<400> 245

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
85 90 95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
100 105 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
115 120 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
130 135 140

```
Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145                 150                 155                 160

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
                165                 170                 175

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
            180                 185                 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
        195                 200                 205

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    210                 215                 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
225                 230                 235                 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                245                 250                 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            260                 265                 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
        275                 280                 285

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    290                 295                 300

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
305                 310                 315                 320

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                325                 330                 335

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            340                 345                 350

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        355                 360                 365

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    370                 375                 380

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
385                 390                 395                 400
```

```
Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
                405                 410                 415

Lys Ile Glu Trp His Glu
            420
```

<210> 246
<211> 422
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena del pomo de Fc del antígeno 4-1BB de macaco

<400> 246

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Leu Gln Asp Leu Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1               5                   10                  15

Asn Arg Ser Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
            20                  25                  30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
        35                  40                  45

Phe Lys Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
    50                  55                  60

Cys Ile Ser Gly Tyr His Cys Leu Gly Ala Glu Cys Ser Met Cys Glu
65                  70                  75                  80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp
                85                  90                  95

Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro
            100                 105                 110

Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr
        115                 120                 125

Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro
    130                 135                 140

Gly Ala Ser Ser Ala Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His
145                 150                 155                 160

Ser Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys
                165                 170                 175
```

```
Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
            180                 185                 190

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
        195                 200                 205

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    210                 215                 220

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
225                 230                 235                 240

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                245                 250                 255

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            260                 265                 270

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
        275                 280                 285

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    290                 295                 300

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
305                 310                 315                 320

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                325                 330                 335

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            340                 345                 350

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        355                 360                 365

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    370                 375                 380

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
385                 390                 395                 400

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
                405                 410                 415

Lys Ile Glu Trp His Glu
            420
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<210> 247
<211> 423
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena del pomo de Fc del antígeno 4-1BB murino

<400> 247

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Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
1               5                  10                  15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
            20                  25                  30

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
        35                  40                  45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
    50                  55                  60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
65                  70                  75                  80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys
                85                  90                  95

Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro
            100                 105                 110

Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr
        115                 120                 125

Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe Ser Pro
    130                 135                 140

Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly His Ser
145                 150                 155                 160

Leu Gln Val Leu Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro
                165                 170                 175

Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
            180                 185                 190

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        195                 200                 205
```

```
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    210                 215                 220

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
225                 230                 235                 240

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                245                 250                 255

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            260                 265                 270

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        275                 280                 285

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    290                 295                 300

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
305                 310                 315                 320

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                325                 330                 335

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            340                 345                 350

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        355                 360                 365

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    370                 375                 380

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
385                 390                 395                 400

Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala
                405                 410                 415

Gln Lys Ile Glu Trp His Glu
            420
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<210> 248
<211> 28
<212> ADN
<213> Secuencia artificial

<220>

<223> Cebador MS63

<400> 248
tttcgcacag taatatacgg ccgtgtcc 28

<210> 249
<211> 321
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(12B3) VL

<400> 249
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatcattcgt atccgcagac gtttggccag 300

ggcaccaaag tcgagatcaa g 321

<210> 250
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(12B3) VH

<400> 250
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

<210> 251
<211> 318
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(25G7) VL

<400> 251
tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactccctt gataggcgcg gtatgtgggt attcggcgga 300

gggaccaagc tgaccgtc 318

<210> 252
<211> 354
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(25G7) VH

<400> 252
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300

ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagt 354

<210> 253
<211> 321
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(11D5) VL

<400> 253
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag cttaattcgt atcctcagac gtttggccag 300

ggcaccaaag tcgagatcaa g 321

<210> 254
<211> 357
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(11D5) VH

<400> 254
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact 300

ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctca 357

<210> 255
<211> 321
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(9B11) VL

<400> 255
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag gttaattctt atccgcagac gtttggccag 300

ggcaccaaag tcgagatcaa g 321

<210> 256
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(9B11) VH

<400> 256
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

<210> 257
<211> 318
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(20G2) VL

<400> 257
gacatccaga tgacccagtc tccatccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag cagcactcgt attatacgtt tggccagggc 300

accaaagtcg agatcaag 318

<210> 258
<211> 360
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN 4-1BB(20G2) VH

<400> 258
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttac 300

tactgggaat cttacccgtt cgactactgg ggccaaggga ccaccgtgac cgtctccagc 360

<210> 259
<211> 642
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 12B3 P329GLALA IgG1

<400> 259
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag tatcattcgt atccgcagac gtttggccag 300

ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 260
<211> 1350
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 12B3 P329GLALA IgG1

<400> 260
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 261

<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera 12B3 P329GLALA IgG1

<400> 261

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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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Gln
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210
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<210> 262
<211> 450
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 12B3 P329GLALA IgG1

<400> 262

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
```

```
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
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<210> 263
<211> 639
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 25G7 P329GLALA IgG1

<400> 263
tcgtctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60

acatgccaag gagacagcct cagaagttat tatgcaagct ggtaccagca gaagccagga 120

caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 180

ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcggaa 240

gatgaggctg actattactg taactccctt gataggcgcg gtatgtgggt attcggcgga 300

gggaccaagc tgaccgtcct aggtcaaccc aaggctgccc ccagcgtgac cctgttcccc 360

cccagcagcg aggaactgca ggccaacaag gccaccctgg tctgcctgat cagcgacttc 420

tacccaggcg ccgtgaccgt ggcctggaag gccgacagca gccccgtgaa ggccggcgtg 480

gagaccacca cccccagcaa gcagagcaac aacaagtacg ccgccagcag ctacctgagc 540

ctgacccccg agcagtggaa gagccacagg tcctacagct gccaggtgac ccacgagggc 600

agcaccgtgg agaaaaccgt ggcccccacc gagtgcagc 639

<210> 264
<211> 1344
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 25G7 P329GLALA IgG1

<400> 264
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300

ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg taaa 1344

<210> 265
<211> 213
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera 25G7 P329GLALA IgG1

<400> 265

Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Leu Asp Arg Arg Gly Met Trp
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
100 105 110

```
Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
        115                 120                 125

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
    130                 135                 140

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
145                 150                 155                 160

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
                165                 170                 175

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
            180                 185                 190

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
        195                 200                 205

Pro Thr Glu Cys Ser
    210
```

<210> 266
<211> 448
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 25G7 P329GLALA IgG1

<400> 266

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350
```

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 267
<211> 642
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 11D5 P329GLALA IgG1

<400> 267
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag cttaattcgt atcctcagac gtttggccag 300

ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 268
<211> 1347
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 11D5 P329GLALA IgG1

<400> 268
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact 300

ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaa 1347

<210> 269
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera 11D5 P329GLALA IgG1

<400> 269

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Gln
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 270
<211> 449
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 11D5 P329GLALA IgG1

<400> 270

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
```

```
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

<210> 271
<211> 642
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 9B11 P329GLALA IgG1

<400> 271

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag gttaattctt atccgcagac gtttggccag 300

ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 272
<211> 1350
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 9B11 P329GLALA IgG1

<400> 272
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 273
<211> 214
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera 9B11 P329GLALA IgG1

<400> 273

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Asn Ser Tyr Pro Gln
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 274
<211> 450
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 9B11 P329GLALA IgG1

<400> 274

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

```
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
```

385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 275
<211> 639
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena ligera 20G2 P329GLALA IgG1

<400> 275
gacatccaga tgacccagtc tccatccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gtgccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180

cgtttcagcg gcagtggatc cgggacagaa ttcactctca ccatcagcag cttgcagcct 240

gatgattttg caacttatta ctgccaacag cagcactcgt attatacgtt tggccagggc 300

accaaagtcg agatcaagcg tacggtggct gcaccatctg tcttcatctt cccgccatct 360

gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420

agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 480

agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540

agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600

agctcgcccg tcacaaagag cttcaacagg ggagagtgt 639

<210> 276
<211> 1350
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN cadena pesada 20G2 P329GLALA IgG1

<400> 276
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttac 300

tactgggaat cttacccgtt cgactactgg ggccaaggga ccaccgtgac cgtctccagc 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 277
<211> 213
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena ligera 20G2 P329GLALA IgG1

<400> 277

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 Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gln His Ser Tyr Tyr Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 278
<211> 450
<212> PRT
<213> Secuencia artificial

<220>
<223> Cadena pesada 20G2 P329GLALA IgG1

<400> 278

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

```
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Tyr Tyr Trp Glu Ser Tyr Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
```

275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 279
<211> 421
<212> PRT
<213> Secuencia artificial

<220>
<223> mu4-1BB D1 / Pomo Fc hu4-1BB D2

<400> 279

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
1 5 10 15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
20 25 30

```
Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
        35                  40                  45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
    50                  55                  60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
65                  70                  75                  80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Asp Cys
                85                  90                  95

Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg Pro Trp
            100                 105                 110

Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr Lys
        115                 120                 125

Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser Pro Gly
    130                 135                 140

Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly His Ser
145                 150                 155                 160

Pro Gln Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys Ser
                165                 170                 175

Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
            180                 185                 190

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        195                 200                 205

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    210                 215                 220

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
225                 230                 235                 240

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                245                 250                 255

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            260                 265                 270

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
```

275 280 285

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
290 295 300

Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
305 310 315 320

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
325 330 335

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
340 345 350

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
355 360 365

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
370 375 380

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
385 390 395 400

Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys
405 410 415

Ile Glu Trp His Glu
420

<210> 280
<211> 424
<212> PRT
<213> Secuencia artificial

<220>
<223> hu4-1BB D1 / Pomo Fc mu4-1BB D2

<400> 280

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

```
Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65                  70                  75                  80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Thr
                85                  90                  95

Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg
            100                 105                 110

Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr Gly
        115                 120                 125

Thr Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe Ser
    130                 135                 140

Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly His
145                 150                 155                 160

Ser Leu Gln Val Leu Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser
                165                 170                 175

Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
            180                 185                 190

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        195                 200                 205

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    210                 215                 220

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
225                 230                 235                 240

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
                245                 250                 255

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            260                 265                 270

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
        275                 280                 285

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    290                 295                 300

Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys
```

305 310 315 320

Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
325 330 335

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
340 345 350

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
355 360 365

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
370 375 380

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
385 390 395 400

Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu
405 410 415

Ala Gln Lys Ile Glu Trp His Glu
420

<210> 281
<211> 354
<212> PRT
<213> Secuencia artificial

<220>
<223> Pomo Fc hu 4-1BB D1

<400> 281

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1 5 10 15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
20 25 30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
35 40 45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
50 55 60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65 70 75 80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Val
85 90 95

```
Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Pro Lys Ser Ala Asp Lys
            100                 105                 110

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
        115                 120                 125

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    130                 135                 140

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
145                 150                 155                 160

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                165                 170                 175

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
            180                 185                 190

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        195                 200                 205

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
    210                 215                 220

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
225                 230                 235                 240

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
                245                 250                 255

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            260                 265                 270

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        275                 280                 285

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    290                 295                 300

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
305                 310                 315                 320

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                325                 330                 335

Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
```

340 345 350

His Glu

<210> 282
<211> 94
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio D1 de 4-1BB murino (N-terminal)

<400> 282

Val Gln Asn Ser Cys Asp Asn Cys Gln Pro Gly Thr Phe Cys Arg Lys
1 5 10 15

Tyr Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile
20 25 30

Gly Gly Gln Pro Asn Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe
35 40 45

Arg Phe Lys Lys Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys
50 55 60

Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys
65 70 75 80

Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys
85 90

<210> 283
<211> 68
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio D2 de 4-1BB humano (C-terminal)

<400> 283

Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys Arg
1 5 10 15

Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly
20 25 30

Thr Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu Ser
35 40 45

Pro Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro Gly
    50   55   60

His Ser Pro Gln
65

<210> 284
<211> 95
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio D1 de 4-1BB humano (N-terminal)

<400> 284

Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn
1   5   10   15

Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser
            20   25   30

Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val
        35   40   45

Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp
    50   55   60

Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu
65   70   75   80

Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys
                85   90   95

<210> 285
<211> 70
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio D2 de 4-1BB murino (C-terminal)

<400> 285

Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys
1   5   10   15

Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr
            20   25   30

Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe
        35   40   45

Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly Gly
50 55 60

His Ser Leu Gln Val Leu
65 70

<210> 286
<211> 2076
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (12B3) VHCH1-Cadena pesada-(28H1) VHCL

<400> 286
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggcccatc cgtgttccct ctggcccctt ccagcaagtc tacctctggc 420

ggcacagccg ctctgggctg cctcgtgaag gactacttcc ccgagcctgt gacagtgtcc 480

tggaactctg gcgccctgac atccggcgtg cacacctttc agctgtgct gcagtcctcc 540

ggcctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg cacccagacc 600

tacatctgca acgtgaacca caagccctcc aacaccaagg tggacaagaa ggtggaaccc 660

aagtcctgcg acaagaccca cacctgtccc ccttgtcctg cccctgaagc tgctggcggc 720

cctagcgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggacccc 780

gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ctagagagga acagtacaac 900

tccacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaaa 960

gagtacaagt gcaaggtgtc caacaaggcc ctgggagccc ccatcgaaaa gaccatctcc 1020

aaggccaagg gccagcctcg cgagcctcag gtgtacaccc tgccccctag cagagatgag 1080

ctgaccaaga accaggtgtc cctgacctgt ctcgtgaaag gcttctaccc ctccgatatc 1140

gccgtggaat gggagagcaa cggccagccc gagaacaact acaagaccac ccccctgtg 1200

ctggactccg acggctcatt cttcctgtac tctaagctga cagtggacaa gtcccggtgg 1260

cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgtccctgtc tcccggggga ggcggaggat ctggcggagg cggatccggt 1380

ggtggcggat ctgggggcgg tggatctgag gtgcagctgc tggaatctgg gggaggactg 1440

gtgcagccag gcggatctct gaggctgtcc tgcgctgctt ccggctttac cttctccagc 1500

cacgccatga gttgggtgcg ccaggcaccc ggaaaaggac tggaatgggt gtcagccatc 1560

tgggcctccg gcgagcagta ctacgccgat agcgtgaagg gccggttcac catctctcgg 1620

gataacagca agaatactct gtacctgcag atgaactccc tgcgcgctga agataccgct 1680

gtgtattact gcgccaaggg ctggctgggc aacttcgatt actggggcca gggaaccctc 1740

gtgactgtct cgagcgcttc tgtggccgct ccctccgtgt tcatcttccc accttccgac 1800

gagcagctga agtccggcac tgcctctgtc gtgtgcctgc tgaacaactt ctaccctcgg 1860

gaagccaagg tgcagtggaa agtggataac gccctgcagt ccggcaactc ccaggaatcc 1920

gtgaccgagc aggactccaa ggacagcacc tactccctga gcagcaccct gaccctgtcc 1980

aaggccgact acgagaagca caaggtgtac gcctgtgaag tgacccacca gggcctgtcc 2040

agccccgtga ccaagtcctt caaccggggc gagtgc 2076

<210> 287
<211> 692
<212> PRT
<213> Secuencia artificial

<220>
<223> (12B3) VHCH1-Cadena pesada-(28H1) VHCL

<400> 287

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
100 105 110

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Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365
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Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
465                 470                 475                 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                485                 490                 495

Thr Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
            500                 505                 510

Gly Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr
        515                 520                 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
    530                 535                 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
545                 550                 555                 560

Val Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly
                565                 570                 575

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser
            580                 585                 590

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
        595                 600                 605

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
```

610 615 620

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
625 630 635 640

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
645 650 655

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
660 665 670

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
675 680 685

Arg Gly Glu Cys
690

<210> 288
<211> 2070
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (25G7) VHCH1-Cadena pesada-(28H1) VHCL

<400> 288
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300

ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgctagc 360

accaagggcc catccgtgtt ccctctggcc ccttccagca agtctacctc tggcggcaca 420

gccgctctgg gctgcctcgt gaaggactac ttccccgagc ctgtgacagt gtcctggaac 480

tctggcgccc tgacatccgg cgtgcacacc tttccagctg tgctgcagtc ctccggcctg 540

tactccctgt cctccgtcgt gacagtgccc tccagctctc tgggcaccca gacctacatc 600

tgcaacgtga accacaagcc ctccaacacc aaggtggaca agaaggtgga acccaagtcc 660

tgcgacaaga cccacacctg tccccccttgt cctgcccctg aagctgctgg cggccctagc 720

gtgttcctgt tccccccaaa gcccaaggac accctgatga tctcccggac ccccgaagtg 780

acctgcgtgg tggtggatgt gtcccacgag gaccctgaag tgaagttcaa ttggtacgtg 840

gacggcgtgg aagtgcacaa tgccaagacc aagcctagag aggaacagta caactccacc 900

taccgggtgg tgtccgtgct gaccgtgctg caccaggatt ggctgaacgg caaagagtac 960

aagtgcaagg tgtccaacaa ggccctggga gcccccatcg aaaagaccat ctccaaggcc 1020

aagggccagc ctcgcgagcc tcaggtgtac accctgcccc ctagcagaga tgagctgacc 1080

aagaaccagg tgtccctgac ctgtctcgtg aaaggcttct acccctccga tatcgccgtg 1140

gaatgggaga gcaacggcca gcccgagaac aactacaaga ccacccccc tgtgctggac 1200

tccgacggct cattcttcct gtactctaag ctgacagtgg acaagtcccg gtggcagcag 1260

ggcaacgtgt tctcctgctc cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgtccc tgtctcccgg gggaggcgga ggatctggcg gaggcggatc cggtggtggc 1380

ggatctgggg gcggtggatc tgaggtgcag ctgctggaat ctgggggagg actggtgcag 1440

ccaggcggat ctctgaggct gtcctgcgct gcttccggct ttaccttctc agccacgcc 1500

atgagttggg tgcgccaggc acccggaaaa ggactggaat gggtgtcagc catctgggcc 1560

tccggcgagc agtactacgc cgatagcgtg aagggccggt tcaccatctc tcgggataac 1620

agcaagaata ctctgtacct gcagatgaac tccctgcgcg ctgaagatac cgctgtgtat 1680

tactgcgcca agggctggct gggcaacttc gattactggg gccagggaac cctcgtgact 1740

gtctcgagcg cttctgtggc cgctccctcc gtgttcatct tcccaccttc cgacgagcag 1800

ctgaagtccg gcactgcctc tgtcgtgtgc ctgctgaaca acttctaccc tcgggaagcc 1860

aaggtgcagt ggaaagtgga taacgccctg cagtccggca actcccagga atccgtgacc 1920

gagcaggact ccaaggacag cacctactcc ctgagcagca ccctgaccct gtccaaggcc 1980

gactacgaga agcacaaggt gtacgcctgt gaagtgaccc accagggcct gtccagcccc 2040

gtgaccaagt ccttcaaccg gggcgagtgc 2070

<210> 289
<211> 690
<212> PRT
<213> Secuencia artificial

<220>
<223> (25G7) VHCH1-Cadena pesada-(28H1) VHCL

<400> 289

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

```
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
        435                 440                 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    450                 455                 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
465                 470                 475                 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                485                 490                 495

Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            500                 505                 510

Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp
        515                 520                 525

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
    530                 535                 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
545                 550                 555                 560
```

```
Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly
                565                 570                 575

Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val Phe
            580                 585                 590

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
        595                 600                 605

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
    610                 615                 620

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
625                 630                 635                 640

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
                645                 650                 655

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
            660                 665                 670

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
        675                 680                 685

Glu Cys
    690
```

<210> 290
<211> 2073
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (11D5) VHCH1-Cadena pesada-(28H1) VHCL

<400> 290

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caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact      300

ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctcagct      360

agcaccaagg gcccatccgt gttccctctg gcccccttcca gcaagtctac ctctggcggc      420

acagccgctc tgggctgcct cgtgaaggac tacttccccg agcctgtgac agtgtcctgg      480

aactctggcg ccctgacatc cggcgtgcac acctttccag ctgtgctgca gtcctccggc      540
```

ctgtactccc tgtcctccgt cgtgacagtg ccctccagct ctctgggcac ccagacctac 600

atctgcaacg tgaaccacaa gccctccaac accaaggtgg acaagaaggt ggaacccaag 660

tcctgcgaca agacccacac ctgtcccccc tgtcctgccc ctgaagctgc tggcggccct 720

agcgtgttcc tgttcccccc aaagcccaag gacaccctga tgatctcccg gacccccgaa 780

gtgacctgcg tggtggtgga tgtgtcccac gaggaccctg aagtgaagtt caattggtac 840

gtggacggcg tggaagtgca caatgccaag accaagccta gagaggaaca gtacaactcc 900

acctaccggg tggtgtccgt gctgaccgtg ctgcaccagg attggctgaa cggcaaagag 960

tacaagtgca aggtgtccaa caaggccctg ggagccccca tcgaaaagac catctccaag 1020

gccaagggcc agcctcgcga gcctcaggtg tacaccctgc cccctagcag agatgagctg 1080

accaagaacc aggtgtccct gacctgtctc gtgaaaggct tctacccctc cgatatcgcc 1140

gtggaatggg agagcaacgg ccagcccgag aacaactaca agaccacccc ccctgtgctg 1200

gactccgacg gctcattctt cctgtactct aagctgacag tggacaagtc ccggtggcag 1260

cagggcaacg tgttctcctg ctccgtgatg cacgaggccc tgcacaacca ctacacccag 1320

aagtccctgt ccctgtctcc cgggggaggc ggaggatctg gcggaggcgg atccggtggt 1380

ggcggatctg ggggcggtgg atctgaggtg cagctgctgg aatctggggg aggactggtg 1440

cagccaggcg gatctctgag gctgtcctgc gctgcttccg gctttacctt ctccagccac 1500

gccatgagtt gggtgcgcca ggcacccgga aaaggactgg aatgggtgtc agccatctgg 1560

gcctccggcg agcagtacta cgccgatagc gtgaagggcc ggttcaccat ctctcgggat 1620

aacagcaaga atactctgta cctgcagatg aactccctgc gcgctgaaga taccgctgtg 1680

tattactgcg ccaagggctg gctgggcaac ttcgattact ggggccaggg aaccctcgtg 1740

actgtctcga gcgcttctgt ggccgctccc tccgtgttca tcttcccacc ttccgacgag 1800

cagctgaagt ccggcactgc ctctgtcgtg tgcctgctga acaacttcta ccctcgggaa 1860

gccaaggtgc agtggaaagt ggataacgcc ctgcagtccg gcaactccca ggaatccgtg 1920

accgagcagg actccaagga cagcacctac tccctgagca gcaccctgac cctgtccaag 1980

gccgactacg agaagcacaa ggtgtacgcc tgtgaagtga cccaccaggg cctgtccagc 2040

cccgtgacca agtccttcaa ccggggcgag tgc 2073

<210> 291
<211> 691
<212> PRT
<213> Secuencia artificial

<220>
<223> (11D5) VHCH1-Cadena pesada-(28H1) VHCL

<400> 291

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
```

```
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
465                 470                 475                 480

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
                485                 490                 495

Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
```

500 505 510

Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala
515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
545 550 555 560

Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln
565 570 575

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser Val
580 585 590

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
595 600 605

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
610 615 620

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
625 630 635 640

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
645 650 655

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
660 665 670

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
675 680 685

Gly Glu Cys
690

<210> 292
<211> 2076
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (9B11) VHCH1-Cadena pesada-(28H1) VHCL

<400> 292
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300
ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360
gctagcacca agggcccatc cgtgttccct ctggcccctt ccagcaagtc tacctctggc 420
ggcacagccg ctctgggctg cctcgtgaag gactacttcc ccgagcctgt gacagtgtcc 480
tggaactctg gcgccctgac atccggcgtg cacacctttc cagctgtgct gcagtcctcc 540
ggcctgtact ccctgtcctc cgtcgtgaca gtgccctcca gctctctggg cacccagacc 600
tacatctgca acgtgaacca caagccctcc aacaccaagg tggacaagaa ggtggaaccc 660
aagtcctgcg acaagaccca cacctgtccc ccttgtcctg cccctgaagc tgctggcggc 720
cctagcgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatctc ccggaccccc 780
gaagtgacct gcgtggtggt ggatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840
tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc ctagagagga acagtacaac 900
tccacctacc gggtggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaaa 960
gagtacaagt gcaaggtgtc caacaaggcc ctgggagccc ccatcgaaaa gaccatctcc 1020
aaggccaagg gccagcctcg cgagcctcag gtgtacaccc tgccccctag cagagatgag 1080
ctgaccaaga accaggtgtc cctgacctgt ctcgtgaaag gcttctaccc ctccgatatc 1140
gccgtggaat gggagagcaa cggccagccc gagaacaact acaagaccac ccccctgtg 1200
ctggactccg acggctcatt cttcctgtac tctaagctga cagtggacaa gtcccggtgg 1260
cagcagggca acgtgttctc ctgctccgtg atgcacgagg ccctgcacaa ccactacacc 1320
cagaagtccc tgtccctgtc tcccggggga ggcggaggat ctggcggagg cggatccggt 1380
ggtggcggat ctgggggcgg tggatctgag gtgcagctgc tggaatctgg gggaggactg 1440
gtgcagccag gcggatctct gaggctgtcc tgcgctgctt ccggctttac cttctccagc 1500
cacgccatga gttgggtgcg ccaggcaccc ggaaaaggac tggaatgggt gtcagccatc 1560
tgggcctccg gcgagcagta ctacgccgat agcgtgaagg gccggttcac catctctcgg 1620
gataacagca agaatactct gtacctgcag atgaactccc tgcgcgctga agataccgct 1680
gtgtattact gcgccaaggg ctggctgggc aacttcgatt actggggcca gggaaccctc 1740
gtgactgtct cgagcgcttc tgtggccgct ccctccgtgt tcatcttccc accttccgac 1800
gagcagctga agtccggcac tgcctctgtc gtgtgcctgc tgaacaactt ctaccctcgg 1860
gaagccaagg tgcagtggaa agtggataac gccctgcagt ccggcaactc ccaggaatcc 1920
gtgaccgagc aggactccaa ggacagcacc tactccctga gcagcaccct gaccctgtcc 1980

aaggccgact acgagaagca caaggtgtac gcctgtgaag tgacccacca gggcctgtcc 2040

agccccgtga ccaagtcctt caaccggggc gagtgc 2076

<210> 293
<211> 692
<212> PRT
<213> Secuencia artificial

<220>
<223> (9B11) VHCH1-Cadena pesada-(28H1) VHCL

<400> 293

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

```
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445
```

```
Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
465                 470                 475                 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                485                 490                 495

Thr Phe Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
            500                 505                 510

Gly Leu Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr
        515                 520                 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
    530                 535                 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
545                 550                 555                 560

Val Tyr Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly
                565                 570                 575

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Val Ala Ala Pro Ser
            580                 585                 590

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
        595                 600                 605

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
    610                 615                 620

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
625                 630                 635                 640

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
                645                 650                 655

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
            660                 665                 670

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
        675                 680                 685

Arg Gly Glu Cys
    690
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<210> 294
<211> 1350
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (12B3) VHCH1-pomo de cadena pesada

<400> 294
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggccctag cgtgttccct ctggccccta gcagcaagag cacaagtgga 420

ggaacagccg ccctgggctg cctggtcaag gactacttcc ccgagcccgt gaccgtgtcc 480

tggaattctg gcgccctgac aagcggcgtg cacacatttc cagccgtgct gcagagcagc 540

ggcctgtact ctctgagcag cgtcgtgacc gtgccctcta gctctctggg cacccagacc 600

tacatctgca acgtgaacca caagcccagc aacaccaaag tggacaagaa ggtggaaccc 660

aagagctgcg acaagaccca cacctgtccc ccttgccctg cccctgaagc tgctggtggc 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc 780

gaagtgacct gcgtggtggt cgatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatg ccgggatgag 1080

ctgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 295
<211> 450
<212> PRT
<213> Secuencia artificial

<220>
<223> (12B3) VHCH1-pomo de cadena pesada

<400> 295

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240
```

```
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
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<210> 296
<211> 1344
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (25G7) VHCH1-pomo de cadena pesada

<400> 296
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300

ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgctagc 360

accaagggcc ctagcgtgtt ccctctggcc cctagcagca agagcacaag tggaggaaca 420

gccgccctgg gctgcctggt caaggactac ttccccgagc ccgtgaccgt gtcctggaat 480

tctggcgccc tgacaagcgg cgtgcacaca tttccagccg tgctgcagag cagcggcctg 540

tactctctga gcagcgtcgt gaccgtgccc tctagctctc tgggcaccca gacctacatc 600

tgcaacgtga accacaagcc cagcaacacc aaagtggaca agaaggtgga acccaagagc 660

tgcgacaaga cccacacctg tccccccttgc cctgcccctg aagctgctgg tggcccttcc 720

gtgttcctgt tcccccccaaa gcccaaggac accctgatga tcagccggac ccccgaagtg 780

acctgcgtgg tggtcgatgt gtcccacgag gaccctgaag tgaagttcaa ttggtacgtg 840

gacggcgtgg aagtgcacaa tgccaagacc aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catgccggga tgagctgacc 1080

aagaaccagg tcagcctgtg gtgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg taaa 1344

<210> 297
<211> 448
<212> PRT
<213> Secuencia artificial

<220>
<223> (25G7) VHCH1-pomo de cadena pesada

<400> 297

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
```

260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 298
<211> 1347
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (11D5) VHCH1-pomo de cadena pesada

<400> 298
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact 300

ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctcagct 360

agcaccaagg gccctagcgt gttccctctg gcccctagca gcaagagcac aagtggagga 420

acagccgccc tgggctgcct ggtcaaggac tacttccccg agcccgtgac cgtgtcctgg 480

aattctggcg ccctgacaag cggcgtgcac acatttccag ccgtgctgca gagcagcggc 540

ctgtactctc tgagcagcgt cgtgaccgtg ccctctagct ctctgggcac ccagacctac 600

atctgcaacg tgaaccacaa gcccagcaac accaaagtgg acaagaaggt ggaacccaag 660

agctgcgaca agacccacac ctgtcccct tgccctgccc ctgaagctgc tggtggccct 720

tccgtgttcc tgttcccccc aaagcccaag gacaccctga tgatcagccg gacccccgaa 780

gtgacctgcg tggtggtcga tgtgtcccac gaggaccctg aagtgaagtt caattggtac 840

gtggacggcg tggaagtgca caatgccaag accaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatgccg ggatgagctg 1080

accaagaacc aggtcagcct gtggtgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtaaa 1347

<210> 299
<211> 449
<212> PRT
<213> Secuencia artificial

<220>
<223> (11D5) VHCH1-pomo de cadena pesada

<400> 299

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300
```

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 300
<211> 1350
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (9B11) VHCH1-pomo de cadena pesada

<400> 300
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggccctag cgtgttccct ctggccccta gcagcaagag cacaagtgga 420

ggaacagccg ccctgggctg cctggtcaag gactacttcc ccgagcccgt gaccgtgtcc 480

tggaattctg gcgccctgac aagcggcgtg cacacatttc agccgtgct gcagagcagc 540

ggcctgtact ctctgagcag cgtcgtgacc gtgccctcta gctctctggg cacccagacc 600

tacatctgca acgtgaacca caagcccagc aacaccaaag tggacaagaa ggtggaaccc 660

aagagctgcg acaagaccca cacctgtccc ccttgccctg cccctgaagc tgctggtggc 720

ccttccgtgt tcctgttccc cccaaagccc aaggacaccc tgatgatcag ccggaccccc 780

gaagtgacct gcgtggtggt cgatgtgtcc cacgaggacc ctgaagtgaa gttcaattgg 840

tacgtggacg gcgtggaagt gcacaatgcc aagaccaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatg ccgggatgag 1080

ctgaccaaga accaggtcag cctgtggtgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 301
<211> 450
<212> PRT
<213> Secuencia artificial

<220>
<223> (9B11) VHCH1-pomo de cadena pesada

<400> 301

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335
```

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 302
<211> 1338
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (8H9) VHCH1-pomo de cadena pesada

<400> 302
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

ggttggatgg actactgggg ccaagggacc accgtgaccg tctcctcagc tagcaccaag 360

ggccctagcg tgttccctct ggcccctagc agcaagagca caagtggagg aacagccgcc 420

ctgggctgcc tggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaattctggc 480

gccctgacaa gcggcgtgca cacatttcca gccgtgctgc agagcagcgg cctgtactct 540

ctgagcagcg tcgtgaccgt gccctctagc tctctgggca cccagaccta catctgcaac 600

gtgaaccaca agcccagcaa caccaaagtg gacaagaagg tggaacccaa gagctgcgac 660

aagacccaca cctgtccccc ttgccctgcc cctgaagctg ctggtggccc ttccgtgttc 720

ctgttccccc caaagcccaa ggacaccctg atgatcagcc ggacccccga agtgacctgc 780

gtggtggtcg atgtgtccca cgaggaccct gaagtgaagt tcaattggta cgtggacggc 840

gtggaagtgc acaatgccaa gaccaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg cccccatgcc gggatgagct gaccaagaac 1080

caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtaaa 1338

<210> 303
<211> 446
<212> PRT
<213> Secuencia artificial

<220>
<223> (8H9) VHCH1-pomo de cadena pesada

<400> 303

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Gly Trp Met Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

```
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
        355                 360                 365
```

```
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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<210> 304
<211> 1752
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de pomo de Fc (49B4) VHCH1 VH (4B9)

<400> 304

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caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc       60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc      120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac      300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc      360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca      420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac      480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc      540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc      600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct      660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca      720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc      780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg      840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg      900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac      960
```

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080

aagaaccagg tgtccctgtg gtgtctggtc aagggcttct accccagcga tatcgccgtg 1140

gagtgggaga gcaacggcca gcctgagaac aactacaaga ccacccccc tgtgctggac 1200

agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260

ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc tgggggcgga 1380

ggttccggag gcggaggatc cgaggtgcag ctgctcgaaa gcggcggagg actggtgcag 1440

cctggcggca gcctgagact gtcttgcgcc gccagcggct tcaccttcag cagctacgcc 1500

atgagctggg tccgccaggc ccctggcaag ggactggaat gggtgtccgc catcatcggc 1560

tctggcgcca gcacctacta cgccgacagc gtgaagggcc ggttcaccat cagccgggac 1620

aacagcaaga acaccctgta cctgcagatg aacagcctgc gggccgagga caccgccgtg 1680

tactactgcg ccaagggatg gttcggcggc ttcaactact ggggacaggg caccctggtc 1740

accgtgtcca gc 1752

<210> 305
<211> 1725
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de agujero de Fc (49B4) VHCH1 VH (4B9)

<400> 305
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggcggcgga 1380

ggttccggag gcggtggatc tgagatcgtg ctgacccagt ctcccggcac cctgtctctg 1440

agccctggcg agagagccac cctgtcctgc agagcctccc agtccgtgac ctcctcctac 1500

ctcgcctggt atcagcagaa gcccggccag gcccctcggc tgctgatcaa cgtgggcagt 1560

cggagagcca ccggcatccc tgaccggttc tccggctctg gctccggcac cgacttcacc 1620

ctgaccatct cccggctgga acccgaggac ttcgccgtgt actactgcca gcagggcatc 1680

atgctgcccc ccacctttgg ccagggcacc aaggtggaaa tcaag 1725

<210> 306
<211> 584
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1 pomo de Fc VH (4B9)

<400> 306

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335
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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
        435                 440                 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    450                 455                 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
465                 470                 475                 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                485                 490                 495

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            500                 505                 510

Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala
        515                 520                 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    530                 535                 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
545                 550                 555                 560

Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln
                565                 570                 575

Gly Thr Leu Val Thr Val Ser Ser
```

580

<210> 307
<211> 575
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1 agujero de Fc VH (4B9)

<400> 307

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

```
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
        355                 360                 365

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
        435                 440                 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
```

450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile
545 550 555 560

Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210> 308
<211> 1749
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de pomo de Fc (49B4) VHCH1 VH (28H1)

<400> 308
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080

aagaaccagg tgtccctgtg gtgtctggtc aagggcttct accccagcga tatcgccgtg 1140

gagtgggaga gcaacggcca gcctgagaac aactacaaga ccacccccc tgtgctggac 1200

agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260

ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc cggaggaggg 1380

ggaagtggcg gcggaggatc tgaggtgcag ctgctggaat ccggcggagg cctggtgcag 1440

cctggcggat ctctgagact gtcctgcgcc gcctccggct tcaccttctc ctcccacgcc 1500

atgtcctggg tccgacaggc tcctggcaaa ggcctggaat gggtgtccgc catctgggcc 1560

tccggcgagc agtactacgc cgactctgtg aagggccggt tcaccatctc ccgggacaac 1620

tccaagaaca ccctgtacct gcagatgaac tccctgcggg ccgaggacac cgccgtgtac 1680

tactgtgcca agggctggct gggcaacttc gactactggg gccagggcac cctggtcacc 1740

gtgtccagc 1749

<210> 309
<211> 1725
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de agujero de Fc (49B4) VHCH1 VH (28H1)

<400> 309
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggtggtggc 1380

ggatctgggg gcggtggatc tgagatcgtg ctgacccagt ctcccggcac cctgagcctg 1440

agccctggcg agagagccac cctgagctgc agagccagcc agagcgtgag ccggagctac 1500

ctggcctggt atcagcagaa gcccggccag gcccccagac tgctgatcat cggcgccagc 1560

acccgggcca ccggcatccc cgatagattc agcggcagcg gctccggcac cgacttcacc 1620

ctgaccatca gccggctgga acccgaggac ttcgccgtgt actactgcca gcagggccag 1680

gtgatccccc ccaccttcgg ccagggcacc aaggtggaaa tcaag 1725

<210> 310
<211> 583
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1 pomo de Fc VH (28H1)

<400> 310

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

```
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
```

290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
485 490 495

Ser Ser His Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
500 505 510

Glu Trp Val Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp
515 520 525

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
530 535 540

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
545 550 555 560

Tyr Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly
565 570 575

Thr Leu Val Thr Val Ser Ser
580

<210> 311
<211> 575
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1 agujero de Fc VH (28H1)

<400> 311

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

```
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
        355                 360                 365

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415
```

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Ser Arg Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Ile Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Gln
545 550 555 560

Val Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210> 312
<211> 1746
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de pomo de Fc (49B4) VHCH1 VH (DP47)

<400> 312
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080

aagaaccagg tgtccctgtg gtgtctggtc aagggcttct accccagcga tatcgccgtg 1140

gagtgggaga gcaacggcca gcctgagaac aactacaaga ccacccccc tgtgctggac 1200

agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260

ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc cggaggaggg 1380

ggaagtggcg gcggaggatc tgaggtgcaa ttgttggagt ctgggggagg cttggtacag 1440

cctgggggt ccctgagact ctcctgtgca gccagcggat tcacctttag cagttatgcc 1500

atgagctggg tccgccaggc tccagggaag gggctggagt gggtctcagc tattagtggt 1560

agtggtggta gcacatacta cgcagactcc gtgaagggcc ggttcaccat ctccagagac 1620

aattccaaga acacgctgta tctgcagatg aacagcctga gagccgagga cacggccgta 1680

tattactgtg cgaaaggcag cggatttgac tactggggcc aaggaaccct ggtcaccgtc 1740

tcgagc 1746

<210> 313
<211> 1725
<212> ADN
<213> Secuencia artificial

<220>
<223> Secuencia nucleotídica de agujero de Fc (49B4) VHCH1 VH (DP47)

<400> 313
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagagaatac 300

taccgtggtc cgtacgacta ctggggccaa gggaccaccg tgaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggaggcggc 1380

ggaagcggag ggggaggctc tgaaattgtg ctgacccaga gccccggcac cctgtcactg 1440

tctccaggcg aaagagccac cctgagctgc agagccagcc agagcgtgtc cagctcttac 1500

ctggcctggt atcagcagaa gcccggacag gcccccagac tgctgatcta cggcgcctct 1560

tctagagcca ccggcatccc cgatagattc agcggcagcg gctccggcac cgacttcacc 1620

ctgacaatca gcagactgga acccgaggac tttgccgtgt attactgcca gcagtacggc 1680

agcagccccc tgacctttgg ccagggcacc aaggtggaaa tcaaa 1725

<210> 314
<211> 582
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1 pomo de Fc VH (DP47)

<400> 314

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

```
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255
```

```
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
        435                 440                 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    450                 455                 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
465                 470                 475                 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                485                 490                 495

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            500                 505                 510
```

```
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
        515                 520                 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    530                 535                 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
545                 550                 555                 560

Tyr Tyr Cys Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr
                565                 570                 575

Leu Val Thr Val Ser Ser
            580
```

<210> 315
<211> 575
<212> PRT
<213> Secuencia artificial

<220>
<223> (49B4) VHCH1 agujero de Fc VL (DP47)

<400> 315

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Tyr Tyr Arg Gly Pro Tyr Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125
```

```
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
        355                 360                 365

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380
```

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
545 550 555 560

Ser Ser Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210> 316
<211> 1758
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (12B3) VHCH1 pomo de Fc VH (4B9) (HC1)

<400> 316
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctggagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcgagt 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccctg cagagatgag 1080

ctgaccaaga accaggtgtc cctgtggtgt ctggtcaagg gcttctaccc cagcgatatc 1140

gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac ccccctgtg 1200

ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccggtgg 1260

cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgagcctgag ccccggcgga ggcggcggaa gcggaggagg aggatctggg 1380

ggcggaggtt ccggaggcgg tggatctgag gtgcagctgc tcgaaagcgg cggaggactg 1440

gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc 1500

tacgccatga gctgggtccg ccaggcccct ggcaagggac tggaatgggt gtccgccatc 1560

atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccggtt caccatcagc 1620

cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc 1680

gccgtgtact actgcgccaa gggatggttc ggcggcttca actactgggg acagggcacc 1740

ctggtcaccg tgtccagc 1758

<210> 317
<211> 1731
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (12B3) VHCH1 agujero de Fc VL (4B9)

<400> 317
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctggagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcgagt 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccggc 1380

ggcggaggtt ccggaggcgg aggatccgag atcgtgctga cccagtctcc cggcaccctg 1440

tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc 1500

tcctacctcg cctggtatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg 1560

ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcaccgac 1620

ttcaccctga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag 1680

ggcatcatgc tgcccccccac ctttggccag ggcaccaagg tggaaatcaa g 1731

<210> 318
<211> 586

<212> PRT
<213> Secuencia artificial

<220>
<223> (12B3) VHCH1 pomo de Fc VH (4B9)

<400> 318

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
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```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
465                 470                 475                 480
```

```
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                485                 490                 495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
            500                 505                 510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
        515                 520                 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
    530                 535                 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
545                 550                 555                 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
                565                 570                 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585
```

<210> 319
<211> 577
<212> PRT
<213> Secuencia artificial

<220>
<223> (12B3) VHCH1 agujero de Fc VL (4B9)

<400> 319

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
            340                 345                 350
```

```
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
465                 470                 475                 480

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
                485                 490                 495

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
            500                 505                 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
        515                 520                 525

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
    530                 535                 540

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
545                 550                 555                 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
                565                 570                 575

Lys
```

<210> 320

<211> 1752
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (25G7) VHCH1 pomo de Fc VH (4B9)

<400> 320
gaggtgcagc tgctggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt caccttcagc agctacgcca tgagctgggt gcgccaggcc 120

cctggaaaag gcctggaatg ggtgtccgcc atctctggca gcggcggcag cacctactac 180

gccgattctg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actattgcgc cagggacgac 300

ccctggcccc cctttgatta ttggggacag ggcaccctcg tgaccgtgtc cagcgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080

aagaaccagg tgtccctgtg gtgtctggtc aagggcttct accccagcga tatcgccgtg 1140

gagtgggaga gcaacggcca gcctgagaac aactacaaga ccaccccccc tgtgctggac 1200

agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260

ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc tgggggcgga 1380

ggttccggag gcggtggatc tgaggtgcag ctgctcgaaa gcggcggagg actggtgcag 1440

cctggcggca gcctgagact gtcttgcgcc gccagcggct tcaccttcag cagctacgcc 1500

atgagctggg tccgccaggc ccctggcaag ggactggaat gggtgtccgc catcatcggc 1560

tctggcgcca gcacctacta cgccgacagc gtgaagggcc ggttcaccat cagccgggac 1620

aacagcaaga acaccctgta cctgcagatg aacagcctgc gggccgagga caccgccgtg 1680

tactactgcg ccaagggatg gttcggcggc ttcaactact ggggacaggg caccctggtc 1740

accgtgtcca gc 1752

<210> 321
<211> 1725
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (25G7) VHCH1 agujero de Fc VL (4B9)

<400> 321
gaggtgcagc tgctggaatc tggcggcgga ctggtgcagc ctggcggatc tctgagactg 60

agctgtgccg ccagcggctt caccttcagc agctacgcca tgagctgggt gcgccaggcc 120

cctggaaaag gcctggaatg ggtgtccgcc atctctggca gcggcggcag cacctactac 180

gccgattctg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actattgcgc cagggacgac 300

ccctggcccc cctttgatta ttggggacag ggcaccctcg tgaccgtgtc cagcgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggcggcgga 1380

ggttccggag gcggaggatc cgagatcgtg ctgacccagt ctcccggcac cctgtctctg 1440

agccctggcg agagagccac cctgtcctgc agagcctccc agtccgtgac ctcctcctac 1500

ctcgcctggt atcagcagaa gcccggccag gcccctcggc tgctgatcaa cgtgggcagt 1560

cggagagcca ccggcatccc tgaccggttc tccggctctg gctccggcac cgacttcacc 1620

ctgaccatct cccggctgga acccgaggac ttcgccgtgt actactgcca gcagggcatc 1680

atgctgcccc ccacctttgg ccagggcacc aaggtggaaa tcaag 1725

<210> 322
<211> 584
<212> PRT
<213> Secuencia artificial

<220>
<223> (25G7) VHCH1 pomo de Fc VH

<400> 322

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

```
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
```

420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
485 490 495

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
500 505 510

Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala
515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
545 550 555 560

Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln
565 570 575

Gly Thr Leu Val Thr Val Ser Ser
580

<210> 323
<211> 575
<212> PRT
<213> Secuencia artificial

<220>
<223> (25G7) VHCH1 agujero de Fc VL (4B9)

<400> 323

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
```

290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
355 360 365

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile
545 550 555 560

Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210> 324
<211> 1755
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (11D5) VHCH1 pomo de Fc VH (4B9)

<400> 324
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg cttccggcgg caccttcagc agctacgcca tttcttgggt gcgccaggcc 120

cctggacagg gcctggaatg gatgggcggc atcatcccca tcttcggcac cgccaactac 180

gcccagaaat tccagggcag agtgaccatc accgccgaca agagcaccag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc cagaagcacc 300

ctgatctacg gctacttcga ctactggggc cagggcacca ccgtgaccgt gtctagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc cccctgcag agatgagctg 1080

accaagaacc aggtgtccct gtggtgtctg gtcaagggct tctaccccag cgatatcgcc 1140

gtggagtggg agagcaacgg ccagcctgag aacaactaca agaccacccc ccctgtgctg 1200

gacagcgacg gcagcttctt cctgtactcc aaactgaccg tggacaagag ccggtggcag 1260

cagggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacccag 1320

aagtccctga gcctgagccc cggcggaggc ggcggaagcg gaggaggagg atctgggggc 1380

ggaggttccg gaggcggtgg atctgaggtg cagctgctcg aaagcggcgg aggactggtg 1440

cagcctggcg gcagcctgag actgtcttgc gccgccagcg gcttcacctt cagcagctac 1500

gccatgagct gggtccgcca ggcccctggc aagggactgg aatgggtgtc cgccatcatc 1560

ggctctggcg ccagcaccta ctacgccgac agcgtgaagg gccggttcac catcagccgg 1620

gacaacagca agaacaccct gtacctgcag atgaacagcc tgcgggccga ggacaccgcc 1680

gtgtactact gcgccaaggg atggttcggc ggcttcaact actggggaca gggcaccctg 1740

gtcaccgtgt ccagc 1755

<210> 325
<211> 1728
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (11D5) VHCH1 agujero de Fc VL (4B9)

<400> 325
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaaggtg 60

tcctgcaagg cttccggcgg caccttcagc agctacgcca tttcttgggt gcgccaggcc 120

cctggacagg gcctggaatg gatgggcggc atcatcccca tcttcggcac cgccaactac 180

gcccagaaat tccagggcag agtgaccatc accgccgaca agagcaccag caccgcctac 240

atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgtgc cagaagcacc 300

ctgatctacg gctacttcga ctactggggc cagggcacca ccgtgaccgt gtctagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tgcaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtggaggc ggcggaagcg gaggaggagg atccggcggc 1380

ggaggttccg gaggcggagg atccgagatc gtgctgaccc agtctcccgg caccctgtct 1440

ctgagccctg gcgagagagc caccctgtcc tgcagagcct cccagtccgt gacctcctcc 1500

tacctcgcct ggtatcagca gaagcccggc caggcccctc ggctgctgat caacgtgggc 1560

agtcggagag ccaccggcat ccctgaccgg ttctccggct ctggctccgg caccgacttc 1620

accctgacca tctcccggct ggaacccgag gacttcgccg tgtactactg ccagcagggc 1680

atcatgctgc cccccacctt tggccagggc accaaggtgg aaatcaag 1728

<210> 326
<211> 585
<212> PRT
<213> Secuencia artificial

<220>
<223> (11D5) VHCH1 pomo de Fc VH (4B9)

<400> 326

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu

130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
450 455 460

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
465 470 475 480

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
485 490 495

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
500 505 510

Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr
515 520 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
530 535 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
545 550 555 560

Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly
565 570 575

Gln Gly Thr Leu Val Thr Val Ser Ser
580 585

<210> 327
<211> 576
<212> PRT
<213> Secuencia artificial

<220>
<223> (11D5) VHCH1 agujero de Fc VL (4B9)

<400> 327

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

```
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
```

```
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser
        355                 360                 365

Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
465                 470                 475                 480

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
                485                 490                 495

Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
            500                 505                 510
```

Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro
515 520 525

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
530 535 540

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly
545 550 555 560

Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210> 328
<211> 1758
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (9B11) VHCH1 pomo de Fc VH (4B9)

<400> 328
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccctg cagagatgag 1080

ctgaccaaga accaggtgtc cctgtggtgt ctggtcaagg gcttctaccc cagcgatatc 1140

gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac ccccctgtg 1200

ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccggtgg 1260

cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgagcctgag ccccggcgga ggcggcggaa gcggaggagg aggatctggg 1380

ggcggaggtt ccggaggcgg tggatctgag gtgcagctgc tcgaaagcgg cggaggactg 1440

gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc 1500

tacgccatga gctgggtccg ccaggcccct ggcaagggac tggaatgggt gtccgccatc 1560

atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccggtt caccatcagc 1620

cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc 1680

gccgtgtact actgcgccaa gggatggttc ggcggcttca actactgggg acagggcacc 1740

ctggtcaccg tgtccagc 1758

<210> 329
<211> 1731
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (9B11) VHCH1 agujero de Fc VL (4B9)

<400> 329
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

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cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccggc 1380

ggcggaggtt ccggaggcgg aggatccgag atcgtgctga cccagtctcc cggcaccctg 1440

tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc 1500

tcctacctcg cctggtatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg 1560

ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcaccgac 1620

ttcaccctga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag 1680

ggcatcatgc tgcccccccac ctttggccag ggcaccaagg tggaaatcaa g 1731

<210> 330
<211> 586
<212> PRT
<213> Secuencia artificial

<220>
<223> (9B11) VHCH1 pomo de Fc VH (4B9)

<400> 330

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350
```

```
Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
465                 470                 475                 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                485                 490                 495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
            500                 505                 510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
        515                 520                 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
    530                 535                 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
545                 550                 555                 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
                565                 570                 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585
```

<210> 331
<211> 577

<212> PRT
<213> Secuencia artificial

<220>
<223> (9B11) VHCH1 agujero de Fc VL (4B9)

<400> 331

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
465                 470                 475                 480
```

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
485 490 495

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
500 505 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
515 520 525

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
530 535 540

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
545 550 555 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
565 570 575

Lys

<210> 332
<211> 1731
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (12B3) VHCH1 pomo de Fc VL (4B9)

<400> 332
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctggagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcgagt 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccctg cagagatgag 1080

ctgaccaaga accaggtgtc cctgtggtgt ctggtcaagg gcttctaccc cagcgatatc 1140

gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac ccccctgtg 1200

ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccggtgg 1260

cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgagcctgag ccccggcgga ggcggcggaa gcggaggagg aggatctggg 1380

ggcggaggtt ccggaggcgg tggatctgag atcgtgctga cccagtctcc cggcaccctg 1440

tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc 1500

tcctacctcg cctggtatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg 1560

ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcaccgac 1620

ttcaccctga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag 1680

ggcatcatgc tgccccccac ctttggccag ggcaccaagg tggaaatcaa g 1731

<210> 333
<211> 1758
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (12B3) VHCH1 agujero de Fc VH (4B9)

<400> 333
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctggagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctgaa 300

ttccgtttct acgctgactt cgactactgg ggccaaggga ccaccgtgac cgtctcgagt 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccggc 1380

ggcggaggtt ccggaggcgg aggatccgag gtgcagctgc tcgaaagcgg cggaggactg 1440

gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc 1500

tacgccatga gctgggtccg ccaggcccct ggcaagggac tggaatgggt gtccgccatc 1560

atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccggtt caccatcagc 1620

cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc 1680

gccgtgtact actgcgccaa gggatggttc ggcggcttca actactgggg acagggcacc 1740

ctggtcaccg tgtccagc 1758

<210> 334
<211> 577
<212> PRT
<213> Secuencia artificial

<220>
<223> (12B3) VHCH1 pomo de Fc VL (4B9)

<400> 334

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

```
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
```

```
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
465                 470                 475                 480

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
                485                 490                 495

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
            500                 505                 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
        515                 520                 525

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
    530                 535                 540

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
```

545 550 555 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
565 570 575

Lys

<210> 335
<211> 586
<212> PRT
<213> Secuencia artificial

<220>
<223> (12B3) VHCH1 agujero de Fc VH (4B9)

<400> 335

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Glu Phe Arg Phe Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

```
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
```

420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
450 455 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
465 470 475 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
485 490 495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
500 505 510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
515 520 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
530 535 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
545 550 555 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
580 585

<210> 336
<211> 1725
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (25G7) VHCH1 pomo de Fc VL (4B9)

<400> 336
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300

ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc cctgcagaga tgagctgacc 1080

aagaaccagg tgtccctgtg gtgtctggtc aagggcttct accccagcga tatcgccgtg 1140

gagtgggaga gcaacggcca gcctgagaac aactacaaga ccaccccccc tgtgctggac 1200

agcgacggca gcttcttcct gtactccaaa ctgaccgtgg acaagagccg gtggcagcag 1260

ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta cacccagaag 1320

tccctgagcc tgagccccgg cggaggcggc ggaagcggag gaggaggatc tgggggcgga 1380

ggttccggag gcggtggatc tgagatcgtg ctgacccagt ctcccggcac cctgtctctg 1440

agccctggcg agagagccac cctgtcctgc agagcctccc agtccgtgac ctcctcctac 1500

ctcgcctggt atcagcagaa gcccggccag gcccctcggc tgctgatcaa cgtgggcagt 1560

cggagagcca ccggcatccc tgaccggttc tccggctctg gctccggcac cgacttcacc 1620

ctgaccatct cccggctgga acccgaggac ttcgccgtgt actactgcca gcagggcatc 1680

atgctgcccc ccacctttgg ccagggcacc aaggtggaaa tcaag 1725

<210> 337
<211> 1752
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (25G7) VHCH1 Fc agujero de Fc VH (4B9)

<400> 337
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gcgtgacgac 300

ccgtggccgc cgttcgacta ctggggccaa ggaaccctgg tcaccgtctc gagtgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagctgcagg gggaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcaagg tctccaacaa agccctcggc gcccccatcg agaaaaccat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtgc accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctctc gtgcgcagtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct cgtgagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggaggcggc ggaagcggag gaggaggatc cggcggcgga 1380

ggttccggag gcggaggatc cgaggtgcag ctgctcgaaa gcggcggagg actggtgcag 1440

cctggcggca gcctgagact gtcttgcgcc gccagcggct tcaccttcag cagctacgcc 1500

atgagctggg tccgccaggc ccctggcaag ggactggaat gggtgtccgc catcatcggc 1560

tctggcgcca gcacctacta cgccgacagc gtgaagggcc ggttcaccat cagccgggac 1620

aacagcaaga acaccctgta cctgcagatg aacagcctgc gggccgagga caccgccgtg 1680

tactactgcg ccaagggatg gttcggcggc ttcaactact ggggacaggg caccctggtc 1740

accgtgtcca gc 1752

<210> 338
<211> 575
<212> PRT
<213> Secuencia artificial

<220>
<223> (25G7) VHCH1 pomo de Fc VL (4B9)

<400> 338

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
```

245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
465 470 475 480

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
485 490 495

Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
500 505 510

Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro Asp
515 520 525

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
530 535 540

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile
545 550 555 560

Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210> 339
<211> 584
<212> PRT
<213> Secuencia artificial

<220>
<223> (25G7) VHCH1 agujero de Fc VH (4B9)

<400> 339

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asp Pro Trp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
355 360 365

Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
465 470 475 480

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
485 490 495

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
500 505 510

Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala
515 520 525

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
530 535 540

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
545 550 555 560

Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln
565 570 575

Gly Thr Leu Val Thr Val Ser Ser
580

<210> 340
<211> 1728
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (11D5) VHCH1 pomo de Fc VL (4B9)

<400> 340
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact 300

ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc agggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc cccctgcag agatgagctg 1080

accaagaacc aggtgtccct gtggtgtctg gtcaagggct tctaccccag cgatatcgcc 1140

gtggagtggg agagcaacgg ccagcctgag aacaactaca agaccacccc ccctgtgctg 1200

gacagcgacg gcagcttctt cctgtactcc aaactgaccg tggacaagag ccggtggcag 1260

cagggcaacg tgttcagctg cagcgtgatg cacgaggccc tgcacaacca ctacacccag 1320

aagtccctga gcctgagccc cggcggaggc ggcggaagcg gaggaggagg atctgggggc 1380

ggaggttccg gaggcggtgg atctgagatc gtgctgaccc agtctcccgg caccctgtct 1440

ctgagccctg gcgagagagc caccctgtcc tgcagagcct cccagtccgt gacctcctcc 1500

tacctcgcct ggtatcagca gaagcccggc caggcccctc ggctgctgat caacgtgggc 1560

agtcggagag ccaccggcat ccctgaccgg ttctccggct ctggctccgg caccgacttc 1620

accctgacca tctcccggct ggaacccgag gacttcgccg tgtactactg ccagcagggc 1680

atcatgctgc cccccacctt tggccagggc accaaggtgg aaatcaag 1728

<210> 341
<211> 1755
<212> ADN
<213> Secuencia artificial

<220>

<223> ADN (11D5) VHCH1 agujero de Fc VH (4B9)

<400> 341
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatctact 300

ctgatctacg gttacttcga ctactggggc caagggacca ccgtgaccgt ctcctcagct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagctgc aggggggaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tgcaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtggaggc ggcggaagcg gaggaggagg atccggcggc 1380

ggaggttccg gaggcggagg atccgaggtg cagctgctcg aaagcggcgg aggactggtg 1440

cagcctggcg gcagcctgag actgtcttgc gccgccagcg gcttcacctt cagcagctac 1500

gccatgagct gggtccgcca ggcccctggc aagggactgg aatgggtgtc cgccatcatc 1560

ggctctggcg ccagcaccta ctacgccgac agcgtgaagg gccggttcac catcagccgg 1620

gacaacagca agaacaccct gtacctgcag atgaacagcc tgcgggccga ggacaccgcc 1680

gtgtactact gcgccaaggg atggttcggc ggcttcaact actggggaca gggcaccctg 1740

gtcaccgtgt ccagc 1755

<210> 342
<211> 576
<212> PRT
<213> Secuencia artificial

<220>
<223> (11D5) VHCH1 pomo de Fc VL (4B9)

<400> 342

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

```
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460
```

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
465 470 475 480

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
485 490 495

Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
500 505 510

Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile Pro
515 520 525

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
530 535 540

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly
545 550 555 560

Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
565 570 575

<210> 343
<211> 585
<212> PRT
<213> Secuencia artificial

<220>
<223> (11D5) VHCH1 agujero de Fc VH (4B9)

<400> 343

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Ser Thr Leu Ile Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr
            340                 345                 350
```

```
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser
        355                 360                 365

Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460

Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
465                 470                 475                 480

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
                485                 490                 495

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
            500                 505                 510

Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr
        515                 520                 525

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
    530                 535                 540

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
545                 550                 555                 560

Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly
                565                 570                 575

Gln Gly Thr Leu Val Thr Val Ser Ser
            580                 585
```

<210> 344
<211> 1731

<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (9B11) VHCH1 pomo de Fc VL (4B9)

<400> 344
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccctg cagagatgag 1080

ctgaccaaga accaggtgtc cctgtggtgt ctggtcaagg gcttctaccc cagcgatatc 1140

gccgtggagt gggagagcaa cggccagcct gagaacaact acaagaccac cccccctgtg 1200

ctggacagcg acggcagctt cttcctgtac tccaaactga ccgtggacaa gagccggtgg 1260

cagcagggca acgtgttcag ctgcagcgtg atgcacgagg ccctgcacaa ccactacacc 1320

cagaagtccc tgagcctgag ccccggcgga ggcggcggaa gcggaggagg aggatctggg 1380

ggcggaggtt ccggaggcgg tggatctgag atcgtgctga cccagtctcc cggcaccctg 1440

tctctgagcc ctggcgagag agccaccctg tcctgcagag cctcccagtc cgtgacctcc 1500

tcctacctcg cctggtatca gcagaagccc ggccaggccc ctcggctgct gatcaacgtg 1560

ggcagtcgga gagccaccgg catccctgac cggttctccg gctctggctc cggcaccgac 1620

ttcaccctga ccatctcccg gctggaaccc gaggacttcg ccgtgtacta ctgccagcag 1680

ggcatcatgc tgccccccac ctttggccag ggcaccaagg tggaaatcaa g 1731

<210> 345
<211> 1758
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN (9B11) VHCH1 agujero de Fc VH (4B9)

<400> 345
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120

cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagatcttct 300

ggtgcttacc cgggttactt cgactactgg ggccaaggga ccaccgtgac cgtctcctca 360

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc tgcaggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcggcgccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtgtgcaccc tgcccccatc ccgggatgag 1080

ctgaccaaga accaggtcag cctctcgtgc gcagtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcgtg agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtgga ggcggcggaa gcggaggagg aggatccggc 1380

ggcggaggtt ccggaggcgg aggatccgag gtgcagctgc tcgaaagcgg cggaggactg 1440

gtgcagcctg gcggcagcct gagactgtct tgcgccgcca gcggcttcac cttcagcagc 1500

tacgccatga gctgggtccg ccaggcccct ggcaagggac tggaatgggt gtccgccatc 1560

atcggctctg gcgccagcac ctactacgcc gacagcgtga agggccggtt caccatcagc 1620

cgggacaaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc 1680

gccgtgtact actgcgccaa gggatggttc ggcggcttca actactgggg acagggcacc 1740

ctggtcaccg tgtccagc 1758

<210> 346
<211> 577
<212> PRT
<213> Secuencia artificial

<220>
<223> (9B11) VHCH1 pomo de Fc VL (4B9)

<400> 346

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

```
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430
```

```
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
465                 470                 475                 480

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
                485                 490                 495

Ser Val Thr Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
            500                 505                 510

Ala Pro Arg Leu Leu Ile Asn Val Gly Ser Arg Arg Ala Thr Gly Ile
        515                 520                 525

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
    530                 535                 540

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
545                 550                 555                 560

Gly Ile Met Leu Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
                565                 570                 575

Lys
```

<210> 347
<211> 586
<212> PRT
<213> Secuencia artificial

<220>
<223> (9B11) VHCH1 agujero de Fc VH (4B9)

<400> 347

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Ser Gly Ala Tyr Pro Gly Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290                 295                 300
```

```
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys
            340                 345                 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    450                 455                 460

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
465                 470                 475                 480

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
                485                 490                 495

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
            500                 505                 510

Gly Leu Glu Trp Val Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr
        515                 520                 525

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
    530                 535                 540

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
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545 550 555 560

Ala Val Tyr Tyr Cys Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp
565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
580 585