LISTADO DE SECUENCIAS

<110> APTEVO RESEARCH Y DEVELOPMENT LLC
Tan, Philip
Blankenship, John W.

<120> POLIPÉPTIDOS DE UNIÓN A CD3

<130> APVO-052/01WO

<150> US 62/221,190
<151> 2015-09-21

<160> 222

<170> PatentIn versión 3.5

<210> 1
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120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
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acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
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ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
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gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
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aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt ggagtctggg
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960

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1080

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1260

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1320

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1440

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<212> PRT
<213> Secuencia artificial

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Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe
305                 310                 315                 320

Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp
                325                 330                 335

Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
385                 390                 395                 400
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Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser
405 410 415

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
420 425 430

Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro
435 440 445

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

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
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Ser Ser Ser

<210> 3
<211> 1569
<212> ADN
<213> Secuencia artificial

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<223> Dominio de unión a CD3 de Fc H7L1 (TSC313)

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180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct
1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

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1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt
1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg
1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc
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1569

<210> 4
<211> 502
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L1 (TSC313)

<400> 4

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1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

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

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    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350
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Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
                485                 490                 495

Gln Ile Thr Ser Ser Ser
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<210> 5
<211> 1572
<212> ADN
<213> Secuencia artificial

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180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct
1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

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1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct
1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca
1320

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1380

tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg
1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt
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1560

tcctccagct aa
1572

<210> 6
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<213> Secuencia artificial

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<223> Dominio de unión a CD3 de Fc H7L4 (TSC314)

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
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Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

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Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
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    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
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<210> 7
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<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L5 (TSC315)

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120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
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660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc
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ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

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1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct
1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

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1260

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1320

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1380

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1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt
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tcctccagct aa
1572

<210> 8
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L5 (TSC315)

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Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

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Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240
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Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460
```

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 9
<211> 1569
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L1 (TSC316)

<400> 9
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt
1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg
1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc
1500

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc
1560

tccagctaa
1569

<210> 10
<211> 502

<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L1 (TSC316)

<400> 10

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

```
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400
```

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Gln Ile Thr Ser Ser Ser
500

<210> 11
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L4 (TSC317)

<400> 11
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct
1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccaacag aaacctggcc aggctcccag gctcctcatc
1380

tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg
1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt
1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 12
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L4 (TSC317)

<400> 12

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

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

```
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

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

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 13
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L5 (TSC318)

<400> 13
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gctcctgatc
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg
1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 14
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L5 (TSC318)
<400> 14

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

```
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300
```

```
Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 15
<211> 1569
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H9L1 (TSC319)

<400> 15
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc
900

tttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaagacacgg ctgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt
1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg
1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc
1500

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc
1560

tccagctaa
1569

<210> 16
<211> 502
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H9L1 (TSC319)

<400> 16

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

```
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
```

```
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    450                 455                 460
```

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Gln Ile Thr Ser Ser Ser
500

<210> 17
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H9L4 (TSC320)

<400> 17
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc
900

tttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaagacacgg ctgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct
1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccaacag aaacctggcc aggctcccag gctcctcatc
1380

tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg
1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt
1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 18
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H9L4 (TSC320)

<400> 18

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

```
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415
```

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 19
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H9L5 (TSC321)

<400> 19
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc
900

tttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaagacacgg ctgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gctcctgatc
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg
1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 20
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H9L5 (TSC321)

<400> 20

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

```
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350
```

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 21
<211> 1569
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L1 (TSC322)

<400> 21
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt
1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg
1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc
1500

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc
1560

tccagctaa
1569

<210> 22
<211> 502
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L1 (TSC322)
<400> 22

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

```
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300
```

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Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
                485                 490                 495

Gln Ile Thr Ser Ser Ser
            500
```

<210> 23
<211> 1572

<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L4 (TSC323)

<400> 23
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct
1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccaacag aaacctggcc aggctcccag gctcctcatc
1380

tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg
1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt
1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 24
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L4 (TSC323)

<400> 24

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

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

```
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255
```

```
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

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

465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 25
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L5 (TSC324)

<400> 25
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gctcctgatc
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg
1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 26
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L5 (TSC324)

<400> 26

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

```
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415
```

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 27
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L6 (TSC334)

<400> 27
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct
1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg
1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 28
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L6 (TSC334)
<400> 28

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

```
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
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Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 29
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L7 (TSC335)

<400> 29
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct
1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct
1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt
1380

tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg
1440

acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt
1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 30
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L7 (TSC335)

<400> 30

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

```
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320
```

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 31
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L8 (TSC336)

<400> 31
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc
1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct
1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 32
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H7L8 (TSC336)

<400> 32

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255
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Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480
```

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 33
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L6 (TSC337)

<400> 33
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg
1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 34
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L6 (TSC337)

<400> 34

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
260 265 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305 310 315 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro

420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 35
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L7 (TSC338)

<400> 35
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct
1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt
1380

tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg
1440

acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt
1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 36
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L7 (TSC338)

<400> 36

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

```
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
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Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 37
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L8 (TSC339)

<400> 37
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg
840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc
900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 38
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H8L8 (TSC339)

<400> 38

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

```
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320
```

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Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 39
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L6 (TSC340)

<400> 39
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg
1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 40
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L6 (TSC340)

<400> 40

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255
```

```
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480
```

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 41
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L7 (TSC341)

<400> 41
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct
1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca
1320

agtgtaagtt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt
1380

tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg
1440

acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt
1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 42
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L7 (TSC341)

<400> 42

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

```
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
```

420 425 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 43
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L8 (TSC342)

<400> 43
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 44
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de Fc H10L8 (TSC342)

<400> 44

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

```
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
```

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Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 45
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC370

<400> 45
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 46
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC370

<400> 46

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

```
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320
```

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 47
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC371

<400> 47
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 48
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC371

<400> 48

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5   10   15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20   25   30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35   40   45

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255
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```
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480
```

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 49
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC372

<400> 49
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 50
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC372

<400> 50

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5                 10                  15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
```

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225 230 235 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
245 250 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
260 265 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
275 280 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
290 295 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305 310 315 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro

420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 51
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC390

<400> 51
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60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 52
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC390

<400> 52

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

```
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
```

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Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
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<210> 53
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC391

<400> 53
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60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 54
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC391

<400> 54

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

```
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320
```

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
325 330 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
340 345 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385 390 395 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 55
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC392

<400> 55
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60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 56
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC392

<400> 56

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255
```

```
Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480
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Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 57
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC393

<400> 57
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60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 58
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC393

<400> 58

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

```
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
```

420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 59
<211> 1572
<212> ADN
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC394

<400> 59
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60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg
120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc
240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag
300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat
360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc
420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg
480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc
540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct
600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc
660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac
720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat
780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg
840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc
900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata
960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc
1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct
1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt
1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga
1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct
1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca
1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt
1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg
1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc
1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg
1560

tcctccagct aa
1572

<210> 60
<211> 503
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 de TSC394

<400> 60

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1. 5 10 15

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

```
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
```

```
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
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<210> 61
<211> 2301
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC408

<400> 61
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60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc
120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca
180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct
240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct
300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa
360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt
420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca
480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg
540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat
600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc
660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca
720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc
780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct
840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg
900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag
960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg
1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac
1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc
1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc
1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc
1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag
1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg
1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg
1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct
1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg
1560

caatctgggc ctgaggtgaa gaagcctggg tcctcggtga aggtctcctg caaggcttct
1620

ggatatacct tcagcagatc tacgatgcac tgggtgcgac aggcccctgg acaagggctt
1680

gagtggatag gatacattaa tcctagcagt gcttatacta attacaatca gaaattcaag
1740

gacagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc
1800

ctgagatctg aggacacggc cgtgtattac tgtgcgagac cccaagtcca ctatgattac
1860

aacgggtttc cttactgggg ccaaggaacc ctggtcaccg tctcctcagg tggaggcggt
1920

tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catccagatg
1980

acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat cacttgcagt
2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag
2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt
2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact
2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag
2280

atcaaacggt cctccagcta a
2301

<210> 62
<211> 746
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC408

<400> 62

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

```
Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
            260                 265                 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380
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```
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
                485                 490                 495

Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser
            500                 505                 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    530                 535                 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            580                 585                 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605
```

```
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
625                 630                 635                 640

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

Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
            660                 665                 670

Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
        675                 680                 685

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    690                 695                 700

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
705                 710                 715                 720

Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly
                725                 730                 735

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745
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<210> 63
<211> 2301
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC409

<400> 63
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc
120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca
180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct
240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct
300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa
360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt
420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca
480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg
540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat
600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc
660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca
720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc
780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct
840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccccaa aacccaagga caccctcatg
900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag
960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg
1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac
1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc
1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc
1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc
1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag
1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg
1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg
1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct
1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg
1560

caatctgggc ctgaggtgaa gaagcctggg tcctcggtga aggtctcctg caaggcttct
1620

ggatatacct tcagcagatc tacgatgcac tgggtgcgac aggcccctgg acaagggctt
1680

gagtggatgg gatacattaa tcctagcagt gcttatacta attacaatca gaaattcaag
1740

gacagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc
1800

ctgagatctg aggacacggc cgtgtattac tgtgcgagac cccaagtcca ctatgattac
1860

aacgggtttc cttactgggg ccaaggaacc ctggtcaccg tctcctcagg tggaggcggt
1920

tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catccagatg
1980

acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat gacttgcagt
2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag
2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt
2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact
2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag
2280

atcaaacggt cctccagcta a
2301

<210> 64
<211> 746
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC409

<400> 64

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

```
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
            260                 265                 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380
```

```
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
                485                 490                 495

Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser
            500                 505                 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
    530                 535                 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            580                 585                 590
```

```
Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
625                 630                 635                 640

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

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
            660                 665                 670

Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
        675                 680                 685

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    690                 695                 700

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
705                 710                 715                 720

Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly
                725                 730                 735

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745
```

<210> 65
<211> 2301
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC410

<400> 65
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc
120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca
180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct
240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct
300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa
360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt
420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca
480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg
540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat
600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc
660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca
720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc
780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct
840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccccaa aacccaagga caccctcatg
900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag
960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg
1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac
1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc
1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc
1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc
1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag
1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg
1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg
1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct
1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg
1560

caatctgggg ctgaggtgaa gaagcctggg tcctcggtga aggtctcctg caaggcttct
1620

ggatatacct tcagcagatc tacgatgcac tgggtgcgac aggcccctgg acaagggctt
1680

gagtggatag gatacattaa tcctagcagt gcttatacta attacaatca gaaattcaag
1740

gacagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc
1800

ctgagatctg aggacacggc cgtgtattac tgtgcgagac cccaagtcca ctatgattac
1860

aacgggtttc cttactgggg ccaaggaacc ctggtcaccg tctcctcagg tggaggcggt
1920

tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catccagatg
1980

acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat gacttgcagt
2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag
2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt
2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact
2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag
2280

atcaaacggt cctccagcta a
2301

<210> 66
<211> 746
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC410

<400> 66

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

```
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
            260                 265                 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
```

```
    370                 375                 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
                485                 490                 495

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser
            500                 505                 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    530                 535                 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            580                 585                 590
```

```
Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
625                 630                 635                 640

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

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
            660                 665                 670

Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
        675                 680                 685

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    690                 695                 700

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
705                 710                 715                 720

Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly
                725                 730                 735

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745
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<210> 67
<211> 2301
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC411

<400> 67
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc
120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca
180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct
240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct
300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa
360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt
420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca
480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg
540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat
600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc
660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca
720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc
780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct
840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg
900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag
960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg
1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac
1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc
1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc
1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc
1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag
1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg
1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg
1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct
1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg
1560

caatctgggc ctgaggtgaa gaagcctggg tcctcggtga aggtctcctg caaggcttct
1620

ggatatacct tcagcagatc tacgatgcac tgggtgcgac aggcccctgg acaagggctt
1680

gagtggatag gatacattaa tcctagcagt gcttatacta attacaatca gaaattcaag
1740

gacagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc
1800

ctgagatctg aggacacggc cgtgtattac tgtgcgagac cccaagtcca ctatgattac
1860

aacgggtttc cttactgggg ccaaggaacc ctggtcaccg tctcctcagg tggaggcggt
1920

tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catccagatg
1980

acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat gacttgcagt
2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag
2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt
2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact
2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag
2280

atcaaacggt cctccagcta a
2301

<210> 68
<211> 746
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC411

<400> 68

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val

```
145                 150                 155                 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
            260                 265                 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365
```

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
                485                 490                 495

Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser
            500                 505                 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    530                 535                 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

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

```
            580                 585                 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
625                 630                 635                 640

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

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
            660                 665                 670

Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
        675                 680                 685

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    690                 695                 700

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr
705                 710                 715                 720

Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly
                725                 730                 735

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745
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<210> 69
<211> 2313
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 CAS105

<400> 69
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt
120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg
180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac
240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac
300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc
360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc
420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc
480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc
540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa
600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca
660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag
720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc
780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac
840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc
900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg
960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg
1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc
1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc
1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga
1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc
1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat
1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc
1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca
1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct
1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct
1560

ccgaattctc aggtccagct ggtggagtct gggggcggag tggtgcagcc tgggcggtca
1620

ctgaggctgt cctgcaaggc ttctggctac acctttacta gatctacgat gcactgggta
1680

aggcaggccc ctggacaagg tctggaatgg attggataca ttaatcctag cagtgcttat
1740

actaattaca atcagaaatt caaggacagg ttcacaatca gcgcagacaa atccaagagc
1800

acagccttcc tgcagatgga cagcctgagg cccgaggaca ccggcgtcta tttctgtgca
1860

cggccccaag tccactatga ttacaacggg tttccttact ggggccaagg gactcccgtc
1920

actgtctcta gcggtggcgg agggtctggg ggtggcggat ccggaggtgg tggctctgca
1980

caagacatcc agatgaccca gtctccaagc agcctgtctg caagcgtggg ggacagggtc
2040

accatgacct gcagtgccag ctcaagtgta agttacatga actggtacca gcagaagccg
2100

ggcaaggccc ccaaaagatg gatttatgac tcatccaaac tggcttctgg agtccctgct
2160

cgcttcagtg gcagtgggtc tgggaccgac tataccctca caatcagcag cctgcagccc
2220

gaagatttcg ccacttatta ctgccagcag tggagtcgta acccacccac gttcggaggg
2280

gggaccaagc tacaaattac atcctccagc taa
2313

<210> 70
<211> 750
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 CAS105

<400> 70

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
130 135 140

```
Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145                 150                 155                 160

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365
```

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
                485                 490                 495

Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly
            500                 505                 510

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
        515                 520                 525

Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp
                565                 570                 575
```

```
Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
            580                 585                 590

Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
    610                 615                 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
625                 630                 635                 640

Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745                 750
```

<210> 71
<211> 2325
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC445

<400> 71

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt
120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg
180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac
240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac
300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc
360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc
420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc
480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc
540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa
600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca
660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag
720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc
780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac
840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc
900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg
960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg
1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc
1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc
1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga
1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc
1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat
1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc
1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca
1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct
1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct
1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg
1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg
1680

cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgcttat
1740

actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc
1800

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg
1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc
1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt
1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga
2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag
2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg
2160

gtcccatcaa ggttcagcgg cagtggatct gggacagagt tcactctcac catcagcagc
2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact
2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa
2325

<210> 72
<211> 754
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC445

<400> 72

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
130 135 140

```
Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145                 150                 155                 160

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350
```

```
Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
                485                 490                 495

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
                565                 570                 575
```

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
580 585 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
595 600 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
610 615 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625 630 635 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
645 650 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
660 665 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
705 710 715 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745 750

Ser Ser

<210> 73
<211> 2325
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC452

<400> 73
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt
120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg
180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac
240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac
300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc
360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc
420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc
480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc
540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa
600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca
660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag
720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc
780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac
840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc
900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg
960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg
1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc
1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc
1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga
1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc
1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat
1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc
1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca
1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct
1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct
1560

ccgaattctc aggtccagct ggtggagtct gggggcggag tggtgcagcc tgggcggtca
1620

ctgaggctgt cctgcaaggc ttctggctac acctttacta gatctacgat gcactgggta
1680

aggcaggccc ctggacaagg tctggaatgg attggataca ttaatcctag cagtgcttat
1740

actaattaca atcagaaatt caaggacagg ttcacaatca gcgcagacaa atccaagagc
1800

acagccttcc tgcagatgga cagcctgagg cccgaggaca ccggcgtcta tttctgtgca
1860

cggccccaag tccactatga ttacaacggg tttccttact ggggccaagg gactcccgtc
1920

actgtctcta gcggtggcgg agggtctggg ggtggcggat ccggcggtgg cggatcgggt
1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga
2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag
2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg
2160

gtcccatcaa ggttcagcgg cagtggatct gggacagagt tcactctcac catcagcagc
2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact
2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa
2325

<210> 74
<211> 754
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC452

<400> 74

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

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

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

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

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

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

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

```
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
                485                 490                 495

Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly
            500                 505                 510

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
        515                 520                 525

Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540
```

```
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp
                565                 570                 575

Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
            580                 585                 590

Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
    610                 615                 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
                645                 650                 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
    690                 695                 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
705                 710                 715                 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
                725                 730                 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
            740                 745                 750

Ser Ser
```

<210> 75
<211> 2322
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC453

<400> 75
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt
120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg
180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac
240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac
300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc
360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc
420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc
480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc
540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa
600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca
660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag
720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc
780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac
840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc
900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg
960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg
1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc
1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc
1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga
1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc
1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat
1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc
1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca
1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct
1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct
1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg
1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg
1680

cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgcttat
1740

actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc
1800

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg
1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc
1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggaggtgg tggctctggt
1980

ggcggcggat ctgacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg
2040

gacagggtca ccatgacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag
2100

cagaagccgg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga
2160

gtccctgctc gcttcagtgg cagtgggtct gggaccgact ataccctcac aatcagcagc
2220

ctgcagcccg aagatttcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg
2280

ttcggagggg ggaccaagct acaaattaca tcctccagct aa
2322

<210> 76
<211> 753
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC453

<400> 76

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300
```

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
                485                 490                 495

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525
```

```
Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
                565                 570                 575

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    610                 615                 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
                645                 650                 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg
    690                 695                 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
705                 710                 715                 720

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
                725                 730                 735
```

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser
740 745 750

Ser

<210> 77
<211> 2325
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC454

<400> 77
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt
120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg
180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac
240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac
300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc
360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc
420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc
480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc
540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa
600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca
660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag
720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc
780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac
840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc
900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg
960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg
1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc
1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc
1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga
1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc
1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat
1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc
1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca
1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct
1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct
1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg
1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg
1680

cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgcttat
1740

actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc
1800

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg
1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc
1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt
1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga
2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag
2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg
2160

gtcccatcaa ggttcagcgg cagtggatct gggacagatt tcactctcac catcagcagc
2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact
2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa
2325

<210> 78
<211> 754
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC454

<400> 78

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285
```

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
                485                 490                 495
```

```
Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly Pro
            500                 505                 510

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
                565                 570                 575

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    610                 615                 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
                645                 650                 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
    690                 695                 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
705                 710                 715                 720
```

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745 750

Ser Ser

<210> 79
<211> 2325
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC455

<400> 79
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt
120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg
180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac
240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac
300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc
360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc
420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc
480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc
540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa
600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca
660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag
720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc
780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac
840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc
900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg
960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg
1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc
1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc
1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga
1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc
1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat
1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc
1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca
1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct
1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct
1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg
1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg
1680

cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgcttat
1740

actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc
1800

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg
1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc
1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt
1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga
2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag
2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg
2160

gtcccatcaa ggttcagcgg cagtggatct gggacagagt atactctcac catcagcagc
2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact
2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa
2325

<210> 80
<211> 754
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC455

<400> 80

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480
```

```
Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
               485                 490                 495

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
               565                 570                 575

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    610                 615                 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
               645                 650                 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685
```

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser
705 710 715 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745 750

Ser Ser

<210> 81
<211> 2325
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC456

<400> 81
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt
120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg
180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac
240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac
300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc
360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc
420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc
480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc
540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa
600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca
660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag
720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc
780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac
840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc
900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg
960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg
1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc
1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc
1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga
1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc
1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat
1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc
1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca
1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct
1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct
1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg
1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg
1680

cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgcttat
1740

actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc
1800

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg
1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc
1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt
1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga
2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag
2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg
2160

gtcccatcaa ggttcagcgg cagtggatct gggacagatt atactctcac catcagcagc
2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact
2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa
2325

<210> 82
<211> 754
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-CD37 X anti-CD3 TSC456

<400> 82

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

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

Thr Leu Ser Cys Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala
            180                 185                 190

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
    210                 215                 220

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240
```

```
Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
               245                 250                 255

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
               325                 330                 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
               405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445
```

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met
                485                 490                 495

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp
                565                 570                 575

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    610                 615                 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
                645                 650                 655

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670
```

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
705 710 715 720

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
725 730 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745 750

Ser Ser

<210> 83
<211> 251
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 TSC455 CD3 scFv

<400> 83

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

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

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

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

Lys Asp 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 Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser
            180                 185                 190

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
    210                 215                 220

Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
                245                 250
```

<210> 84
<211> 251
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 TSC456 CD3 scFv

<400> 84

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

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

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

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

Lys Asp 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 Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110

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

Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
130 135 140

Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
145 150 155 160

Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser
180 185 190

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
210 215 220

Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
245 250

<210> 85
<211> 247
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 DRA222 CD3 scFv

<400> 85

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

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

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

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

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

Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

```
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160

Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Leu Gln Ile Thr Ser Ser Ser
                245
```

<210> 86
<211> 121
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 TSC455 y TSC456 dominio variable pesado

<400> 86

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

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

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

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

Lys Asp 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 Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 87
<211> 121
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 DRA222 dominio variable pesado
<400> 87

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

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

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

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

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

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly

100 105 110

Gln Gly Thr Pro Val Thr Val Ser Ser
115 120

<210> 88
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 TSC455 dominio variable ligero

<400> 88

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

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

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

<210> 89
<211> 108
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 TSC456 dominio variable ligero

<400> 89

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

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

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

<210> 90
<211> 107
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 DRA222 dominio variable ligero

<400> 90

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

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

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

<210> 91
<211> 5
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VH CDR1 (Kabat)

<400> 91

Arg Ser Thr Met His
1. 5

<210> 92
<211> 16
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VH CDR2 (Kabat)

<400> 92

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

<210> 93
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VH CDR3 (Kabat)

<400> 93

Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr
1. 5 10

<210> 94
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VL CDR1 (Kabat)

<400> 94

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn
1. 5 10

<210> 95
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VL CDR2 (Kabat)

<400> 95

Asp Ser Ser Lys Leu Ala Ser
1. 5

<210> 96
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VL CDR3 (Kabat)

<400> 96

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1. 5

<210> 97
<211> 2304
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR133

<400> 97
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
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ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
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tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
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2280

ctacaaatta catcctccag ctaa
2304

<210> 98
<211> 747
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR133

<400> 98

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

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

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

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

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

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

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

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

```
Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365
```

```
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
                565                 570                 575
```

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
580 585 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625 630 635 640

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

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 99
<211> 2316
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR193

<400> 99

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120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

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1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

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1620

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1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac
1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc
1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga
1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc
2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca
2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca
2160

aggttcagcg gcagtggatc tgggacagag tatactctca ccatcagcag cctgcagcct
2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga
2280

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2316

<210> 100
<211> 751
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR193

<400> 100

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

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

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

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

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

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

```
Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350
```

```
Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575
```

```
Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
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<210> 101
<211> 2304
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR134

<400> 101
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120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc gactcggtga agggccggtt caccatctcc
660

cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc
720

gccgtgtact tctgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg
1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag
2280

ctacaaatta catcctccag ctaa
2304

<210> 102
<211> 747
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR134

<400> 102

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

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

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

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

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

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

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

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

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

```
    130                 135                 140

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

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

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350
```

```
Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
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565 570 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
580 585 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625 630 635 640

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

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 103
<211> 2316
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR189

<400> 103
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc gactcggtga agggccggtt caccatctcc
660

cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc
720

gccgtgtact tctgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc
1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc
1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac
1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc
1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga
1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc
2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca
2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca
2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct
2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga
2280

gggaccaagg tggagatcaa acggtcctcc agctaa
2316

<210> 104
<211> 751
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR189

<400> 104

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

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

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

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

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

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

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

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

```
Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

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

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
```

```
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560
```

```
Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
```

<210> 105
<211> 2304
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR154

<400> 105
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg
1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag
2280

ctacaaatta catcctccag ctaa
2304

<210> 106
<211> 747
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR154

<400> 106

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

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

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

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

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

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

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

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

```
Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335
```

```
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560
```

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
565 570 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
580 585 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625 630 635 640

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

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 107
<211> 2316
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR185

<400> 107
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc
1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc
1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac
1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc
1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga
1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc
2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca
2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca
2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct
2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga
2280

gggaccaagg tggagatcaa acggtcctcc agctaa
2316

<210> 108
<211> 751
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR185

<400> 108

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

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

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

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

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

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

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

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335
```

```
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540
```

```
Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
```

<210> 109
<211> 2304

<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR179

<400> 109
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ctggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg
1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag
2280

ctacaaatta catcctccag ctaa
2304

<210> 110
<211> 747
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR179

<400> 110

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

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

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

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

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

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

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

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
```

```
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540
```

```
Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
                565                 570                 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
            580                 585                 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625                 630                 635                 640

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

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            660                 665                 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
        675                 680                 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
    690                 695                 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705                 710                 715                 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
                725                 730                 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
```

<210> 111

<211> 2316
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR186

<400> 111
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ctggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc
1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc
1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac
1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc
1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga
1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc
2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca
2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca
2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct
2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga
2280

gggaccaagg tggagatcaa acggtcctcc agctaa
2316

<210> 112
<211> 751
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR186

<400> 112

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

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

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

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

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

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

Tyr Trp Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly

```
            100                 105                 110

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320
```

```
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
```

```
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
```

<210> 113
<211> 2304
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR181

<400> 113
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg tgtccggcac cgacatcaac
540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc gactcggtga agggccggtt caccatctcc
660

cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc
720

gccgtgtact tctgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg
1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag
2280

ctacaaatta catcctccag ctaa
2304

<210> 114
<211> 747
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR181

<400> 114

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

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

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

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

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

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

```
Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

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

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

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

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320
```

```
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525
```

```
Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
                565                 570                 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
            580                 585                 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625                 630                 635                 640

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

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            660                 665                 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
        675                 680                 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
    690                 695                 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705                 710                 715                 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
                725                 730                 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
```

<210> 115
<211> 2316
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR191

<400> 115
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg tgtccggcac cgacatcaac
540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc gactcggtga agggccggtt caccatctcc
660

cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc
720

gccgtgtact tctgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc
1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc
1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac
1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc
1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga
1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc
2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca
2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca
2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct
2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga
2280

gggaccaagg tggagatcaa acggtcctcc agctaa
2316

<210> 116
<211> 751
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR191

<400> 116

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

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

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

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

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

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

```
Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

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

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

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

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300
```

```
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525
```

```
Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735
```

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 117
<211> 2304
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR182

<400> 117
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg
1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag
2280

ctacaaatta catcctccag ctaa
2304

<210> 118
<211> 747
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR182

<400> 118

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

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

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

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

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

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser

85 90 95

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

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
180 185 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
195 200 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
210 215 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
260 265 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
290 295 300

```
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
```

```
        515                 520                 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
                565                 570                 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
            580                 585                 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625                 630                 635                 640

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

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            660                 665                 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
        675                 680                 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
    690                 695                 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705                 710                 715                 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
                725                 730                 735
```

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 119
<211> 2316
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR192

<400> 119
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

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1740

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2100

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2220

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<220>
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<400> 120

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

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

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

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

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

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

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

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
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    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510
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Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
515 520 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
530 535 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545 550 555 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
565 570 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
580 585 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
595 600 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625 630 635 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
645 650 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
660 665 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
675 680 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
690 695 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro

725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

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

<220>
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<400> 121

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1. 5 10 15

<210> 122
<211> 15
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<400> 122

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1. 5 10 15

<210> 123
<211> 15
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<400> 123

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1. 5 10 15

<210> 124
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<400> 124

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
1. 5 10 15

<210> 125
<211> 15
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<400> 125

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1. 5 10 15

<210> 126
<211> 15
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<400> 126

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
1. 5 10 15

<210> 127
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<400> 127

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1. 5 10 15

<210> 128
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<213> Secuencia artificial

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<400> 128

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1. 5 10 15

<210> 129
<211> 15
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<400> 129

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1. 5 10 15

<210> 130
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<400> 130

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1. 5 10 15

<210> 131
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<212> PRT
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<400> 131

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1. 5 10 15

<210> 132

<211> 15
<212> PRT
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<400> 132

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1. 5 10 15

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<220>
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<400> 133

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1. 5 10 15

<210> 134
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<212> PRT
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<220>
<223> Bisagra scs(p)-hIgG1

<400> 134

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1. 5 10 15

<210> 135
<211> 6
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<220>
<223> Enlazador Scppcp

<400> 135

Ser Cys Pro Pro Cys Pro
1. 5

<210> 136
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador STD1

<400> 136

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1. 5 10 15

Ser Gly Asn Ser
20

<210> 137
<211> 38
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador STD2

<400> 137

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1. 5 10 15

Ser Gly Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Asn Ser
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<210> 138
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<220>
<223> Enlazador H1

<400> 138

Asn Ser
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<210> 139
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<212> PRT
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<220>
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<400> 139

Gly Gly Gly Gly Ser Gly Asn Ser
1. 5

<210> 140
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H3

<400> 140

Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser
1. 5 10

<210> 141
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H4

<400> 141

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
1. 5 10

<210> 142
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H5

<400> 142

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser

1. 5 10 15

<210> 143
<211> 18
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H6

<400> 143

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

Asn Ser

<210> 144
<211> 8
<212> PRT
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<220>
<223> Enlazador H7

<400> 144

Gly Cys Pro Pro Cys Pro Asn Ser
1. 5

<210> 145
<211> 15
<212> PRT
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<220>
<223> Enlazador (G4S)3

<400> 145

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

<210> 146
<211> 16
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H105

<400> 146

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

<210> 147
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador (G4S)4

<400> 147

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

Gly Gly Gly Ser
20

<210> 148
<211> 21
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H75 (mutante cuádruple de NKG2A)

<400> 148

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1. 5 10 15

His Ser Pro Asn Ser
20

<210> 149
<211> 16
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H83 (derivado de NKG2A)

<400> 149

Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
1. 5 10 15

<210> 150
<211> 18
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H106 (derivado de NKG2A)

<400> 150

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1. 5 10 15

His Ser

<210> 151
<211> 14
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H81 (derivado de NKG2D)

<400> 151

Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
1. 5 10

<210> 152
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H91 (derivado de NKG2D)

<400> 152

Asn Ser Leu Ala Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1. 5 10 15

Ser Pro Asn Ser
20

<210> 153
<211> 19
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H94

<400> 153

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

Pro Asn Ser

<210> 154
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H16

<400> 154

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1. 5 10 15

<210> 155
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H17

<400> 155

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Cys Pro Pro
1. 5 10 15

Cys Pro Asn Ser
20

<210> 156
<211> 15
<212> PRT

<213> Secuencia artificial

<220>
<223> Bisagra H18

<400> 156

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
1. 5 10 15

<210> 157
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H19

<400> 157

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro
1. 5 10 15

Cys Pro Asn Ser
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<210> 158
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H20

<400> 158

Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Asn Ser
1. 5 10 15

<210> 159
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H21

<400> 159

Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Cys Pro Pro

1. 5 10 15

Cys Pro Asn Ser
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<210> 160
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H22

<400> 160

Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Asn Ser
1. 5 10 15

<210> 161
<211> 21
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H23

<400> 161

Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Ser Cys Pro
1. 5 10 15

Pro Cys Pro Asn Ser
20

<210> 162
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H24

<400> 162

Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Asn Ser
1. 5 10 15

<210> 163

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

<220>
<223> Bisagra H25

<400> 163

Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Cys Pro Pro
1. 5 10 15

Cys Pro Asn Ser
20

<210> 164
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H26

<400> 164

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1. 5 10 15

<210> 165
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H27

<400> 165

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Cys Pro Pro
1. 5 10 15

Cys Pro Asn Ser
20

<210> 166
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H28

<400> 166

Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Ser Asn Ser
1. 5 10 15

<210> 167
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H30

<400> 167

Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Asn Ser
1. 5 10 15

<210> 168
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H32

<400> 168

Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
1. 5 10 15

<210> 169
<211> 20
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H33

<400> 169

Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Cys Pro Pro
1. 5 10 15

Cys Pro Asn Ser
20

<210> 170
<211> 13
<212> PRT
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<220>
<223> Bisagra H36

<400> 170

Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
1. 5 10

<210> 171
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H40

<400> 171

Gly Cys Pro Pro Cys Pro Ala Asn Ser
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<210> 172
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H41

<400> 172

Gly Cys Pro Pro Cys Pro Ala Asn Ser
1. 5

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

<220>
<223> Bisagra H42

<400> 173

Gly Cys Pro Pro Cys Pro Asn Ser

1. 5

<210> 174
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H44

<400> 174

Gly Gly Gly Ala Ser Cys Pro Pro Cys Pro Gly Asn Ser
1. 5 10

<210> 175
<211> 13
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H45

<400> 175

Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
1. 5 10

<210> 176
<211> 12
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H46

<400> 176

Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Asn Ser
1. 5 10

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

<220>
<223> Bisagra H47

<400> 177

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1. 5 10 15

<210> 178
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H48

<400> 178

Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1. 5 10

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

<220>
<223> Bisagra H50

<400> 179

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
1. 5 10 15

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

<220>
<223> Bisagra H51

<400> 180

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
1. 5 10 15

<210> 181
<211> 11
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H52

<400> 181

Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ser
1. 5 10

<210> 182
<211> 16
<212> PRT
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<220>
<223> Bisagra H53

<400> 182

Ser Gln Pro Glu Ile Val Pro Ile Ser Cys Pro Pro Cys Pro Asn Ser
1. 5 10 15

<210> 183
<211> 19
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H54

<400> 183

Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro Cys
1. 5 10 15

Pro Asn Ser

<210> 184
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H55

<400> 184

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1. 5 10 15

<210> 185

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

<220>
<223> Bisagra H56

<400> 185

Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1. 5 10

<210> 186
<211> 10
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H57

<400> 186

Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
1. 5 10

<210> 187
<211> 15
<212> PRT
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<220>
<223> Bisagra H58

<400> 187

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
1. 5 10 15

<210> 188
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H59

<400> 188

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
1. 5 10 15

<210> 189
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H60

<400> 189

Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Asn Ser
1. 5 10 15

<210> 190
<211> 21
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H61

<400> 190

Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu Leu Gln Lys Asp Ser
1. 5 10 15

Asp Cys Pro Asn Ser
20

<210> 191
<211> 21
<212> PRT
<213> Secuencia artificial

<220>
<223> Bisagra H62

<400> 191

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
1. 5 10 15

His Cys Pro Asn Ser
20

<210> 192
<211> 20
<212> PRT

<213> Secuencia artificial

<220>
<223> Bisagra H63

<400> 192

Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1. 5 10 15

Cys Pro Asn Ser
20

<210> 193
<211> 15
<212> PRT
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<220>
<223> Enlazador ((Gly4Ser)3)

<400> 193

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

<210> 194
<211> 25
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador (Gly4Ser)n

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<221> MISC_FEATURE
<222> (6)..(25)
<223> pueden faltar residuos de aminoácidos

<400> 194

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 195

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

<220>
<223> secuencia señal de secreción

<400> 195

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1. 5 10 15

Asp Thr Thr Gly
20

<210> 196
<211> 19
<212> PRT
<213> Secuencia artificial

<220>
<223> Enlazador H111

<400> 196

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

Pro Gly Ser

<210> 197
<211> 751
<212> PRT
<213> Secuencia artificial

<220>
<223> anti-CD123 (VLVH) x anti-CD3 (TSC456) biespecífica quimérica
Dominio de unión a CD3 scFv-Fc-scFv

<400> 197

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

Glu Lys Phe Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe Phe Gly
20 25 30

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

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

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

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

Tyr Tyr Asn Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110

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

Gly Gly Gly Gly Ser Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
    130                 135                 140

Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Asp Tyr Ser
145                 150                 155                 160

Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
                165                 170                 175

Lys Leu Glu Trp Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr
            180                 185                 190

Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
        195                 200                 205

Asn Gln Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala
    210                 215                 220

Thr Tyr Tyr Cys Ser Arg Gly Glu Gly Phe Tyr Phe Asp Ser Trp Gly
225                 230                 235                 240

Gln Gly Thr Thr Leu Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460
```

```
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685
```

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
690 695 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705 710 715 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
725 730 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 198
<211> 753
<212> PRT
<213> Secuencia artificial

<220>
<223> anti-CD123 (VHVL) x anti-CD3 (TSC456) biespecífica quimérica
Dominio de unión a CD3 scFv-Fc-scFv

<400> 198

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

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

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

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

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

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

Arg Gly Glu Gly Phe Tyr Phe Asp Ser Trp Gly Gln Gly Thr Thr Leu

```
            100                 105                 110

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

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Met Met Ser Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ala Val Ser Val Gly Glu Lys Phe Thr Met Thr Cys Lys
145                 150                 155                 160

Ser Ser Gln Ser Leu Phe Phe Gly Ser Thr Gln Lys Asn Tyr Leu Ala
                165                 170                 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Ala Ile Ser Ser Val Met Pro Glu Asp
    210                 215                 220

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Trp Thr Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270

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

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

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320
```

```
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380

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

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480

Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                485                 490                 495

Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu
            500                 505                 510

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
        515                 520                 525

Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly
```

```
    530                 535                 540

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
545                 550                 555                 560

Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys
                565                 570                 575

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
            580                 585                 590

Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        595                 600                 605

Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    610                 615                 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala
                645                 650                 655

Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val
            660                 665                 670

Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg
        675                 680                 685

Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe
    690                 695                 700

Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu
705                 710                 715                 720

Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn
                725                 730                 735

Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser
            740                 745                 750
```

Ser

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

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VH CDR1 (IMGT)

<400> 199

Gly Tyr Thr Phe Thr Arg Ser Thr
1. 5

<210> 200
<211> 8
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VH CDR2 (IMGT)

<400> 200

Ile Asn Pro Ser Ser Ala Tyr Thr
1. 5

<210> 201
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VH CDR3 (IMGT)

<400> 201

Ala Arg Pro Gln Val His Tyr Asn Gly Phe Pro Tyr
1. 5

<210> 202
<211> 7
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VL CDR1 (IMGT)

<400> 202

Ala Ser Ser Ser Val Ser Tyr
1. 5

<210> 203
<211> 3
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VL CDR2 (IMGT)

<400> 203

Asp Ser Ser
1

<210> 204
<211> 9
<212> PRT
<213> Secuencia artificial

<220>
<223> Dominio de unión a CD3 Cris7 y DRA222 VL CDR3 (IMGT)

<400> 204

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1. 5

<210> 205
<211> 2286
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC471

<400> 205
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc
120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca
180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct
240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct
300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa
360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt
420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca
480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg
540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat
600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc
660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca
720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc
780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct
840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg
900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag
960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg
1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac
1080

tggctgaatg gcaaggaata caagtgcgcg gtctccaaca aagccctccc agcccccatc
1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc
1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc
1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag
1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg
1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg
1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gttccggagg tggcggttcg
1500

ggaggtggcg ggtcaggagg tgggggctct ccttcacagg tgcagctggt gcagtctggt
1560

cctgaggtga aaaagcctgg ctccagcgtg aaggtgtcct gcaaggccag cggatacacc
1620

tttagccggt ccaccatgca ttgggtgagg caggctcctg gacagggcct ggagtggatc
1680

ggctacatca accccagcag cgcttatacc aactacaatc agaagtttaa ggaccgggtg
1740

accatcaccg ccgataagtc caccagcacc gcctacatgg agctgtccag cctgaggagc
1800

gaggataccg ccgtgtacta ttgcgcccgg ccccaggtcc attacgacta caacggcttc
1860

ccctattggg gccagggaac cctggtgacc gtgtccagcg gtggcggtgg cagcggcggc
1920

ggcggctctg gcggaggtgg cagcggcgga gggggctccg acattcagat gacccagtcc
1980

ccctccaccc tgtccgctag cgtgggcgat cgggtgacca tgacctgcag cgccagcagc
2040

tccgtgtcct acatgaactg gtaccagcag aagcccggca aggctcccaa gaggtggatt
2100

tacgactcca gcaagctggc ctctggtgtc cccagcaggt tctctggtag cggcagcggc
2160

acagactaca ccctgaccat ctcctccctg cagcccgacg atttcgccac ctactattgc
2220

cagcagtggt cccggaatcc ccctaccttt ggcggcggca ccaaggtgga gatcaagagg
2280

agctaa
2286

<210> 206
<211> 741
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC471

<400> 206

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

```
Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
            260                 265                 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
```

385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Pro Ser Gln Val Gln Leu
485 490 495

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
500 505 510

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
515 520 525

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
530 535 540

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
545 550 555 560

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
565 570 575

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
580 585 590

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
595 600 605

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
610 615 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
625 630 635 640

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
645 650 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
660 665 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
675 680 685

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
705 710 715 720

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
725 730 735

Glu Ile Lys Arg Ser
740

<210> 207
<211> 2307
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR243

<400> 207
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60

gacatccaga tgacccagtc cccttcctcc ctgtccgcta gcgtgggcga tagggtgacc
120

atcaactgcc aggcctccca gtccattgac tccaatctgg cctggttcca gcagaagccc
180

ggacagcccc ccaagctgct gatttacagg gcctccaacc tggcttccgg cgtgcctgac
240

aggttctccg gatccggcag cggcaccgac ttcaccctga ccatctcctc cctggaggcc
300

gaggatgtcg ccacctacta ctgtctgggc ggcgtgggcg ctgtgagcta tcggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggcggcggcg gcagcggcgg cggcggcagc
420

ggcggcggag gctccggcgg cggcggcagc gaggtgcagc tggtggaaag cggaggaggc
480

ctggtgcagc ctggaaggtc cctgaggctg tcctgcacag ccagcggctc cgacatcaac
540

gactacccca tcacctgggt gaggcaggct cctggccagg gcctggaatg gatcggcttt
600

atcaacagcg gcggcagcac ctggtatgct tcctgggtga agggccggtt caccattagc
660

agggacgact ccaagtccat tgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact actgcgccag gggctacagc acctattacc gggactttaa catctggggc
780

cagggcacac tggtcaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttccggag gaggggttc aggtgggga ggttctggcg gcgggggaag cccttcacag
1560

gtgcaactgg tgcagagtgg acccgaggtt aaaaaaccag ggtcctccgt taaggttagc
1620

tgcaaagcct ctggctacac attttccagg agtacaatgc actgggtgag gcaggctcct
1680

ggacagggac tcgagtggat cgggtatatc aacccatcta gcgcctatac caattacaac
1740

caaaagttta aggaccgagt taccattacc gctgacaaat ccaccagtac agcttatatg
1800

gagctgtcat ctcttaggtc cgaggacact gctgtttatt actgcgctcg tcctcaggtt
1860

cactatgact ataatggttt tccctactgg ggtcagggaa ccctggtgac tgtctcttct
1920

ggcggtggag gcagcggtgg gggtgggtct ggaggcggtg gcagtggcgg cggaggctct
1980

gatattcaga tgactcagtc tcctagcact ctcagcgcca gcgtggggga tcgtgtgaca
2040

atgacttgct ccgctagcag tagtgtgtct tacatgaatt ggtatcagca gaagcccggg
2100

aaagcaccta agcgctggat ctatgactct tccaagctgg caagtggtgt cccctcacgg
2160

ttctctggct caggttctgg tactgactat actttgacta tctcctccct ccagcccgat
2220

gatttcgcta cctattattg tcagcagtgg agccgtaacc cacccacttt cggaggcggt
2280

accaaagtgg agatcaagag gtcatga
2307

<210> 208
<211> 748
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR243

<400> 208

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

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

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

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

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

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

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

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

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
165 170 175

```
Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380
```

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
            500                 505                 510

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

Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    530                 535                 540

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn
545                 550                 555                 560

Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
                565                 570                 575

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            580                 585                 590

Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro
        595                 600                 605
```

```
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    610                 615                 620

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
                645                 650                 655

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            660                 665                 670

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        675                 680                 685

Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    690                 695                 700

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
705                 710                 715                 720

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                725                 730                 735

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
            740                 745
```

<210> 209
<211> 2289
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC266

<400> 209
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc
120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca
180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct
240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct
300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa
360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt
420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca
480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg
540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat
600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc
660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca
720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc
780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct
840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccccaa aacccaagga caccctcatg
900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag
960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg
1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac
1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc
1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc
1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc
1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag
1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg
1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg
1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct
1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg
1560

gagtctgggg gcggagtggt gcagcctggg cggtcactga ggctgtcctg caaggcttct
1620

ggctacacct ttactagatc tacgatgcac tgggtaaggc aggcccctgg acaaggtctg
1680

gaatggattg gatacattaa tcctagcagt gcttatacta attacaatca gaaattcaag
1740

gacaggttca caatcagcgc agacaaatcc aagagcacag ccttcctgca gatggacagc
1800

ctgaggcccg aggacaccgg cgtctatttc tgtgcacggc cccaagtcca ctatgattac
1860

aacgggtttc cttactgggg ccaagggact cccgtcactg tctctagcgg tggcggaggg
1920

tctgggggtg gcggatccgg aggtggtggc tctgcacaag acatccagat gacccagtct
1980

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca
2040

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt
2100

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg
2160

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc
2220

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc
2280

tccagctaa
2289

<210> 210
<211> 742
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-PSMA X anti-CD3 TSC266

<400> 210

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
85 90 95

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

```
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
            260                 265                 270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305                 310                 315                 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                325                 330                 335

Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380
```

```
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
                485                 490                 495

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
            500                 505                 510

Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    530                 535                 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu
                565                 570                 575

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
            580                 585                 590
```

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
595 600 605

Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
610 615 620

Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
625 630 635 640

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
645 650 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
660 665 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
675 680 685

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
705 710 715 720

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
725 730 735

Gln Ile Thr Ser Ser Ser
740

<210> 211
<211> 2301
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR206

<400> 211
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg
1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag
2280

ctacaaatta catcctccag c
2301

<210> 212
<211> 767
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR206

<400> 212

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1. 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
50 55 60

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

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

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145 150 155 160

```
Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

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

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
```

```
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly
        515                 520                 525

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
            580                 585                 590
```

```
Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
        595                 600                 605

Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            660                 665                 670

Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
        675                 680                 685

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
    690                 695                 700

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
705                 710                 715                 720

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
                725                 730                 735

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
            740                 745                 750

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
        755                 760                 765
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<210> 213
<211> 2313
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR207

<400> 213

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc
1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc
1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac
1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc
1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga
1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc
2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca
2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca
2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct
2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga
2280

gggaccaagg tggagatcaa acggtcctcc agc
2313

<210> 214
<211> 771
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR207

<400> 214

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1. 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
50 55 60

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

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

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

```
Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

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

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350
```

```
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
        515                 520                 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575
```

```
Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
            580                 585                 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
        595                 600                 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
            660                 665                 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
        675                 680                 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    690                 695                 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705                 710                 715                 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                725                 730                 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            740                 745                 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        755                 760                 765

Ser Ser Ser
    770
```

<210> 215
<211> 2301
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR208

<400> 215
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg
1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc
1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc
1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct
1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc
1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc
2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc
2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt
2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc
2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag
2280

ctacaaatta catcctccag c
2301

<210> 216
<211> 767
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR208

<400> 216

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1. 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
50 55 60

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

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

Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val

```
            100                 105                 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

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

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320
```

```
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly
        515                 520                 525

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
```

530 535 540

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
545 550 555 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
565 570 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
580 585 590

Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
595 600 605

Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
610 615 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
660 665 670

Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
675 680 685

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
690 695 700

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
705 710 715 720

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
725 730 735

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
740 745 750

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
755 760 765

<210> 217
<211> 2313
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR209

<400> 217
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt
60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc
120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc
180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac
240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc
300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc
420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc
480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac
540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc
600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc
660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc
780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct
1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc
1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc
1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac
1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac
1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa
1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc
1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga
1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc
2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca
2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca
2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct
2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga
2280

gggaccaagg tggagatcaa acggtcctcc agc
2313

<210> 218
<211> 771
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR209

<400> 218

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1. 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
50 55 60

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

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

Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
            100                 105                 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

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

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
```

```
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510
```

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
515 520 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
530 535 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545 550 555 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
565 570 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
580 585 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
595 600 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
610 615 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
660 665 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
675 680 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
690 695 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705 710 715 720

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

725 730 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
740 745 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
755 760 765

Ser Ser Ser
770

<210> 219
<211> 2313
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR231

<400> 219
atggaggcac ccgcccagct gctgttcttg ttgctgctgt ggctccctga taccaccgga
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gacatccaga tgacccaatc cccttctagt ctctccgcta gcgtcggaga ccgcgtgacc
120

atcaattgtc aagcatctca gagtattgac agcaatctcg cctggtttca gcagaagcca
180

ggaaagccac ccaagctcct gatttatagg gctagcaacc tggcttctgg tgtccctagt
240

aggttcagcg gctctgggag tggcacagac ttcaccctga ccattagtag tctgcagccc
300

gaagatgtcg ctacctatta ctgcctcgga ggagtgggtg ccgtttctta tcgcacctca
360

tttggaggtg gcaccaaagt ggagatcaaa ggtggtggcg gctccggggg tggcgggtca
420

ggggggggag ggtctggagg cggcggatca gaagttcagc tggtggaatc tggaggaggt
480

ctggtgcagc caggcaggtc cctccggctg agctgcactg catccggctc tgacattaat
540

gactacccta tcacctgggt gaggcaggcc cccggtaaag gcctggagtg gatcgggttc
600

atcaattctg gtggatctac ttggtacgca agctgggtga aaggacgctt cacaattagt
660

agagacgact ctaagtctat cgcatatctg cagatgaata gcttgaagac agaggacacc
720

gccgtgtact attgtgcaag aggatactcc acttactacc gcgatttcaa tatctggggc
780

cagggaaccc tggtgacagt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttccggag gcggcggctc cggcggcggc ggcagcggcg gcggcggcag ccccggatcc
1560

caggtgcagc tggtgcagtc tggtcctgag gtgaaaaagc ctggctccag cgtgaaggtg
1620

tcctgcaagg ccagcggata cacctttagc cggtccacca tgcattgggt gaggcaggct
1680

cctggacagg gcctggagtg gatcggctac atcaacccca gcagcgctta taccaactac
1740

aatcagaagt ttaaggaccg ggtgaccatc accgccgata agtccaccag caccgcctac
1800

atggagctgt ccagcctgag gagcgaggat accgccgtgt actattgcgc ccggccccag
1860

gtccattacg actacaacgg cttcccctat tggggccagg gaaccctggt gaccgtgtcc
1920

agcggaggcg gcggcagcgg cggcggcggc agcggcggag gaggcagcgg cggaggaggc
1980

tccgacattc agatgaccca gtccccctcc accctgtccg ctagcgtggg cgatcgggtg
2040

accatgacct gcagcgccag cagctccgtg tcctacatga actggtacca gcagaagccc
2100

ggcaaggctc ccaagaggtg gatttacgac tccagcaagc tggcctctgg tgtccccagc
2160

aggttctctg gtagcggcag cggcacagac tacaccctga ccatctcctc cctgcagccc
2220

gacgatttcg ccacctacta ttgccagcag tggtcccgga atccccctac ctttggcggc
2280

ggcaccaagg tggagatcaa gaggagctcc agc
2313

<210> 220
<211> 771
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR231

<400> 220

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1. 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

```
Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
    50                  55                  60

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

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

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
            100                 105                 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
                245                 250                 255
```

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Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480
```

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
515 520 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
530 535 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545 550 555 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
565 570 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
580 585 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
595 600 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
610 615 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
660 665 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
675 680 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
690 695 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
725 730 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
740 745 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
755 760 765

Ser Ser Ser
770

<210> 221
<211> 2313
<212> ADN
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR233

<400> 221
atggaggctc ccgctcagct gctgttcctc ctgctgctct ggctgcccga caccacaggc
60

gacatccaga tgacccagtc cccttcctcc ctgtccgcta gcgtgggcga tagggtgacc
120

atcaactgcc aggcctccca gtccattgac tccaatctgg cctggttcca gcagaagccc
180

ggacagcccc ccaagctgct gatttacagg gcctccaacc tggcttccgg cgtgcctgac
240

aggttctccg gatccggcag cggcaccgac ttcaccctga ccatctcctc cctggaggcc
300

gaggatgtcg ccacctacta ctgtctgggc ggcgtgggcg ctgtgagcta tcggacctcc
360

ttcggcggcg gcaccaaggt ggagatcaag ggcggcggcg gcagcggcgg cggcggcagc
420

ggcggcggag gctccggcgg cggcggcagc gaggtgcagc tggtggaaag cggaggaggc
480

ctggtgcagc ctggaaggtc cctgaggctg tcctgcacag ccagcggctc cgacatcaac
540

gactacccca tcacctgggt gaggcaggct cctggccagg gcctggaatg gatcggcttt
600

atcaacagcg gcggcagcac ctggtatgct tcctgggtga agggccggtt caccattagc
660

agggacgact ccaagtccat tgcctacctg cagatgaact ccctgaagac cgaggacacc
720

gccgtgtact actgcgccag gggctacagc acctattacc gggactttaa catctggggc
780

cagggcacac tggtcaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca
840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа
900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac
960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat
1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc
1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac
1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa
1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg
1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg
1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc
1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc
1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg
1500

ggttccggag gcggcggctc cggcggcggc ggcagcggcg gcggcggcag ccccggatcc
1560

caggtgcagc tggtgcagtc tggtcctgag gtgaaaaagc ctggctccag cgtgaaggtg
1620

tcctgcaagg ccagcggata cacctttagc cggtccacca tgcattgggt gaggcaggct
1680

cctggacagg gcctggagtg gatcggctac atcaacccca gcagcgctta taccaactac
1740

aatcagaagt ttaaggaccg ggtgaccatc accgccgata agtccaccag caccgcctac
1800

atggagctgt ccagcctgag gagcgaggat accgccgtgt actattgcgc ccggccccag
1860

gtccattacg actacaacgg cttcccctat tggggccagg gaaccctggt gaccgtgtcc
1920

agcggaggcg gcggcagcgg cggcggcggc agcggcggag gaggcagcgg cggaggaggc
1980

tccgacattc agatgaccca gtccccctcc accctgtccg ctagcgtggg cgatcgggtg
2040

accatgacct gcagcgccag cagctccgtg tcctacatga actggtacca gcagaagccc
2100

ggcaaggctc ccaagaggtg gatttacgac tccagcaagc tggcctctgg tgtccccagc
2160

aggttctctg gtagcggcag cggcacagac tacaccctga ccatctcctc cctgcagccc
2220

gacgatttcg ccacctacta ttgccagcag tggtcccgga atccccctac ctttggcggc
2280

ggcaccaagg tggagatcaa gaggagctcc agc
2313

<210> 222
<211> 771
<212> PRT
<213> Secuencia artificial

<220>
<223> Molécula biespecífica Anti-ROR1 X anti-CD3 ROR233

<400> 222

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro

1. 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
50 55 60

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

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

Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145 150 155 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
165 170 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
180 185 190

Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
195 200 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
210 215 220

```
Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

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

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

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

435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
500 505 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
515 520 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
530 535 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545 550 555 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
565 570 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
580 585 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
595 600 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
610 615 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

```
Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
            660                 665                 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
        675                 680                 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    690                 695                 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705                 710                 715                 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                725                 730                 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            740                 745                 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        755                 760                 765

Ser Ser Ser
    770
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