

LISTADO DE SECUENCIAS

<110> Solicitante: DAIICHI SANKYO COMPANY, LIMITED;
THE UNIVERSITY OF TOKYO

<120> Título de la invención: ANTICUERPO ANTI-TLR7 HUMANO

<130> Número de referencia: FA1511-19113

<150> Número de solicitud previa: JP 2018-104676

<151> Fecha de presentación de la solicitud previa: 31-05-2018

<160> Número de secuencias: 86

<170> Software: PatentIn versión 3.5

<210> SEQ ID NO: 1

<211> Longitud: 3150

<212> Tipo: ADN

<213> Organismo: Homo sapiens

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<210> SEQ ID NO: 2
<211> Longitud: 1049
<212> Tipo: PRT
<213> Organismo: Homo sapiens

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<400> Secuencia: 2

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Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys
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Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile
          35           40           45

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Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro
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Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile
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Ser Pro Ala Ser Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe
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Arg Cys Asn Cys Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys
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Ile Lys Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr
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Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160

Phe Ser Ile Arg Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile
 165 170 175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser
 180 185 190

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

Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro
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Ser Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
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Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu
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Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro
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Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala
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Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys Leu Gln Glu Leu Asp
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Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu
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His Phe Leu Pro Ser Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu
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Leu Gln Val Tyr Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser
 355 360 365

Leu Lys Ser Leu Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu
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Leu Lys Ser Phe Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu
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Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met
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Phe Lys Gln Phe Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys
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Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu
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Ala Phe Glu Glu Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn
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Ser His Tyr Phe Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr
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Lys Asn Leu Lys Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile
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Ser Ser Ser Thr Ser Arg Thr Met Glu Ser Glu Ser Leu Arg Thr Leu
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Glu Phe Arg Gly Asn His Leu Asp Val Leu Trp Arg Glu Gly Asp Asn
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Arg Tyr Leu Gln Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp
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Ile Ser Lys Asn Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly
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Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys
 675 680 685

Ser Phe Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu
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Asp Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn
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Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile Arg
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Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg Tyr Leu
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Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr Ser Phe Pro
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Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu His His Asn Arg
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Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr
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Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser
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Val Ser Leu Phe Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe
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Trp Asp Val Trp Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly
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Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
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Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln
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Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu
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Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys
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Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro
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Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val
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<210> SEQ ID NO: 3
 <211> Longitud: 3150
 <212> Tipo: ADN
 <213> Organismo: Homo sapiens

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<210> SEQ ID NO: 4
 <211> Longitud: 1049
 <212> Tipo: PRT
 <213> Organismo: Homo sapiens

<400> Secuencia: 4

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Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys
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```

```

Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile
          35              40              45

```

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Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro
          50              55              60

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Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile
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Ser Pro Ala Ser Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe
          85              90              95

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Arg Cys Asn Cys Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys
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Ile Lys Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr
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Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
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Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
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Ser	Thr	Leu	Thr	Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile
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Val	Pro	Pro	Arg	Trp	Phe	Lys	Asn	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Asp
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Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu
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His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu
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Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser
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Leu	Lys	Ser	Leu	Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu
	370					375					380				

Leu Lys Ser Phe Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu
 385 390 395 400

Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met
 405 410 415

Phe Lys Gln Phe Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys
 420 425 430

Ile Ser Pro Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala
 435 440 445

Arg Thr Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His
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Tyr Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
 465 470 475 480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln
 485 490 495

Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp
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Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu
 515 520 525

Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu
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Ala Phe Glu Glu Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn
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Lys Asn Leu Lys Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile
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Ile Ser Lys Asn Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly
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Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys
 675 680 685

Ser Phe Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu
 690 695 700

Asp Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn
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Cys Ser Arg Ser His Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile Arg
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Ser Pro Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg Tyr Leu
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Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr Ser Phe Pro
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Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu His His Asn Arg
 770 775 780

Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His
 785 790 795 800

Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly
 805 810 815

Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr
 820 825 830

Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser
 835 840 845

Val Ser Leu Phe Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe
 850 855 860

Trp Asp Val Trp Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly
 865 870 875 880

Tyr Gln Arg Leu Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val
 885 890 895

Tyr Asp Thr Lys Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu
 900 905 910

Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu
 915 920 925

Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser
 930 935 940

Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
 945 950 955 960

Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln
 965 970 975

Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu
 980 985 990

Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys
 995 1000 1005

Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro
 1010 1015 1020

Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr Asp Asn His
 1025 1030 1035

Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val
 1040 1045

<210> SEQ ID NO: 5
 <211> Longitud: 116
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 5

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

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

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

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

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

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

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

Thr Val Ser Ser
 115

<210> SEQ ID NO: 6
 <211> Longitud: 348
 <212> Tipo: ADN
 <213> Organismo: Mus musculus

<400> Secuencia: 6

caggtgcagc tgcagcagcc tggcgccgaa ctcggtgaaac ctggcgccctc cgtgaacctg 60
 agctgcaagg ccagcggcta caccttcacc aacaactggc tgcactgggt caagcagagg 120
 cccggcagag gcctggaatg gatcggcgac atctaccca gcaacggccg gaccaactac 180
 aacgagcagt tcaagaccaa ggccaccctg accgtggaca agagcagcag caccgcctac 240
 atgcagctgt ccagcctgac cagcgaggac agcgccgtgt acttctgcgc cagagagcgg 300
 ggctacttcg actattgggg ccaggaacc gctctgaccg tcagctca 348

<210> SEQ ID NO: 7
 <211> Longitud: 122
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 7

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

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

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

Met Gly His Ile Ser Tyr Arg Gly Asn Thr Asn Tyr Asn Pro Ser Leu
 50 55 60

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

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

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

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

<210> SEQ ID NO: 8
 <211> Longitud: 366
 <212> Tipo: ADN
 <213> Organismo: Mus musculus

<400> Secuencia: 8

gacgtgcagc tgcaggaatc tggccctggc ctggtgaagc ctagccagag cctgagcctg	60
acatgcaccg tgaccggcta cagcatcacc agcgactacg cctggaactg gatccggcag	120
ttccccggca acaagctgga atggatgggc cacatcagct accggggcaa caccaactac	180
aaccccagcc tgaagtcccg gatctccatc acccgggaca ccagcaagaa ccagttcttt	240
ctgcagctga acagcgtgac caccgaggac accgccacct actactgcgc cagctggaac	300

tactacggct acgtggacta tgccatggac tactggggcc agggcacctc cgtgaccgtc 360
agctca 366

<210> SEQ ID NO: 9
<211> Longitud: 121
<212> Tipo: PRT
<213> Organismo: Mus musculus

<400> Secuencia: 9

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

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

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

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

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

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

Arg Asp Lys Gly Tyr Asp Gly Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> SEQ ID NO: 10
<211> Longitud: 363
<212> Tipo: ADN
<213> Organismo: Mus musculus

<400> Secuencia: 10

caggtgcagc tgaaagagtc tggccctgga ctggtggccc ctagccagag cctgagcatc 60

acctgtaccg tgtccggctt cagcctgacc ggctacggcg tgaactgggt gcgccagcct 120

cctggcaaag gcctggaatg gctgggcatg atctggggcg acggcagcac cgactacaac 180

```

agcgccctga agtcccggct gagcatccgg aaggacaaca gcaagtccca ggtgttcctg      240
aagatgaaca gcctgcagac cgacgacacc gcccggtact actgcgccag agacaagggc      300
tacgacggct actactacgc catggactac tggggccagg gcacctctgt gaccgtcagc      360
tca                                                                    363

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<210> SEQ ID NO: 11
 <211> Longitud: 106
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 11

```

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

```

```

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

```

```

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

```

```

His Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
          50           55           60

```

```

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

```

```

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

```

```

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

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<210> SEQ ID NO: 12
 <211> Longitud: 318
 <212> Tipo: ADN
 <213> Organismo: Mus musculus

<400> Secuencia: 12

```

gacatccaga tgaccagag ccctagcagc ctgagcacia gcctgggdcg caaagtgacc      60
atcacatgca aggccagcca ggacatcaac aagtatatcg cctggtatca gcacaaaccc      120
ggcaagggcc ccagactgct gattcactac accagcacc cgcagcccgg catccccagc      180

```

```

agattttctg gcagcgggctc cggcagagac tacagcttca gcatcagcaa cctggaaccc      240
gaggatatcg ccacctacta ctgcctgcag tacgactacc tgctgacctt cggagccggc      300
accaagctgg aactgaag                                          318

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<210> SEQ ID NO: 13
<211> Longitud: 106
<212> Tipo: PRT
<213> Organismo: Mus musculus

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<400> Secuencia: 13

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```

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

```

```

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

```

```

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

```

```

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
              50              55              60

```

```

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

```

```

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

```

```

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

```

```

<210> SEQ ID NO: 14
<211> Longitud: 318
<212> Tipo: ADN
<213> Organismo: Mus musculus

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<400> Secuencia: 14

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gacatccaga tgacccagac acccagcagc ctgagcgcca gcctggggcga tagagtgacc      60
atcagctgca gagccagcca ggacatcagc aactacctga actggtatca gcagaaaccc      120
gacggcaccg tgaagctgct gatctactac accagcagac tgacacagcg cggtgccacg      180
agattttctg gcagcgggctc cggcaccgac tacagcctga ccatcaacaa cctggaacag      240

```

gaagatatcg ctacctactt ctgtcagcaa ggcgacacct tccccacctt cggcggaggc 300
 accaagctgg aaatcaag 318

<210> SEQ ID NO: 15
 <211> Longitud: 107
 <212> Tipo: PRT
 <213> Organismo: Mus musculus
 <400> Secuencia: 15

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
 20 25 30

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

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

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

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His His Tyr Gly Ile Pro Tyr
 85 90 95

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

<210> SEQ ID NO: 16
 <211> Longitud: 321
 <212> Tipo: ADN
 <213> Organismo: Mus musculus

<400> Secuencia: 16
 gacatccaga tgacacagtc tcccgcacgc ctgagcgcct ctgtgggaga gacagtgacc 60
 atcacctgtc gggccagcga gaacatctac agctacctgg cctggtatca gcagaagcag 120
 ggcaagagcc ccagctgct ggtgtacgat gccaaagacac tggccgaggg cgtgccccagc 180
 agattttctg gcagcggctc cggcaccacag ttacgcctga agatcaacag cctgcagccc 240
 gaggacttcg gcagctacta ctgccagcac cactacggca tcccttacac cttcggcgga 300

ggcaccaagc tggaaatcaa g

321

<210> SEQ ID NO: 17
 <211> Longitud: 10
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 17

Gly Tyr Thr Phe Thr Asn Asn Trp Leu His
 1 5 10

<210> SEQ ID NO: 18
 <211> Longitud: 10
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 18

Asp Ile Tyr Pro Ser Asn Gly Arg Thr Asn
 1 5 10

<210> SEQ ID NO: 19
 <211> Longitud: 7
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 19

Glu Arg Gly Tyr Phe Asp Tyr
 1 5

<210> SEQ ID NO: 20
 <211> Longitud: 11
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 20

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

<210> SEQ ID NO: 21
 <211> Longitud: 7
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 21

Tyr Thr Ser Thr Leu Gln Pro
 1 5

<210> SEQ ID NO: 22
 <211> Longitud: 8
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 22

Leu Gln Tyr Asp Tyr Leu Leu Thr
 1 5

<210> SEQ ID NO: 23
 <211> Longitud: 11
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 23

Gly Tyr Ser Ile Thr Ser Asp Tyr Ala Trp Asn
 1 5 10

<210> SEQ ID NO: 24
 <211> Longitud: 9
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 24

His Ile Ser Tyr Arg Gly Asn Thr Asn
 1 5

<210> SEQ ID NO: 25
 <211> Longitud: 13
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 25

Trp Asn Tyr Tyr Gly Tyr Val Asp Tyr Ala Met Asp Tyr
 1 5 10

<210> SEQ ID NO: 26
 <211> Longitud: 11
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 26

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

<210> SEQ ID NO: 27
 <211> Longitud: 7
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 27

Tyr Thr Ser Arg Leu His Ser
 1 5

<210> SEQ ID NO: 28
 <211> Longitud: 8
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 28

Gln Gln Gly Asp Thr Phe Pro Thr
 1 5

<210> SEQ ID NO: 29
 <211> Longitud: 10
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 29

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

<210> SEQ ID NO: 30
 <211> Longitud: 9
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 30

Met Ile Trp Gly Asp Gly Ser Thr Asp
 1 5

<210> SEQ ID NO: 31
 <211> Longitud: 13
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 31

Asp Lys Gly Tyr Asp Gly Tyr Tyr Tyr Ala Met Asp Tyr
 1 5 10

<210> SEQ ID NO: 32

<211> Longitud: 11
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 32

Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
 1 5 10

<210> SEQ ID NO: 33
 <211> Longitud: 7
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 33

Asp Ala Lys Thr Leu Ala Glu
 1 5

<210> SEQ ID NO: 34
 <211> Longitud: 9
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 34

Gln His His Tyr Gly Ile Pro Tyr Thr
 1 5

<210> SEQ ID NO: 35
 <211> Longitud: 465
 <212> Tipo: PRT
 <213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la cadena pesada del anticuerpo anti-TLR7 humano quimérico AT01 (cAT01)

<400> Secuencia: 35

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

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

Pro Gly Ala Ser Val Asn Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Asn Trp Leu His Trp Val Lys Gln Arg Pro Gly Arg Gly Leu
 50 55 60

Glu Trp Ile Gly Asp Ile Tyr Pro Ser Asn Gly Arg Thr Asn Tyr Asn
 65 70 75 80

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

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Phe Cys Ala Arg Glu Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 115 120 125

Thr Ala Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 130 135 140

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 145 150 155 160

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 165 170 175

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 180 185 190

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 195 200 205

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 210 215 220

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
 225 230 235 240

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 275 280 285

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 290 295 300

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

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 340 345 350

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 355 360 365

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 420 425 430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 450 455 460

Lys
 465

<210> SEQ ID NO: 36

<211> Longitud: 233

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la cadena ligera del anticuerpo anti-TLR7 humano quimérico AT01 (cAT01)

<400> Secuencia: 36

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

Ile Asn Lys Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro
50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
85 90 95

Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
100 105 110

Tyr Leu Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
 210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> SEQ ID NO: 37

<211> Longitud: 471

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la cadena pesada del anticuerpo anti-TLR7 humano quimérico NB7 (cNB7)

<400> Secuencia: 37

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

Val Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30

Pro Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile
 35 40 45

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

Leu Glu Trp Met Gly His Ile Ser Tyr Arg Gly Asn Thr Asn Tyr Asn
 65 70 75 80

Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn
 85 90 95

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

Tyr Tyr Cys Ala Ser Trp Asn Tyr Tyr Gly Tyr Val Asp Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
 130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
 225 230 235 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
385					390					395					400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

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<210> SEQ ID NO: 38
<211> Longitud: 233
<212> Tipo: PRT
<213> Organismo: Secuencia Artificial
```

<220> Característica:
<223> Otra Información: Secuencia de aminoácidos de la cadena ligera del anticuerpo anti-TLR7 humano quimérico NB7 (cNB7)

<400> Secuencia: 38

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Thr Pro Ser Ser Leu Ser
20 25 30

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

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
 50 55 60

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn
 85 90 95

Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp
 100 105 110

Thr Phe Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
 115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
 165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
 180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
 210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> SEQ ID NO: 39

<211> Longitud: 470

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la cadena pesada del anticuerpo anti-TLR7 humano quimérico FAN2 (cFAN2)

<400> Secuencia: 39

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

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

Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45

Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

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

Ala Leu Lys Ser Arg Leu Ser Ile Arg Lys Asp Asn Ser Lys Ser Gln
85 90 95

Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr
100 105 110

Tyr Cys Ala Arg Asp Lys Gly Tyr Asp Gly Tyr Tyr Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
 225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

Ser Leu Ser Pro Gly Lys
 465 470

<210> SEQ ID NO: 40

<211> Longitud: 234

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la cadena ligera del anticuerpo anti-TLR7 humano quimérico FAN2 (cFAN2)

<400> Secuencia: 40

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
 20 25 30

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
 35 40 45

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

Gln Leu Leu Val Tyr Asp Ala Lys Thr Leu Ala Glu Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His His Tyr
 100 105 110

Gly Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 130 135 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> SEQ ID NO: 41

<211> Longitud: 116

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la región variable de
 cadena pesada de huAT01_H1_IgG1LALA

<400> Secuencia: 41

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

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

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

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

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

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

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

Thr Val Ser Ser
115

<210> SEQ ID NO: 42

<211> Longitud: 116

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la región variable de
cadena pesada de huAT01_H3_IgG1LALA

<400> Secuencia: 42

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

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

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

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

Gln Gly Arg Val Thr Leu Thr Val 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 Phe Cys
85 90 95

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

Thr Val Ser Ser

115

<210> SEQ ID NO: 43
 <211> Longitud: 106
 <212> Tipo: PRT
 <213> Organismo: Secuencia Artificial

 <220> Característica:
 <223> Otra Información: Secuencia de aminoácidos de la región variable de
 cadena ligera de huAT01_L1

<400> Secuencia: 43

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

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

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

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

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

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

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

<210> SEQ ID NO: 44
 <211> Longitud: 106
 <212> Tipo: PRT
 <213> Organismo: Secuencia Artificial

 <220> Característica:
 <223> Otra Información: Secuencia de aminoácidos de la región variable de
 cadena ligera de huAT01_L2

<400> Secuencia: 44

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

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

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

His Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

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

<210> SEQ ID NO: 45

<211> Longitud: 465

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huAT01_H1_IgG1LALA

<400> Secuencia: 45

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

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Asn Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Asp Ile Tyr Pro Ser Asn Gly Arg Thr Asn Tyr Ala
 65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Glu Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
130 135 140

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
145 150 155 160

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
165 170 175

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
180 185 190

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
195 200 205

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
210 215 220

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
225 230 235 240

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
275 280 285

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
290 295 300

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

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 340 345 350

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 355 360 365

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 420 425 430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 450 455 460

Lys
 465

<210> SEQ ID NO: 46

<211> Longitud: 465

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huAT01_H3_IgG1LALA

<400> Secuencia: 46

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

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Asn Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Tyr Pro Ser Asn Gly Arg Thr Asn Tyr Ala
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Phe Cys Ala Arg Glu Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
130 135 140

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
145 150 155 160

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
165 170 175

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
180 185 190

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
195 200 205

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
210 215 220

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
225 230 235 240

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
275 280 285

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
290 295 300

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

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
340 345 350

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
355 360 365

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
420 425 430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 450 455 460

Lys
 465

<210> SEQ ID NO: 47

<211> Longitud: 462

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huAT01_H3_IgG4Pro

<400> Secuencia: 47

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

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Asn Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Asp Ile Tyr Pro Ser Asn Gly Arg Thr Asn Tyr Ala
 65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Phe Cys Ala Arg Glu Arg Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
 115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 130 135 140

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
145 150 155 160

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
165 170 175

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
180 185 190

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
195 200 205

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
210 215 220

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
275 280 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 405 410 415

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
 420 425 430

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 450 455 460

<210> SEQ ID NO: 48

<211> Longitud: 233

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huAT01_L1

<400> Secuencia: 48

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

Gly Ala Tyr 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 Thr Cys Lys Ala Ser Gln Asp
 35 40 45

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

Lys Leu Leu Ile His Tyr Thr Ser Thr Leu Gln Pro Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
100 105 110

Tyr Leu Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> SEQ ID NO: 49

<211> Longitud: 233

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huAT01_L2

<400> Secuencia: 49

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr 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 Thr Cys Lys Ala Ser Gln Asp
 35 40 45

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

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

Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Thr Leu Thr Ile Ser
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
 100 105 110

Tyr Leu Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
 165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
 180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
 210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> SEQ ID NO: 50
 <211> Longitud: 122
 <212> Tipo: PRT
 <213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la región variable de cadena pesada de huNB7_H3_IgG1LALA

<400> Secuencia: 50

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

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

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

Ile Gly His Ile Ser Tyr Arg Gly Asn Thr Asn Tyr Asn Pro Ser Leu
 50 55 60

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

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

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

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

<210> SEQ ID NO: 51
 <211> Longitud: 106
 <212> Tipo: PRT
 <213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de la región variable de cadena ligera de huNB7_L3

<400> Secuencia: 51

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

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

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

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

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

<210> SEQ ID NO: 52

<211> Longitud: 471

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huNB7_H3_IgG1LALA

<400> Secuencia: 52

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

Val Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30

Pro Ser Asp Thr Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile
 35 40 45

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

Leu Glu Trp Ile Gly His Ile Ser Tyr Arg Gly Asn Thr Asn Tyr Asn
65 70 75 80

Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn
85 90 95

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Ser Trp Asn Tyr Tyr Gly Tyr Val Asp Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225 230 235 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 450 455 460

Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> SEQ ID NO: 53

<211> Longitud: 233

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huNB7_L3

<400> Secuencia: 53

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr 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 Thr Cys Arg Ala Ser Gln Asp
35 40 45

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

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp
100 105 110

Thr Phe Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
 210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> SEQ ID NO: 54

<211> Longitud: 468

<212> Tipo: PRT

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de aminoácidos de huNB7_H3_IgG4Pro

<400> Secuencia: 54

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Val Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
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Pro Ser Asp Thr Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile
 35 40 45

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

Leu Glu Trp Ile Gly His Ile Ser Tyr Arg Gly Asn Thr Asn Tyr Asn
 65 70 75 80

Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn
 85 90 95

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Ser Trp Asn Tyr Tyr Gly Tyr Val Asp Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
 145 150 155 160

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys
 210 215 220

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
 225 230 235 240

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
 245 250 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
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Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
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Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
 340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
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Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
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Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
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Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
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Ser Leu Gly Lys
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<210> SEQ ID NO: 55

<211> Longitud: 1794

<212> Tipo: ADN

<213> Organismo: Homo sapiens

<400> Secuencia: 55

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<210> SEQ ID NO: 56
 <211> Longitud: 3153
 <212> Tipo: ADN
 <213> Organismo: Mus musculus

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<210> SEQ ID NO: 57

<211> Longitud: 3153

<212> Tipo: ADN

<213> Organismo: Rattus norvegicus

<400> Secuencia: 57

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<210> SEQ ID NO: 58
<211> Longitud: 3150
<212> Tipo: ADN
<213> Organismo: Macaca mulatta

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<400> Secuencia: 58
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<210> SEQ ID NO: 59

<211> Longitud: 449

<212> Tipo: ADN

<213> Organismo: Homo sapiens

<400> Secuencia: 59

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 cctgagcagc accctgaccc tgagcaaagc cgactacgag aagcacaagg tgtacgcctg 360
 cgaggtgacc caccaggggc tgagctcccc cgtcaccaag agcttcaaca ggggggagtg 420
 ttagggggccc gtttaaacgg gggaggcta 449

<210> SEQ ID NO: 60
 <211> Longitud: 1132
 <212> Tipo: ADN
 <213> Organismo: Homo sapiens

<400> Secuencia: 60
 gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tgggtggcagc 60
 tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag 120
 ggccaagcg tcttccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 180
 ctgggctgcc tgggtcaagga ctacttcccc gaaccctga ccgtgagctg gaactcaggc 240
 gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 300
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacctc catctgcaac 360
 gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 420
 aaaactcaca catgcccacc ctgccagca cctgaactcc tgggggggacc ctcagtcttc 480
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 540
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600
 gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 660
 gtggtcagcg tcttcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720
 aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggc 780
 cagccccggg aaccacaggt gtacaccctg ccccatccc gggaggagat gaccaagaac 840
 caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatgc cgtggagtgg 900
 gagagcaatg gccagcccga gaacaactac aagaccacc ctcccgctgt ggactccgac 960
 ggctccttct tctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1020
 gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacca gaagagcctc 1080
 tccctgtctc ccggcaaagt agatatcggg ccggtttaaa cgggggaggc ta 1132

<210> SEQ ID NO: 61

<211> Longitud: 1395

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la cadena pesada del anticuerpo cAT01

<400> Secuencia: 61

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag	60
gtgcagctgc agcagcctgg cgccgaactc gtgaaacctg ggcctccgt gaacctgagc	120
tgcaaggcca gcggctacac cttcaccaac aactggctgc actgggtcaa gcagaggccc	180
ggcagaggcc tggaatggat cggcgacatc taccocagca acggccggac caactacaac	240
gagcagttca agaccaaggc caccctgacc gtggacaaga gcagcagcac cgcctacatg	300
cagctgtcca gctgaccag cgaggacagc gccgtgtact tctgcgccag agagcggggc	360
tacttcgact attggggcca gggaaccgct ctgaccgtca gctcagcctc caccaagggc	420
ccaagcgtct tccccctggc accctcctcc aagagcacct ctggcgggcac agccgccttg	480
ggctgcctgg tcaaggacta cttccccgaa cccgtgaccg tgagctggaa ctcaggcgcc	540
ctgaccagcg gcgtgcacac cttccccgct gtctctcagt cctcaggact ctactccctc	600
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	660
aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa	720
actcacacat gccacacctg ccagcacct gaactcctgg ggggaccctc agtcttcctc	780
ttccccccaa aaccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	840
gtggtggacg tgagccacga agacctgag gtcaagttca actggtacgt ggacggcgtg	900
gaggtgcata atgccaagac aaagccccgg gaggagcagt acaacagcac gtaccgggtg	960
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	1020
gtctccaaca aagccctccc agccccatc gagaaaacca tctccaaagc caaaggccag	1080
ccccgggaac cacaggtgta caccctgccc ccatccccgg aggagatgac caagaaccag	1140
gtcagcctga cctgcctggc caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1200
agcaatggcc agcccgagaa caactacaag accaccctc ccgtgctgga ctccgacggc	1260
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc	1320
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acaccagaa gagcctctcc	1380
ctgtctcccg gcaaa	1395

<210> SEQ ID NO: 62
 <211> Longitud: 749
 <212> Tipo: ADN
 <213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos del fragmento de ADN que comprende la secuencia de nucleótidos que codifica la cadena ligera del anticuerpo cAT01

<400> Secuencia: 62
 ccagcctccg gactctagag ccaccatggt gctgcagacc caggtgttca tcagcctgct 60
 gctgtggatc agcggcgccct acggcgacat ccagatgacc cagagcccta gcagcctgag 120
 cacaagcctg ggcgggcaaag tgaccatcac atgcaaggcc agccaggaca tcaacaagta 180
 tatcgctctg tatcagcaca aaccgcggcaa gggccccaga ctgctgattc actacaccag 240
 caccctgcag cccggcatcc ccagcagatt ttctggcagc ggctccggca gagactacag 300
 cttcagcatc agcaacctgg aacccgagga tatcgccacc tactactgcc tgcagtacga 360
 ctacctgctg accttcggag cgggcaccaa gctggaactg aagagagccg tggccgctcc 420
 ctccgtgttc atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt 480
 gtgcctgctg aacaacttct acccccgcga ggccaagggt cagtggaagg tggacaatgc 540
 cctgcagagc ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta 600
 cagcctgtcc tcacacctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc 660
 ctgcgaagtg acccaccagg gcctgagcag ccctgtgacc aagagcttca accggggcga 720
 gtgctgagtt taaacggggg aggctaact 749

<210> SEQ ID NO: 63
 <211> Longitud: 1413
 <212> Tipo: ADN
 <213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la cadena pesada del anticuerpo cNB7

<400> Secuencia: 63
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgac 60
 gtgcagctgc aggaatctgg ccctggcctc gtgaagccta gccagagcct gagcctgaca 120
 tgcaccgtga ccggctacag catcaccagc gactacgcct ggaactggat ccggcagttc 180

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cccggcaaca agctggaatg gatggggccac atcagctacc ggggcaacac caactacaac      240
cccagcctga agtcccggat ctccatcacc cgggacacca gcaagaacca gttctttctg      300
cagctgaaca gcgtgaccac cgaggacacc gccacctact actgcgccag ctggaactac      360
tacggctacg tggactatgc catggactac tggggccagg gcacctccgt gaccgtcagc      420
tcagcctcca ccaagggccc aagcgtcttc cccctggcac cctcctccaa gagcacctct      480
ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg      540
agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc      600
tcaggactct actcctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag      660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag      720
cccaaattctt gtgacaaaac tcacacatgc ccacctgcc cagcacctga actcctgggg      780
ggacctcag tcttctctct cccccaaaa cccaaggaca cctcatgat ctcccgacc      840
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      900
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccccggga ggagcagtac      960
aacagcacgt accgggtggt cagcgtcttc accgtctgc accaggactg gctgaatggc     1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1080
tccaaagcca aaggccagcc ccgggaacca caggtgtaca cctgcccc atcccgggag     1140
gagatgacca agaaccaggt cagcctgacc tgctggtca aaggcttcta tcccagcgac     1200
atcgccgtgg agtgggagag caatggccag ccgagaaca actacaagac caccctccc     1260
gtgctggact ccgacggctc cttcttctc tacagcaagc tcaccgtgga caagagcagg     1320
tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1380
accagaaga gcctctccct gtctcccggc aaa                                  1413

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<210> SEQ ID NO: 64

<211> Longitud: 749

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos del fragmento de ADN que comprende la secuencia de nucleótidos que codifica la cadena ligera del anticuerpo cNB7

<400> Secuencia: 64

```
ccagcctccg gactctagag ccaccatggt gctgcagacc caggtgttca tcagcctgct      60
```

```

gctgtggatc agcggcgccct acggcgacat ccagatgacc cagacacca gcagcctgag      120
cgccagcctg ggcgatagag tgaccatcag ctgcagagcc agccaggaca tcagcaacta      180
cctgaactgg tatcagcaga aacccgacgg caccgtgaag ctgctgatct actacaccag      240
cagactgcac agcggcggtgc ccagcagatt ttctggcagc ggctccggca ccgactacag      300
cctgaccatc aacaacctgg aacaggaaga tatcgctacc tactttctgtc agcaaggcga      360
caccttcccc accttcggcg gaggcaccaa gctggaaatc aagagagccg tggccgctcc      420
ctccgtgttc atcttccac ctagcgacga gcagctgaag tctggcacag ccagcgtcgt      480
gtgcctgctg aacaacttct acccccgcga ggccaagggt cagtgggaagg tggacaatgc      540
cctgcagagc ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta      600
ctccctgagc agcacccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc      660
ctgcgaagtg acccaccagg gcctgtctag ccccgtagcc aagagcttca accggggcgga      720
gtgttgagtt taaacggggg aggctaact      749

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<210> SEQ ID NO: 65

<211> Longitud: 1410

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la cadena pesada del anticuerpo cFAN2

<400> Secuencia: 65

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atgaaacacc tgtgtgttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag      60
gtgcagctga aagagtctgg ccctggactg gtggccccta gccagagcct gagcatcacc      120
tgtaccgtgt ccggcttcag cctgaccggc tacggcgtga actgggtgcg ccagcctcct      180
ggcaaaggcc tggaatggct gggcatgata tggggcgacg gcagcaccga ctacaacagc      240
gccctgaagt cccggctgag catccggaag gacaacagca agtcccagggt gttcctgaag      300
atgaacagcc tgcagaccga cgacaccgcc cgggtactact gcgccagaga caagggctac      360
gacggctact actacgccat ggactactgg ggccagggca cctctgtgac cgtcagctca      420
gcctccacca agggcccaag cgtcttcccc ctggcaccct cctccaagag cacctctggc      480
ggcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gaccgtgagc      540
tggaactcag gcgcctgac cagcggcggtg cacaccttcc ccgtgtcct gcagtcctca      600
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      660

```

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc	720
aaatcttgtg acaaaactca cacatgccc cctgcccag cacctgaact cctgggggga	780
ccctcagtct tctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	840
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cccgggagga gcagtacaac	960
agcacgtacc ggggtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	1020
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1080
aaagccaaag gccagccccg ggaaccacag gtgtacaccc tgccccatc ccgggaggag	1140
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc	1200
gccgtggagt gggagagcaa tggccagccc gagaacaact acaagaccac ccctcccgtg	1260
ctggactccg acggctcctt ctctctctac agcaagctca ccgtggacaa gagcaggtgg	1320
cagcagggca acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacc	1380
cagaagagcc tctccctgtc tcccggcaaa	1410

<210> SEQ ID NO: 66

<211> Longitud: 752

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos del fragmento de ADN que comprende la secuencia de nucleótidos que codifica la cadena ligera del anticuerpo cFAN2

<400> Secuencia: 66

ccagcctccg gactctagag ccaccatggt gctgcagacc caggtgttca tcagcctgct	60
gctgtggatc agcggcgccct acggcgacat ccagatgaca cagtctcccg ccagcctgag	120
cgcctctgtg ggagagacag tgaccatcac ctgtcggggc agcgagaaca tctacagcta	180
cctggcctgg tatcagcaga agcagggcaa gagccccag ctgctggtgt acgatgcaa	240
gacactggcc gagggcgtgc ccagcagatt ttctggcagc ggctccggca ccagttcag	300
cctgaagatc aacagcctgc agcccgagga ctccggcagc tactactgcc agcaccacta	360
cggcatccct tacaccttcg gcggaggcac caagctggaa atcaagagag ccgtggccgc	420
tccctccgtg ttcatcttcc cacctagcga cgagcagctg aagtccggca cagctagcgt	480
cgtgtgcttg ctgaacaact tctacccccg cgaggccaag gtgcagtgga aggtggacaa	540

tgccctgcag agcgggaaca gccaggaaag cgtgaccgag caggacagca aggactccac	600
ctacagcctg tccagcacc tgaccctgag caaggccgac tacgagaagc acaaggtgta	660
cgcctgcgaa gtgaccacc agggcctgag cagcccagtg accaagagct tcaaccgggg	720
cgagtgtga gtttaaacgg gggaggctaa ct	752

<210> SEQ ID NO: 67
 <211> Longitud: 1395
 <212> Tipo: ADN
 <213> Organismo: Secuencia Artificial

<220> Característica:
 <223> Otra Información: Secuencia de nucleótidos que codifica
 huAT01_H1_IgG1LALA

<400> Secuencia: 67	
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag	60
gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc	120
tgcaaggcca gcggctacac ctttaccac aactggctgc actgggtgcg ccaggctcca	180
ggacagggac tggaatggat gggcgacatc taccocagca acggccggac caactacgcc	240
cagaaattcc agggcagagt gaccatcacc gccgacaaga gcaccagcac cgcctacatg	300
gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag agagcggggc	360
tacttcgact attggggcca gggcacactc gtgaccgtca gctcagcctc caccaagggc	420
ccaagcgtct tccccctggc accctcctcc aagagcacct ctggcgggcac agccgccctg	480
ggctgcctgg tcaaggacta cttccccgaa cccgtgaccg tgagctggaa ctcaggcgcc	540
ctgaccagcg gcgtgcacac cttccccgct gtctcgcagt cctcaggact ctactccctc	600
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	660
aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaata ttgtgacaaa	720
actcacacat gccacccctg ccagcacct gaagccgcgg ggggaccctc agtcttctc	780
ttccccccaa aaccacagga caccctcatg atctcccga cccctgaggt cacatgcgtg	840
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	900
gaggtgcata atgccaagac aaagccccgg gagggagcagt acaacagcac gtaccgggtg	960
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	1020
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag	1080

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ccccgggaac cacaggtgta caccctgccc ccatccccggg aggagatgac caagaaccag      1140
gtcagcctga cctgcctggg caaaggcttc tatcccagcg acatcgccgt ggagtgggag      1200
agcaatggcc agcccagaaa caactacaag accacccttc ccgtgctgga ctccgacggc      1260
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca gggcaacgtc      1320
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acaccagaa gagcctctcc      1380
ctgtctcccg gcaaa                                         1395

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<210> SEQ ID NO: 68

<211> Longitud: 1395

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica
huAT01_H3_IgG1LALA

<400> Secuencia: 68

```

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag      60
gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag ggcgcagcgt gaaggtgtcc      120
tgcaaggcca gcggctacac ctttaccac aactggctgc actgggtgcg ccaggctcca      180
ggacagggac tggaatggat gggcgacatc taccacagca acggccggac caactacgcc      240
cagaaattcc agggcagagt gaccctgacc gtggacaaga gcaccagcac cgcctacatg      300
gaactgagca gcctgcggag cgaggatacc gccgtgtact tctgtgccag agagcggggc      360
tacttcgact actggggcca gggaaacactc gtgaccgtca gctcagcctc caccaagggc      420
ccaagcgtct tccccctggc accctcctcc aagagcacct ctggcgggcac agccgccctg      480
ggctgcctgg tcaaggacta cttccccgaa cccgtgaccg tgagctggaa ctcaggcgcc      540
ctgaccagcg gcgtgcacac cttccccgct gtccctgcagt cctcaggact ctactccctc      600
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg      660
aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa      720
actcacacat gccaccctg cccagcacct gaagccgcgg ggggaccctc agtcttcctc      780
ttccccccaa aaccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg      840
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcggtg      900
gagggtgcata atgccaaagc aaagccccgg gaggagcagt acaacagcac gtaccgggtg      960
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag      1020

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gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaaggccag      1080
ccccgggaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag      1140
gtcagcctga cctgcctggg caaaggcttc tatcccagcg acatcgccgt ggagtgggag      1200
agcaatggcc agcccagaaa caactacaag accacccttc ccgtgctgga ctccgacggc      1260
tcctttcttc tctacagcaa gctcacctg gacaagagca ggtggcagca gggcaacgtc      1320
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acaccagaa gagcctctcc      1380
ctgtctcccg gcaaa                                         1395

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<210> SEQ ID NO: 69

<211> Longitud: 1386

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica
huAT01_H3_IgG4Pro

<400> Secuencia: 69

```

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag      60
gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag gcgccagcgt gaaggtgtcc      120
tgcaaggcca gcggctacac ctttaccac aactggctgc actgggtgcg ccaggctcca      180
ggacagggac tggaatggat gggcgacatc taccacagca acggccggac caactacgcc      240
cagaaattcc agggcagagt gaccctgacc gtggacaaga gcaccagcac cgcctacatg      300
gaactgagca gctgcgagg cgaggatacc gccgtgtact tctgtgccag agagcggggc      360
tacttcgact actggggcca gggaacactc gtgaccgtca gctcagcctc caccaagggc      420
cctagcgtgt tccctctggc cccttgtagc agaagcacca gcgagtctac agccgccctg      480
ggctgcctcg tgaaggacta ctttcccgag cccgtgaccg tgtcctggaa ctctggcgct      540
ctgacaagcg gcgtgcacac ctttccagcc gtgctgcaga gcagcggcct gtactctctg      600
tccagcgtcg tgactgtgcc cagcagctct ctgggcacca agacctacac ctgtaacgtg      660
gaccacaagc ccagcaacac caaggtggac aagcgggtgg aatctaagta cggccctccc      720
tgccctcctt gccagcccc tgaatttctg ggcggaacct ccgtgttcct gttcccccca      780
aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt ggtggtggat      840
gtgtcccagg aagatcccg ggtgcagttc aattgggtac tggacggcgt ggaagtgcac      900

```

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aacgccaaaga ccaagcctag agaggaacag ttcaacagca cctaccgggt ggtgtccgtg      960
ctgacagtgc tgcaccagga ctggctgaac ggcaaagagt acaagtgcaa ggtgtccaac      1020
aagggcctgc ccagctccat cgagaaaacc atcagcaagg ccaagggcca gccccgcgaa      1080
ccccaggtgt acacactgcc tccaagccag gaagagatga ccaagaatca ggtgtccctg      1140
acctgtctcg tgaaaggctt ctaccctcc gatatcgccg tggaatggga gagcaacggc      1200
cagccccgaga acaactacaa gaccaccccc cctgtgctgg actccgatgg ctattcttc      1260
ctgtacagca gactgaccgt ggacaagagc cgggtggcagg aaggcaacgt gttcagctgc      1320
tccgtgatgc acgaggccct gcacaaccac tacaccaga agtcctgtc tctgagcctg      1380
ggcaaa                                           1386

```

<210> SEQ ID NO: 70

<211> Longitud: 699

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica huAT01_L1

<400> Secuencia: 70

```

atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc      60
gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtgggcca cagagtgacc      120
atcacatgca aggccagcca ggacatcaac aagtatatcg cctggatatca gcagaagccc      180
ggcaaggccc ccaagctgct gatccactac accagcacac tgcagcctgg cgtgcccagc      240
agattttccg gctctggcag cggcagagac ttcacctga ccatcagcag cctgcagccc      300
gaggacttcg ccacctacta ctgcctgcag tacgactacc tgctgacctt cggccagggc      360
accaaggtgg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccctcc      420
gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc      480
agagaggcca aggtgcagtg gaaggtggac aacgcctgc agtcgggaa ctcccaggag      540
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg      600
agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg      660
agctcccccg tcaccaagag cttcaacagg ggggagtg      699

```

<210> SEQ ID NO: 71

<211> Longitud: 699

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica huAT01_L2

<400> Secuencia: 71

```

atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc      60
gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtgggcca cagagtgacc      120
atcacatgca aggccagcca ggacatcaac aagtatatcg cctggtatca gcagaagccc      180
ggcaaggccc ccaagctgct gatccactac accagcacac tgcagcccgg catccccagc      240
agattttccg gctctggcag cggcagagac tacacctga ccatcagcag cctgcagcca      300
gaggacttgc ccacctacta ctgcctgcag tacgactacc tgctgacctt cggccagggc      360
accaaggtgg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccctcc      420
gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc      480
agagaggcca aggtgcagtg gaaggtggac aacgccttgc agtccgggaa ctcccaggag      540
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg      600
agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg      660
agctcccccg tcaccaagag cttcaacagg ggggagtgt      699

```

<210> SEQ ID NO: 72

<211> Longitud: 1413

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica huNB7_H3_IgG1LALA

<400> Secuencia: 72

```

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgac      60
gtgcagctgc aggaatctgg ccctggcctc gtgaagccca gcgataccct gagcctgacc      120
tgtaccgtga ccggctacag catcaccagc gactacgcct ggaactggat cagacagccc      180
cctggcaaca agctggaatg gatcggccac atcagctacc ggggcaacac caactacaac      240
cccagcctga agtccagagt gaccatcagc cgggacacca gcaagaacca gttctccctg      300
aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag ctggaactac      360
tacggctacg tggactatgc catggactac tggggccagg gcaccacagt gaccgtcagc      420
tcagcctcca ccaagggccc aagcgtcttc ccctggcac cctcctccaa gagcacctct      480

```

```

ggcggcacag cgcacctggg ctgcctgggc aaggactact tccccgaacc cgtgaccgtg      540
agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc      600
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag      660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag      720
cccaaattct gtgacaaaac tcacacatgc ccacctgcc cagcacctga agccgcgggg      780
ggacctcag tcttctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc      840
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgagggt caagttcaac      900
tggtacgtgg acggcgtgga ggtgcataat gccaaagaaa agccccggga ggagcagtac      960
aacagcacgt accgggtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc     1020
aaggagtaca agtgcaagggt ctccaacaaa gccctccag ccccatcga gaaaaccatc     1080
tcaaagcca aaggccagcc cggggaacca caggtgtaca ccctgcccc atcccgggag     1140
gagatgacca agaaccagggt cagcctgacc tgcttggtca aaggcttcta tcccagcgac     1200
atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac caccctccc     1260
gtgctggact ccgacggctc cttcttctc tacagcaagc tcaccgtgga caagagcagg     1320
tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1380
accagaaga gcctctccct gtctcccgcc aaa                                  1413

```

<210> SEQ ID NO: 73

<211> Longitud: 1404

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica
huNB7_H3_IgG4Pro

<400> Secuencia: 73

```

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgac      60
gtgcagctgc aggaatctgg cctggcctc gtgaagccca gcgataccct gagcctgacc     120
tgtaccgtga ccggctacag catcaccagc gactacgcct ggaactggat cagacagccc     180
cctggcaaca agctggaatg gatcggccac atcagctacc ggggcaacac caactacaac     240
cccagcctga agtccagagt gaccatcagc cgggacacca gcaagaacca gttctccctg     300
aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag ctggaactac     360

```

tacggctacg tggactatgc catggactac tggggccagg gcaccacagt gaccgtcagc	420
tcagcctcca ccaagggccc tagcgtgttc cctctggccc cttgttagcag aagcaccagc	480
gagtctacag ccgccctggg ctgcctcgtg aaggactact ttcccagagc cgtgaccgtg	540
tcctggaact ctggcgctct gacaagcggc gtgcacacct ttccagccgt gctgcagagc	600
agcggcctgt actctctgtc cagcgtcgtg actgtgccc gcagctctct gggcaccaag	660
acctacacct gtaacgtgga ccacaagccc agcaacacca aggtggacaa gcgggtggaa	720
tctaagtacg gccctccctg ccctccttgc ccagcccctg aatttctggg cggaccctcc	780
gtgttcctgt tcccccaaa gcccaaggac accctgatga tcagccggac cccgaagtg	840
acctgcgtgg tgggtgatgt gtcccaggaa gatcccgagg tgcagttcaa ttggtacgtg	900
gacggcgtgg aagtgcacaa cgccaagacc aagcctagag aggaacagtt caacagcacc	960
taccgggtgg tgtccgtgct gacagtgtg caccaggact ggctgaacgg caaagagtac	1020
aagtgcagg tgtccaacaa gggcctgccc agctccatcg agaaaaccat cagcaaggcc	1080
aagggccagc cccgcgaacc ccaggtgtac aactgcctc caagccagga agagatgacc	1140
aagaatcagg tgtccctgac ctgtctcgtg aaaggcttct acccctccga tatcgccgtg	1200
gaatgggaga gcaacggcca gcccgagaac aactacaaga ccaccccccc tgtgctggac	1260
tccgatggct cattcttcct gtacagcaga ctgaccgtgg acaagagccg gtggcaggaa	1320
ggcaacgtgt tcagctgctc cgtgatgcac gaggccctgc acaaccacta caccagaag	1380
tccctgtctc tgagcctggg caaa	1404

<210> SEQ ID NO: 74

<211> Longitud: 699

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica huNB7_L3

<400> Secuencia: 74

atggtgctgc agaccaggt gttcatctcc ctgctgctgt ggatctccgg cgcgtacggc	60
gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtgggcca cagagtgacc	120
atcacctgta gagccagcca ggacatcagc aactacctga actggtatca gcagaaacct	180
ggcaaggccg tgaagctgct gatctactac accagcagac tgacacagcg cgtgccagc	240
agattttctg gcagcggctc cggcaccgac tacacctga caatcagcag cctgcagccc	300

gaggacttcg ctacctactt ctgtcagcaa ggcgacacct tccccacctt cggccagggc 360
 accaaggtgg aaatcaagcg tacggtggcc gccccctccg tgttcattctt cccccctcc 420
 gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480
 agagaggcca aggtgcagtg gaaggtggac aacgcctgc agtccgggaa ctcccaggag 540
 agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600
 agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660
 agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> SEQ ID NO: 75
 <211> Longitud: 1137
 <212> Tipo: ADN
 <213> Organismo: Homo sapiens

<400> Secuencia: 75
 ccagcctccg gactctagag ccaccatgaa acacctgtgg ttcttctctc tgctgggtggc 60
 agtccccaga tgggtgctga gccaggtgca attgtgcagg cggttagctc agcctccacc 120
 aagggcccaa gcgtcttccc cctggcaccc tctccaaga gcacctctgg cggcacagcc 180
 gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgaccgtgag ctggaactca 240
 ggcgccctga ccagcggcgt gcacaccttc cccgctgtcc tgcagtcctc aggactctac 300
 tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 360
 aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt 420
 gacaaaactc acacatgccc accctgccc gacactgaag ccgcgggggg accctcagtc 480
 ttctcttctc cccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 540
 tgctgtgggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 600
 ggctgtggagg tgcataatgc caagacaaag ccccgaggagg agcagtacaa cagcacgtac 660
 cgggtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 720
 tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 780
 ggccagcccc gggaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag 840
 aaccaggtca gcctgacctg cctgggtcaa ggcttctatc ccagcgacat cgccgtggag 900
 tgggagagca atggccagcc cgagaacaac tacaagacca cccctcccggt gctggactcc 960
 gacggctcct tcttctctta cagcaagctc accgtggaca agagcaggtg gcagcagggc 1020
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac ccagaagagc 1080

ctctccctgt ctcccggcaa atgagatatc gggcccgttt aaacggggga ggctaac 1137

<210> SEQ ID NO: 76
 <211> Longitud: 1117
 <212> Tipo: ADN
 <213> Organismo: Homo sapiens

<400> Secuencia: 76
 ccagcctccg gactctagag ccaccatgaa acacctgtgg ttcttctctc tgctgggtggc 60
 agctcccaga tgggtgctga gccagggtgca attgtgcagg cggtttagctc agcctccacc 120
 aaggggcccta gcgtgttccc tctggcccct tgtagcagaa gcaccagcga gtctacagcc 180
 gccctgggct gcctcgtgaa ggactacttt cccgagcccg tgaccgtgtc ctggaactct 240
 ggcgtctctga caagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac 300
 tctctgtcca gcgtcgtgac tgtgcccagc agctctctgg gcaccaagac ctacacctgt 360
 aacgtggacc acaagcccag caacaccaag gtggacaagc ggggtggaatc taagtacggc 420
 cctccctgcc ctccctgccc agcccctgaa tttctgggcg gaccctccgt gttcctgttc 480
 ccccaaagc ccaaggacac cctgatgac agccggaccc ccgaagtgac ctgcgtgggtg 540
 gtggatgtgt cccaggaaga tcccagagtg cagttcaatt ggtacgtgga cggcgtggaa 600
 gtgcacaacg ccaagaccaa gcctagagag gaacagttca acagcaccta ccgggtgggtg 660
 tccgtgctga cagtgtctga ccaggactgg ctgaacggca aagagtacaa gtgcaagggtg 720
 tccaacaagg gcctgcccag ctccatcgag aaaaccatca gcaaggccaa gggccagccc 780
 cgcgaacccc aggtgtacac actgcctcca agccaggaag agatgaccaa gaatcagggtg 840
 tccctgacct gtctcgtgaa aggtttctac cctccgata tcgccgtgga atgggagagc 900
 aacggccagc ccgagaacaa ctacaagacc accccccctg tgctggactc cgatgggtca 960
 ttcttctgt acagcagact gaccgtggac aagagccggt ggcaggaagg caacgtgttc 1020
 agctgctccg tgatgcacga ggccctgcac aaccactaca ccagaagtc cctgtctctg 1080
 agcctgggca aatgagttta aacgggggag gctaact 1117

<210> SEQ ID NO: 77
 <211> Longitud: 348
 <212> Tipo: ADN
 <213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la región variable de cadena pesada de huAT01_H1

<400> Secuencia: 77

```
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggtg      60
tcttgcaagg ccagcgggcta cacctttacc aacaactggc tgcactgggt gcgccagggt      120
ccaggacagg gactggaatg gatgggcgac atctaccca gcaacggccg gaccaactac      180
gccagaaat tccagggcag agtgaccatc accgccgaca agagcaccag caccgcctac      240
atggaactga gcagcctgcg gagcgaggac accgccgtgt actactgcmc cagagagcgg      300
ggctacttcg actattgggg ccagggcaca ctcgtagccg tcagctca      348
```

<210> SEQ ID NO: 78

<211> Longitud: 348

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la región variable de cadena pesada de huAT01_H3

<400> Secuencia: 78

```
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggtg      60
tcttgcaagg ccagcgggcta cacctttacc aacaactggc tgcactgggt gcgccagggt      120
ccaggacagg gactggaatg gatgggcgac atctaccca gcaacggccg gaccaactac      180
gccagaaat tccagggcag agtgaccctg accgtggaca agagcaccag caccgcctac      240
atggaactga gcagcctgcg gagcgaggat accgccgtgt acttctgtgc cagagagcgg      300
ggctacttcg actactgggg ccaggggaaca ctcgtagccg tcagctca      348
```

<210> SEQ ID NO: 79

<211> Longitud: 318

<212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la región variable de cadena ligera de huAT01_L1

<400> Secuencia: 79

```
gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtgggcca cagagtgacc      60
atcacatgca aggccagcca ggacatcaac aagtatatcg cctggatatca gcagaagccc      120
ggcaaggccc ccaagctgct gatccactac accagcacac tgcagcctgg cgtgccccagc      180
```

```

agattttccg gctctggcag cggcagagac ttcacctga ccatcagcag cctgcagccc      240
gaggacttcg ccacctacta ctgcctgcag tacgactacc tgctgacctt cggccagggc      300
accaaggtgg aaatcaag                                                    318

```

```

<210> SEQ ID NO: 80
<211> Longitud: 318
<212> Tipo: ADN
<213> Organismo: Secuencia Artificial

```

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la región variable de cadena ligera de huAT01_L2

```

<400> Secuencia: 80
gacatccaga tgaccagag ccctagcagc ctgagcgcca gcgtggggcga cagagtgacc      60
atcacatgca aggccagcca ggacatcaac aagtatatcg cctggtatca gcagaagccc      120
ggcaaggccc ccaagctgct gatccactac accagcacac tgcagcccgg catccccagc      180
agattttccg gctctggcag cggcagagac tacacctga ccatcagcag cctgcagcca      240
gaggacttcg ccacctacta ctgcctgcag tacgactacc tgctgacctt cggccagggc      300
accaaggtgg aaatcaag                                                    318

```

```

<210> SEQ ID NO: 81
<211> Longitud: 366
<212> Tipo: ADN
<213> Organismo: Secuencia Artificial

```

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la región variable de cadena pesada de huNB7_H3

```

<400> Secuencia: 81
gacgtgcagc tgcaggaatc tggccctggc ctgctgaagc ccagcgatac cctgagcctg      60
acctgtaccg tgaccggcta cagcatcacc agcgactacg cctggaactg gatcagacag      120
ccccctggca acaagctgga atggatcggc cacatcagct accggggcaa caccaactac      180
aaccacagcc tgaagtccag agtgaccatc agccggggaca ccagcaagaa ccagttctcc      240
ctgaagctga gcagcgtgac agccgccgat accgccgtgt actactgcg cagctggaac      300
tactacggct acgtggacta tgccatggac tactgggggc agggcaccac agtgaccgtc      360
agctca                                                                    366

```

```

<210> SEQ ID NO: 82

```

<211> Longitud: 318
 <212> Tipo: ADN
 <213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos que codifica la región variable de cadena ligera de huNB7_L3

<400> Secuencia: 82
 gacatccaga tgacccagag ccctagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
 atcacctgta gagccagcca ggacatcagc aactacctga actggtatca gcagaaaccc 120
 ggcaaggccg tgaagctgct gatctactac accagcagac tgcacagcgg cgtgcccagc 180
 agattttctg gcagcggctc cggcaccgac tacaccctga caatcagcag cctgcagccc 240
 gaggacttcg ctacctactt ctgtcagcaa ggcgacacct tccccacctt cggccagggc 300
 accaaggtgg aaatcaag 318

<210> SEQ ID NO: 83
 <211> Longitud: 1050
 <212> Tipo: PRT
 <213> Organismo: Mus musculus

<400> Secuencia: 83

Met Val Phe Ser Met Trp Thr Arg Lys Arg Gln Ile Leu Ile Phe Leu
 1 5 10 15

Asn Met Leu Leu Val Ser Arg Val Phe Gly Phe Arg Trp Phe Pro Lys
 20 25 30

Thr Leu Pro Cys Glu Val Lys Val Asn Ile Pro Glu Ala His Val Ile
 35 40 45

Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Glu Gly Ile Pro
 50 55 60

Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Ser Ile
 65 70 75 80

Ser Pro Asp Ser Phe Arg Arg Leu Asn His Leu Glu Glu Ile Asp Leu
 85 90 95

Arg Cys Asn Cys Val Pro Val Leu Leu Gly Ser Lys Ala Asn Val Cys
 100 105 110

Thr Lys Arg Leu Gln Ile Arg Pro Gly Ser Phe Ser Gly Leu Ser Asp
 115 120 125

Leu Lys Ala Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140

Asp Leu Pro Ser Ser Leu His Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160

Phe Ser Ile Thr Lys Glu Asn Leu Thr Glu Leu Val Asn Ile Glu Thr
 165 170 175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Asn Val Ser
 180 185 190

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

Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu Pro
 210 215 220

Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys Ile
 225 230 235 240

Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Val Leu Asp Leu
 245 250 255

Ser Gly Asn Cys Pro Arg Cys Tyr Asn Val Pro Tyr Pro Cys Thr Pro
 260 265 270

Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn Ser
 275 280 285

Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300

Val Pro Pro Thr Trp Phe Lys Asn Met Arg Asn Leu Gln Glu Leu Asp
 305 310 315 320

Leu Ser Gln Asn Tyr Leu Ala Arg Glu Ile Glu Glu Ala Lys Phe Leu
 325 330 335

His Phe Leu Pro Asn Leu Val Glu Leu Asp Phe Ser Phe Asn Tyr Glu
 340 345 350

Leu Gln Val Tyr His Ala Ser Ile Thr Leu Pro His Ser Leu Ser Ser
 355 360 365

Leu Glu Asn Leu Lys Ile Leu Arg Val Lys Gly Tyr Val Phe Lys Glu
 370 375 380

Leu Lys Asn Ser Ser Leu Ser Val Leu His Lys Leu Pro Arg Leu Glu
 385 390 395 400

Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asp Leu Asn Ile
 405 410 415

Phe Lys His Phe Glu Asn Leu Lys Leu Ile Asp Leu Ser Val Asn Lys
 420 425 430

Ile Ser Pro Ser Glu Glu Ser Arg Glu Val Gly Phe Cys Pro Asn Ala
 435 440 445

Gln Thr Ser Val Asp Arg His Gly Pro Gln Val Leu Glu Ala Leu His
 450 455 460

Tyr Phe Arg Tyr Asp Glu Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
 465 470 475 480

Glu Pro Pro Ser Phe Leu Pro Leu Asn Ala Asp Cys His Ile Tyr Gly
 485 490 495

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

Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn
 515 520 525

Thr Ile Gly Gln Thr Leu Asn Gly Ser Glu Leu Trp Pro Leu Arg Glu
 530 535 540

Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp Leu Leu Tyr Ser
 545 550 555 560

Thr Ala Phe Glu Glu Leu Gln Ser Leu Glu Val Leu Asp Leu Ser Ser
 565 570 575

Asn Ser His Tyr Phe Gln Ala Glu Gly Ile Thr His Met Leu Asn Phe
 580 585 590

Thr Lys Lys Leu Arg Leu Leu Asp Lys Leu Met Met Asn Asp Asn Asp
 595 600 605

Ile Ser Thr Ser Ala Ser Arg Thr Met Glu Ser Asp Ser Leu Arg Ile
 610 615 620

Leu Glu Phe Arg Gly Asn His Leu Asp Val Leu Trp Arg Ala Gly Asp
 625 630 635 640

Asn Arg Tyr Leu Asp Phe Phe Lys Asn Leu Phe Asn Leu Glu Val Leu
 645 650 655

Asp Ile Ser Arg Asn Ser Leu Asn Ser Leu Pro Pro Glu Val Phe Glu
 660 665 670

Gly Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu
 675 680 685

Lys Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile
 690 695 700

Leu Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala
 705 710 715 720

Asn Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile
 725 730 735

Arg Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr
 740 745 750

Leu Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe
 755 760 765

Pro Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn
 770 775 780

Arg Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn
785 790 795 800

His Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val
805 810 815

Gly Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr
820 825 830

Thr Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile
835 840 845

Ser Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe
850 855 860

Phe Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys
865 870 875 880

Gly Tyr Gln His Leu Gln Ser Met Glu Ser Cys Tyr Asp Ala Phe Ile
885 890 895

Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu
900 905 910

Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys
915 920 925

Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu
930 935 940

Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln
945 950 955 960

Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His
965 970 975

Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu
980 985 990

Glu Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu
995 1000 1005

Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His
 1010 1015 1020

Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn
 1025 1030 1035

His Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val
 1040 1045 1050

<210> SEQ ID NO: 84

<211> Longitud: 1050

<212> Tipo: PRT

<213> Organismo: Rattus norvegicus

<400> Secuencia: 84

Met Val Phe Pro Met Trp Thr Leu Lys Arg Gln Ser Phe Ile Phe Leu
 1 5 10 15

Asn Met Ile Leu Val Ser Arg Val Leu Gly Phe Arg Trp Tyr Pro Lys
 20 25 30

Thr Leu Pro Cys Asp Val Ser Leu Asp Ser Thr Asn Thr His Val Ile
 35 40 45

Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Glu Gly Ile Pro
 50 55 60

Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Ser Ile
 65 70 75 80

Ser Pro Asp Ser Phe His Arg Leu Lys His Leu Glu Glu Leu Asp Leu
 85 90 95

Arg Cys Asn Cys Val Pro Ile Leu Leu Gly Ser Lys Ala Asn Val Cys
 100 105 110

Thr Lys Arg Leu Gln Ile Arg Pro Gly Ser Phe Ser Gly Leu Ser Asp
 115 120 125

Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140

Asp Leu Pro Ser Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160

Phe Ser Ile Thr Lys Glu Asn Leu Ser Glu Leu Val Asn Ile Glu Ser
 165 170 175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Asn Val Ser
 180 185 190

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

Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Ile Leu Pro
 210 215 220

Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Arg Ile
 225 230 235 240

Gln Glu His Asp Phe Asn Lys Leu Ser Gln Leu Gln Val Leu Asp Leu
 245 250 255

Ser Gly Asn Cys Pro Arg Cys Tyr Asn Val Pro Tyr Pro Cys Thr Pro
 260 265 270

Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asp Ser
 275 280 285

Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300

Val Pro Ala Glu Trp Phe Lys Asn Met Ser Asn Leu Gln Glu Leu Asp
 305 310 315 320

Leu Ser Gln Asn Tyr Leu Ala Arg Glu Ile Glu Glu Ala Lys Phe Leu
 325 330 335

Asn Ser Leu Pro Asn Leu Val Gln Leu Asp Leu Ser Phe Asn Tyr Glu
 340 345 350

Leu Gln Val Tyr His Ala Ser Ile Thr Leu Pro His Ser Leu Ser Ser
 355 360 365

Leu Thr Lys Leu Lys Asn Leu Tyr Ile Lys Gly Tyr Val Phe Lys Glu
 370 375 380

Leu Lys Asp Ser Ser Leu Ser Val Leu His Asn Leu Ser Asn Leu Glu
 385 390 395 400

Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asp Leu Asn Ile
 405 410 415

Phe Gln Gln Phe Glu Asn Leu Lys Phe Ile Asp Leu Ser Val Asn Lys
 420 425 430

Ile Ser Pro Ser Glu Glu Ser Arg Glu Val Gly Leu Cys Pro Asn Ala
 435 440 445

Gln Thr Ser Val Asp Trp His Gly Pro Gln Val Leu Glu Ala Leu His
 450 455 460

Tyr Phe Arg Tyr Asp Glu Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
 465 470 475 480

Glu Pro Pro Thr Phe Leu Pro Leu Asn Ala Asp Cys His Thr Tyr Gly
 485 490 495

Lys Thr Leu Asp Leu Ser Arg Asn Asn Ile Phe Phe Ile Lys Pro Ser
 500 505 510

Asp Phe Lys His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn
 515 520 525

Ala Ile Gly Gln Thr Leu Asn Gly Ser Glu Leu Gln Pro Leu Arg Glu
 530 535 540

Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp Leu Leu Tyr Ser
 545 550 555 560

Thr Ala Phe Glu Glu Leu Gln Asn Leu Glu Ile Leu Asp Leu Ser Ser
 565 570 575

Asn Ser His Tyr Phe Gln Ala Glu Gly Ile Thr His Met Leu Asn Phe
 580 585 590

Thr	Lys	Lys	Leu	Arg	His	Leu	Glu	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp		
		595					600					605					
Ile	Ser	Thr	Ser	Ala	Ser	Arg	Thr	Met	Glu	Ser	Glu	Ser	Leu	Arg	Val		
	610					615					620						
Leu	Glu	Phe	Arg	Gly	Asn	His	Leu	Asp	Val	Leu	Trp	Arg	Asp	Gly	Asp		
625					630					635					640		
Asn	Arg	Tyr	Leu	Asp	Phe	Phe	Lys	Asn	Leu	Leu	Asn	Leu	Glu	Glu	Leu		
				645					650					655			
Asp	Ile	Ser	Arg	Asn	Ser	Leu	Asn	Ser	Val	Pro	Pro	Gly	Val	Phe	Glu		
			660					665					670				
Gly	Met	Pro	Pro	Asn	Leu	Thr	Thr	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu		
	675						680					685					
Arg	Ser	Phe	Ser	Trp	Gly	Arg	Leu	Gln	Leu	Leu	Lys	His	Leu	Lys	Asn		
	690					695					700						
Leu	Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Ala	Arg	Leu	Ala		
705					710					715					720		
Asn	Cys	Ser	Lys	Ser	Leu	Thr	Lys	Leu	Ile	Leu	Asn	His	Asn	Gln	Ile		
				725					730					735			
Arg	Gln	Leu	Thr	Lys	Tyr	Phe	Leu	Glu	Asp	Ala	Leu	Gln	Leu	Arg	Tyr		
			740					745					750				
Leu	Asp	Ile	Ser	Ser	Asn	Lys	Ile	Gln	Val	Ile	Gln	Lys	Thr	Ser	Phe		
	755						760					765					
Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Asn	Met	Leu	Leu	Leu	His	His	Asn		
	770					775					780						
Arg	Phe	Leu	Cys	Asn	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn		
785					790					795					800		
His	Thr	Asp	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Ala		
				805					810					815			

Gly Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr
 820 825 830

Thr Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile
 835 840 845

Ser Ser Val Leu Phe Leu Met Ile Val Met Thr Thr Ser His Leu Phe
 850 855 860

Phe Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys
 865 870 875 880

Gly Tyr Gln His Leu Gln Ser Met Glu Ser Cys Tyr Asp Ala Phe Ile
 885 890 895

Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu
 900 905 910

Leu Val Val Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys
 915 920 925

Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu
 930 935 940

Ser Gln Ser Ile Gln Leu Ser Arg Lys Thr Val Phe Val Met Thr Gln
 945 950 955 960

Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His
 965 970 975

Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu
 980 985 990

Glu Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu
 995 1000 1005

Cys Ser Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln Ala His
 1010 1015 1020

Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn
 1025 1030 1035

His Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val
 1040 1045 1050

<210> SEQ ID NO: 85
 <211> Longitud: 1049
 <212> Tipo: PRT
 <213> Organismo: Macaca mulatta

<400> Secuencia: 85

Met Met Phe Pro Val Trp Thr Leu Lys Arg Gln Ile Leu Ile Leu Phe
 1 5 10 15

Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys
 20 25 30

Thr Leu Pro Cys Asp Val Thr Leu Asp Val Ser Lys Asn His Val Ile
 35 40 45

Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro
 50 55 60

Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile
 65 70 75 80

Ser Pro Ala Ser Phe His Arg Leu Val His Leu Val Glu Ile Asp Phe
 85 90 95

Arg Cys Asn Cys Val Pro Ile Arg Leu Gly Ser Lys Ser Asn Met Cys
 100 105 110

Pro Arg Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr
 115 120 125

Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140

Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160

Phe Ser Ile Arg Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile
 165 170 175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser
 180 185 190

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

Leu Ser Leu Lys Asp Asn Asn Val Thr Thr Val Pro Thr Val Leu Pro
 210 215 220

Ser Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Glu Ile
 225 230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu
 245 250 255

Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Thr Pro
 260 265 270

Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala
 275 280 285

Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300

Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Asn Leu Gln Glu Leu Asp
 305 310 315 320

Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu
 325 330 335

His Phe Leu Pro Asn Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu
 340 345 350

Leu Gln Val Tyr Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser
 355 360 365

Leu Lys Ser Leu Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu
 370 375 380

Leu Lys Ser Phe Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu
 385 390 395 400

Val	Leu	Asp	Leu	Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	405	410	415	
Phe	Lys	Gln	Phe	Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	420	425	430	
Ile	Ser	Pro	Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	435	440	445	
Arg	Thr	Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	Tyr	450	455	460	
Tyr	Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	465	470	475	480
Glu	Ala	Ser	Phe	Thr	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	Gln	485	490	495	
Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Ile	Lys	Ser	Ser	Asp	500	505	510	
Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	Gly	Asn	Leu	515	520	525	
Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	Leu	Ala	Glu	Leu	530	535	540	
Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	Leu	Leu	His	Ser	Thr	545	550	555	560
Ala	Phe	Glu	Glu	Leu	Arg	Lys	Leu	Glu	Val	Leu	Asp	Ile	Ser	Ser	Asn	565	570	575	
Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	Thr	His	Met	Leu	Asn	Phe	Thr	580	585	590	
Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	595	600	605	
Ser	Ser	Ser	Thr	Ser	Arg	Thr	Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	610	615	620	

Glu Phe Arg Gly Asn His Leu Asp Val Leu Trp Arg Asp Gly Asp Asn
625 630 635 640

Arg Tyr Leu Gln Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp
645 650 655

Ile Ser Lys Asn Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly
660 665 670

Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys
675 680 685

Ser Phe Ile Trp Glu Lys Leu Arg Tyr Leu Lys Asn Leu Glu Thr Leu
690 695 700

Asp Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn
705 710 715 720

Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile Arg
725 730 735

Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg Tyr Leu
740 745 750

Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr Ser Phe Pro
755 760 765

Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu His His Asn Arg
770 775 780

Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His
785 790 795 800

Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly
805 810 815

Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr
820 825 830

Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser
835 840 845

Val Ser Leu Phe Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe
 850 855 860

Trp Asp Val Trp Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly
 865 870 875 880

Tyr Gln Arg Leu Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val
 885 890 895

Tyr Asp Thr Lys Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu
 900 905 910

Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu
 915 920 925

Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser
 930 935 940

Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
 945 950 955 960

Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln
 965 970 975

Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu
 980 985 990

Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys
 995 1000 1005

Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro
 1010 1015 1020

Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr Asp Asn His
 1025 1030 1035

Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val
 1040 1045

<210> SEQ ID NO: 86
 <211> Longitud: 1797
 <212> Tipo: ADN

<213> Organismo: Secuencia Artificial

<220> Característica:

<223> Otra Información: Secuencia de nucleótidos del gen Unc93B1 humano D34A mutante-HA×2

<400> Secuencia: 86

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cccaactaca atgaggagga ggaagagcgc cgctactacc gccgcaagcg cctcggagtg	180
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ctcctgcaga tgcaactgat cctgcactat gatgagacct acagagaggt gaagtatggc	300
aacatggggc tgccggacat cgatagcaag atgctgatgg gtatcaacgt gacgcctatc	360
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gagcagggac ctcagcagcg cccaccacga ggttcccacg caccctatct cctggttttc	660
caggccatct totatagctt cttccacttg agcttcgcgt gtgcccagct gcccatgatt	720
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gccatctttg ttgtgtacct gggctccagc ttgcccatga aggccaaagct ggcagtgttg	1500

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